1000 Fungal Genomes project.
Nominate New Species!

Genomic Encyclopedia of Fungi
- **Plant Feedstock Health**
  - Mycorrhizal Symbiosis
  - Plant Pathogenicity
  - Biocontrol
- **Biorefinery**
  - Lignocellulose Degradation
  - Sugar Fermentation
  - Industrial Organisms
- **Fungal Diversity**

Submit CSP proposal

Announcements

- March 6-9, 2014
Neurospora meeting, Asilomar,CA, U.S.A.
- March 18-20, 2014
Fungal genomics workshop @ JGI User
- March 23-27, 2014
European Conference on Fungal Genetics, Seville, Spain
- June 8-12, 2014
Mycological Society of America, East Lansing, Michigan

Releases

- September 12, 2014
Coniochaeta sp. PMI_546 v1.0
- September 12, 2014
Clavulina sp. PMI_390 v1.0
- September 12, 2014
Thozetella sp. PMI_491 v2.0
- September 8, 2014
Trametes ljubarskyi CIRM1659 v1.0
- September 8, 2014
Artolenzites elegans CIRM1663 v1.0

more »

Genomic Encyclopedia of Fungi

The **Genomic Encyclopedia of Fungi** is the key project of the JGI Fungal Genomics Program to focus fungal genome sequencing in the areas of:

- Plant Feedstock Health
  - Mycorrhizal Symbiosis
  - Plant Pathogenicity
  - Biocontrol
- Biorefinery
  - Lignocellulose Degradation
  - Sugar Fermentation
  - Industrial Organisms
- Fungal Diversity

Plant health maintenance is critical for sustainable growth of biofuel feedstock and fungi, as symbionts, pathogens, and biocontrol agents, dramatically affect plant health.

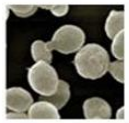
Symbionts such as mycorrhizae can increase productivity of bioenergy feedstock plants. Mycorrhizae enter symbiotic relationships with plants and effectively extend the host root system towards regions of decaying organic matter to provide nutrients such as nitrogen and phosphorus. Optimizing feedstock plant growth therefore is dependent on understanding molecular mechanisms of interactions between plants and mycorrhizae.

Pathogens can have dramatic negative effects on bioenergy crops as witnessed with the 1970 epidemic of corn leaf blight. Understanding mechanisms of virulence and pathogenicity, host specificity and the life cycle of pathogenic fungi hold keys to developing methods to control growth of pathogenic fungi and protecting plants. Feedstock protection can also be achieved by biocontrol fungi, which kill fungi, nematodes, and insects pathogenic to plants and are attractive alternatives to the chemical treatments used now.

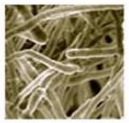
Comparing genomes of pathogenic and symbiotic fungi to closely related fungi that lack these features will help find specific traits from each group of fungi and will help to understand the mechanisms of their interaction with plants. Reference genomes of mycorrhiza and other soil-inhabiting fungi will also facilitate comprehensive metagenomics studies of the rhizosphere, studies which until now have been mostly limited to bacterial communities.

Biorefinery methods convert biopolymers such as cellulose into simple sugars (eg, glucose and xylose) and then into biofuels employing fungal hosts optimized for large scale industrial processes. Knowing the enzymes and processes employed by diverse fungi in lignocellulose degradation and sugar fermentation as well as understanding the molecular biology of strains adopted by industry are essential for development robust platforms for biomass-to-biofuel production on an industrial scale. Genome sequencing in this area will provide a comprehensive catalog of enzymes, metabolic processes, and regulatory and secretory mechanisms. Resequencing of industrial strains should help to map desirable properties such as morphology, hyperproductivity, thermostability to genomic blueprints.

Fungal diversity. Over a million species in the Kingdom Fungi have evolved over millions of years to occupy diverse ecological niches and have accumulated an enormous but yet undiscovered natural arsenal of potentially useful innovations. While the number of fungal genome sequencing projects continues to increase, the phylogenetic breadth of current sequencing targets is extremely limited. Exploration of phylogenetic and ecological diversity of fungi by genome sequencing is therefore a potentially rich source of valuable metabolic pathways and enzyme activities that will remain undiscovered and unexploited until a systematic survey of phylogenetically diverse genome sequences is undertaken.

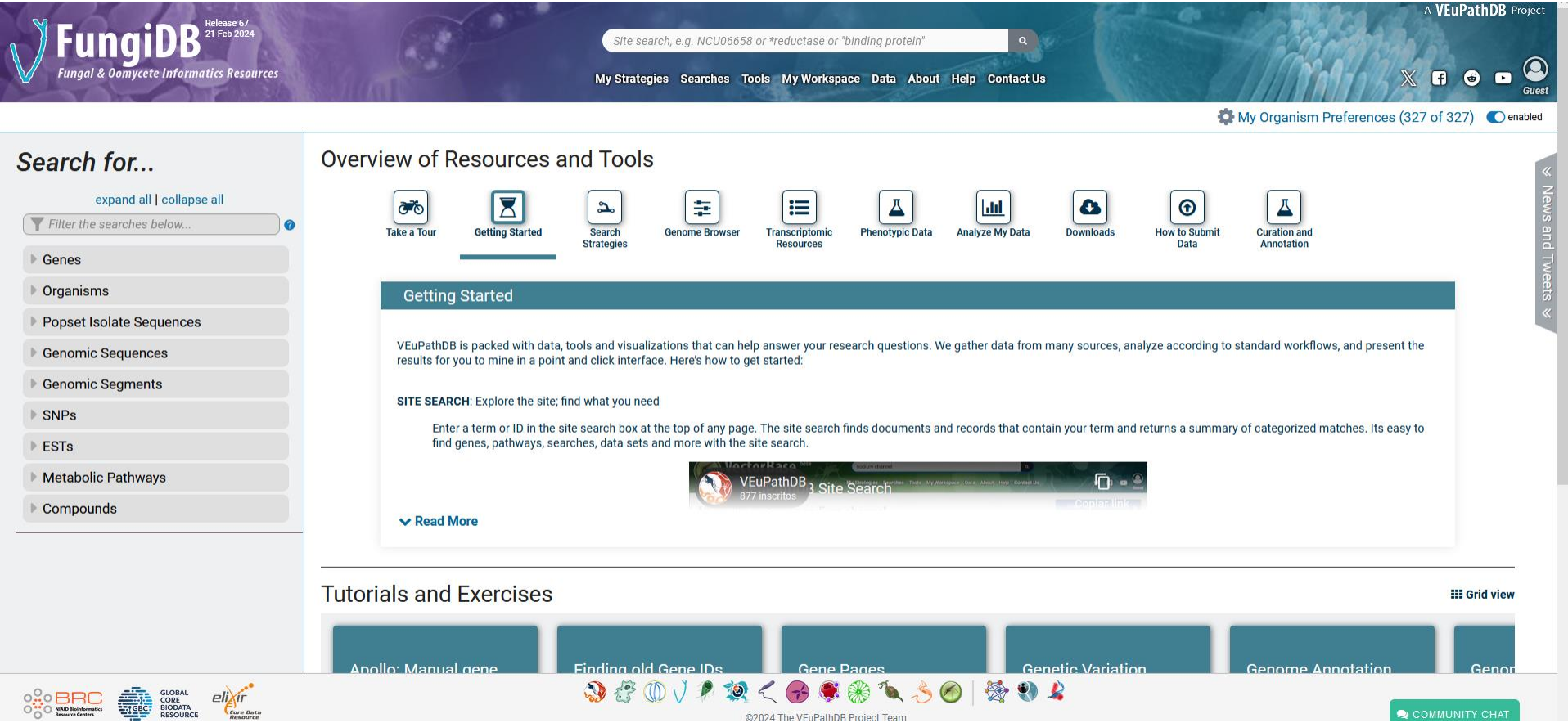






Genome Portal version:7.0.13.eab574e content:eab574e clustering:fdef11e synteny:fdef11e gp-edge4.jgi-psf.org 27-Sep-2014 15:02:18.612 PDT

Organização do genoma de fungos filamentosos



https://fungidb.org/fungidb/app/#getting-started

FungiDB: an integrated functional genomics database for fungi. Stajich JE, Harris T, Brunk BP, Brestelli J, Fischer S, Harb OS, Kissinger JC, Li W, Nayak V, Pinney DF, Stoeckert CJ Jr, Roos DS. Nucleic Acids Res. 2012 Jan 1;40(D1):D675-D681. http://fungidb.org/

Organism	Strain	ncbi_tax_id	Mega base Pairs	All Genes	Prot Genes	Non Prot Genes
Ajellomyces capsulatus G186AR	G186AR	447093	30.44	9399	9233	166
Aspergillus flavus NRRL3357	NRRL3357	332952	36.89	13731	13485	246
Aspergillus fumigatus Af293	Af293	330879	29.42	9981	9784	197
Aspergillus nidulans FGSC A4	Aspergillus nidulans FGSC A4	227321	30.48	10931	10751	180
Aspergillus niger ATCC 1015	ATCC 1015	380704	34.85	11223	10947	276
Coprinopsis cinerea okayama7#130	okayama7#130	240176	36.15	13610	13342	268
Cryptococcus neoformans var. grubii H99	var. grubii H99	235443	18.90	8505	6975	1530
Fusarium graminearum PH-1	PH-1	229533	36.45	14148	13826	322
Fusarium oxysporum f. sp. lycopersici 4287	f. sp. lycopersici 4287	426428	61.36	18016	17708	308
Fusarium verticillioides 7600	7600	334819	41.78	14476	14180	296
Magnaporthe oryzae 70-15	70-15	242507	41.70	11395	11052	343
Malassezia globosa CBS 7966	CBS 7966	425265	8.96	4369	4286	83
Neurospora crassa OR74A	OR74A	367110	41.10	11243	10812	431
Phanerochaete chrysosporium RP-78	RP-78	273507	35.15	10263	10048	215
Phytophthora infestans T30-4	T30-4	403677	228.54	24898	17909	6989
Rhizopus delemar RA 99-880	RA 99-880	246409	46.13	17952	17459	493
Sclerotinia sclerotiorum 1980 UF-70	1980 UF-70	665079	38.33	14684	14493	191
Sordaria macrospora k-hell	k-hell	771870	39.96	11772	10827	945
Talaromyces marneffei ATCC 18224	ATCC 18224	441960	28.64	10289	10027	262
Trichoderma reesei QM6a	QM6a	431241	33.40	9316	9120	196
Ustilago maydis 521	521	237631	19.67	6897	6786	111

Fonte: FungiDB, http://fungidb.org/ (Setembro-2014).

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PLANT SCIENCE

ORIGINAL RESEARCH ARTICLE
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doi: 10.3389/fpls.2014.00422

Genome size analyses of Pucciniales reveal the largest fungal genomes

*Sílvia Tavares[1,2], Ana Paula Ramos[3], Ana Sofia Pires[1,2], Helena G. Azinheira[1,3], Patrícia Caldeirinha[4], Tobias Link[5], Rita Abranches[2], Maria do Céu Silva[1,3], Ralf T. Voegele[5], João Loureiro[4] and Pedro Talhinhas[1,2,3]**

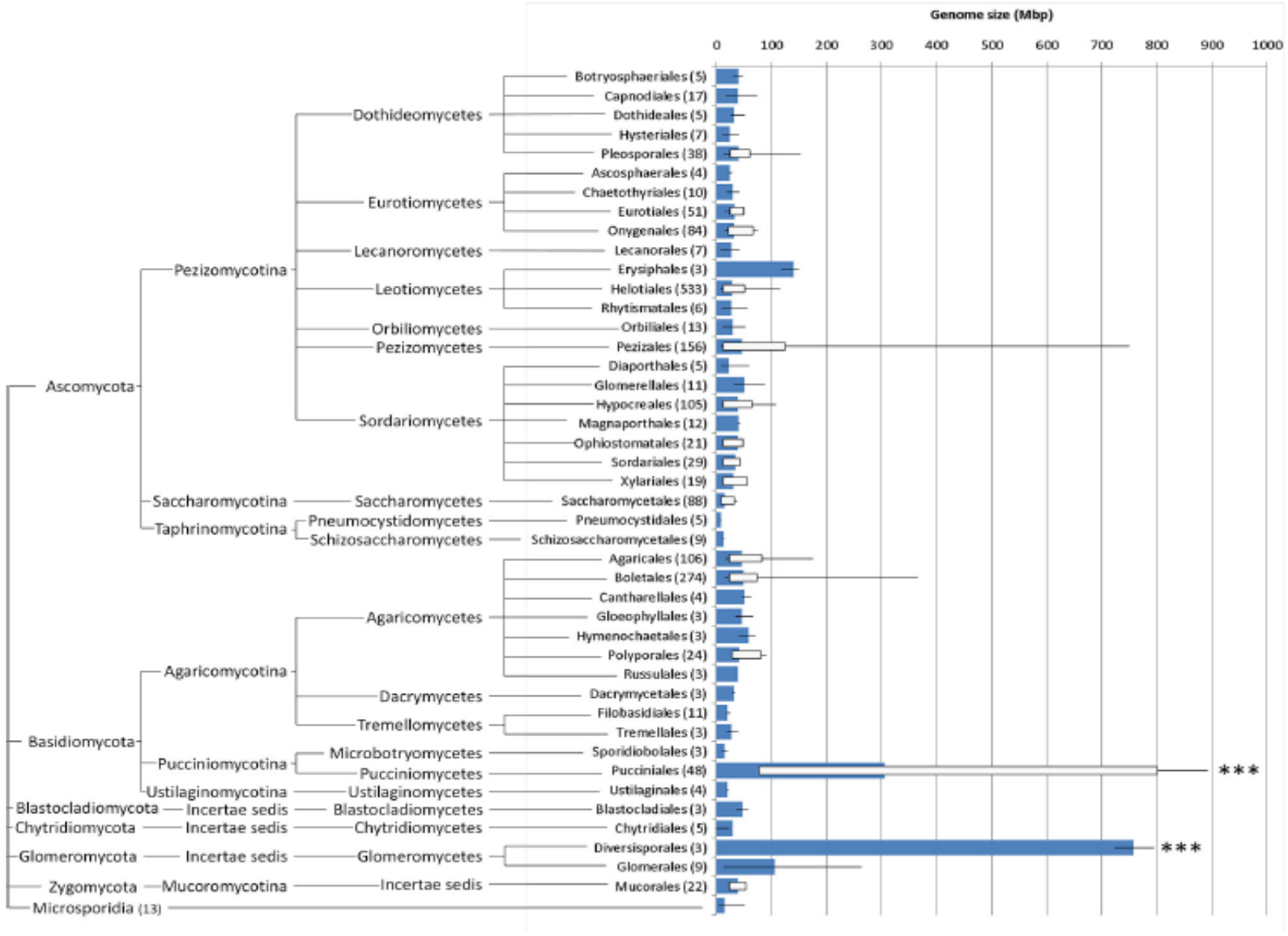
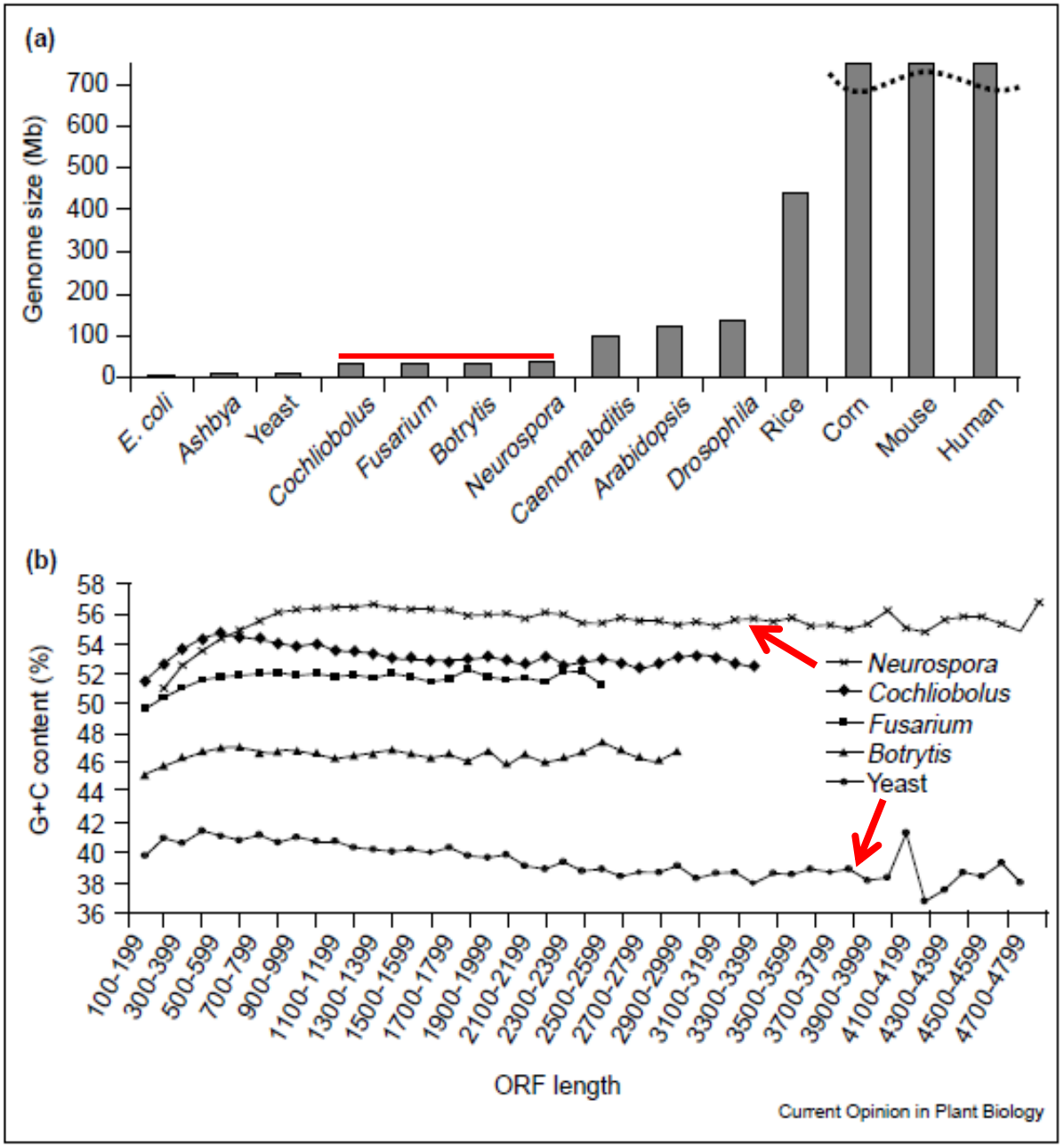


Table 1: Fungi Genome size (Mbp)

KINGDOM	PHYLUM	average	minimum	maximum
	Ascomycota	31,82	6,50	750,00
	Basidiomycota	**70,39**	**8,90**	**893,20**
	Blastocladiomycota	47,46	36,22	57,06
	Chytridiomycota	34,91	23,70	71,02
	Glomeromycota	268,64	13,93	795,00
	Microsporidia	14,14	2,90	71,30
	Zygomycota	49,83	21,84	350,00
Fungi		44,24	2,90	893,20

- *Gymnosporangium confusum* possesses the largest fungal genome ever reported (**893.2Mbp**).
- *Mixia osmundae* (**8,9 Mbp**)

(a) Sizes of filamentous fungal genomes compared to those of various model organisms. **(b)** G+C content of five fungi plotted against open reading frame (ORF) length.



Yoder and Turgeon. Current Opinion in Plant Biology 2001, 4:315–321

Islam et al. BMC Genomics 2012, 13:493
http://www.biomedcentral.com/1471-2164/13/493

BMC Genomics

RESEARCH ARTICLE Open Access

Tools to kill: Genome of one of the most destructive plant pathogenic fungi *Macrophomina phaseolina*

fungal pathogens that infect more than 500 plant species

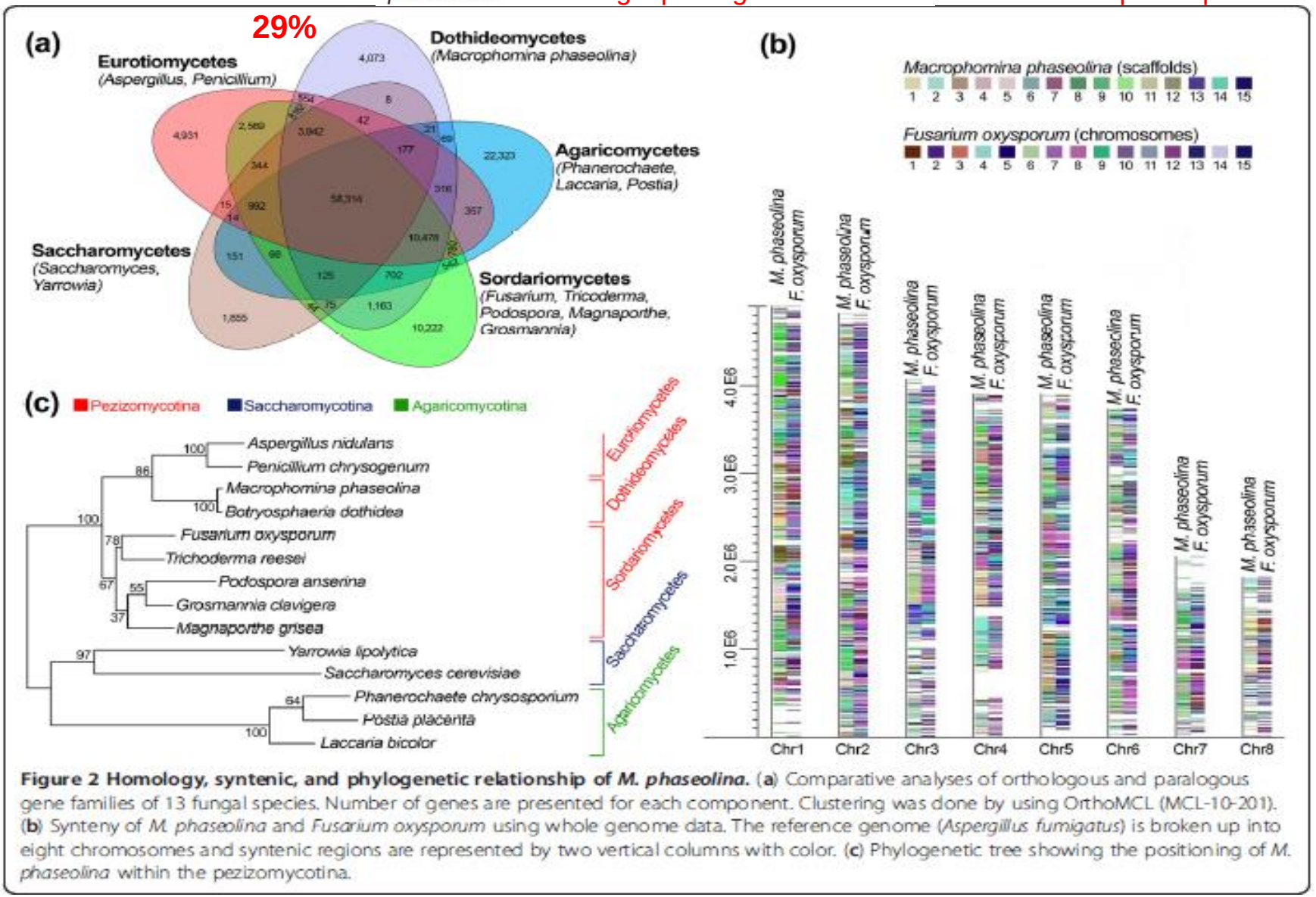


Figure 2 Homology, syntenic, and phylogenetic relationship of *M. phaseolina*. (**a**) Comparative analyses of orthologous and paralogous gene families of 13 fungal species. Number of genes are presented for each component. Clustering was done by using OrthoMCL (MCL-10-201). (**b**) Synteny of *M. phaseolina* and *Fusarium oxysporum* using whole genome data. The reference genome (*Aspergillus fumigatus*) is broken up into eight chromosomes and syntenic regions are represented by two vertical columns with color. (**c**) Phylogenetic tree showing the positioning of *M. phaseolina* within the pezizomycotina.

Table 2 Sizes of selected protein families in *M. phaseolina* and other fungi

Protein family[a]	MP[b]	FO	FG	MO	BC	SS	NC	AN	AF	PCH	PP
Fungal specific transcription factors	156	101	192	95	118	90	89	209	169	65	63
C2H2 zinc finger transcription factors	66	73	85	58	48	54	63	58	51	77	42
Zn2/Cys6 transcription factors	113	370	376	155	142	108	110	307	230	146	118
Major facilitator superfamily	270	352	274	198	225	167	110	279	232	141	184
Cytochrome P450	256	178	112	137	129	93	40	116	74	155	236
Pth11-like G-protein coupled receptor	44	55	51	60	22	23	28	39	15	14	26
Protein kinases	140	160	129	129	124	164	111	127	131	106	56
Histidine kinase	1	37	20	6	3	5	8	12	6	19	24
Heterokaryon incompatibility	65	82	88	41	59	34	45	7	8	3	2
Serine proteases	1	12	60/150[c]	56/91	19/34	20/33	32/74	53/136	29/46	0	2
Subtilisin	19	36	16/24	26/29	4/7	4/6	6/10	3/4	3/7	12	33
Trypsin	2	3	2/3	3/3	1/1	1/1	0/2	1/2	0/0	0	0
Carboxypeptidase	19	31	12/21	7/8	7/9	8/ 11	6/9	5/12	14/15	24	22
Aspartic protease	4	0	15/18	14/19	11/14	9/21	15/19	7/16	7/9	38	18
Threonine protease	0	0	3/18	2/18	2/13	2/13	2/20	0/20	1/17	0	0
Cysteine protease	3	0	5/57	4/31	3/24	1/27	4/41	6/57	3/31	0	0
Metalloprotease	8	26	32/111	38/91	6/50	7/48	21/81	22/105	20/77	0	0
All proteases	113	261	354	250	135	142	235	334	180	228	325
Lipase	53	61	4/31	2/23	3/28	2/25	0/16	2/27	3/25	23	40
Esterase/thioesterase	108	95	70	64	70	58	42	63	52	74	69
Glycoside hydrolase related	219	168	159	198	120	126	137	200	165	180	144
Transposases	101	19	17	15	73	426	15	15	109	12	11
Cutinase	10	12	12	18	11	8	3	4	5	0	0
Polysaccharide lyase	16	23	25	9	25	20	5	24	27	4	6
Secondary metabolite backbone genes	75	34	37	32	37	29	15	58	40	51	39

[a]Corresponding InterPro codes are listed in Additional file 1: Table S4.
[b]Fungal species are MP, *Macrophomina phaseolina*; FO, *Fusarium oxysporum*; FG, *Fusarium graminearum*; MO, *Magnaporthe oryzae*; BC, *Botrytis cinerea*; SS, *Sclerotinia sclerotiorum*; NC, *Neurospora crassa*; AN, *Aspergillus nidulans*; AF, *A. fumigatus*; PCH, *Phanerochaete chrysosporium*, and PP, *Postia placenta*.

Table 2

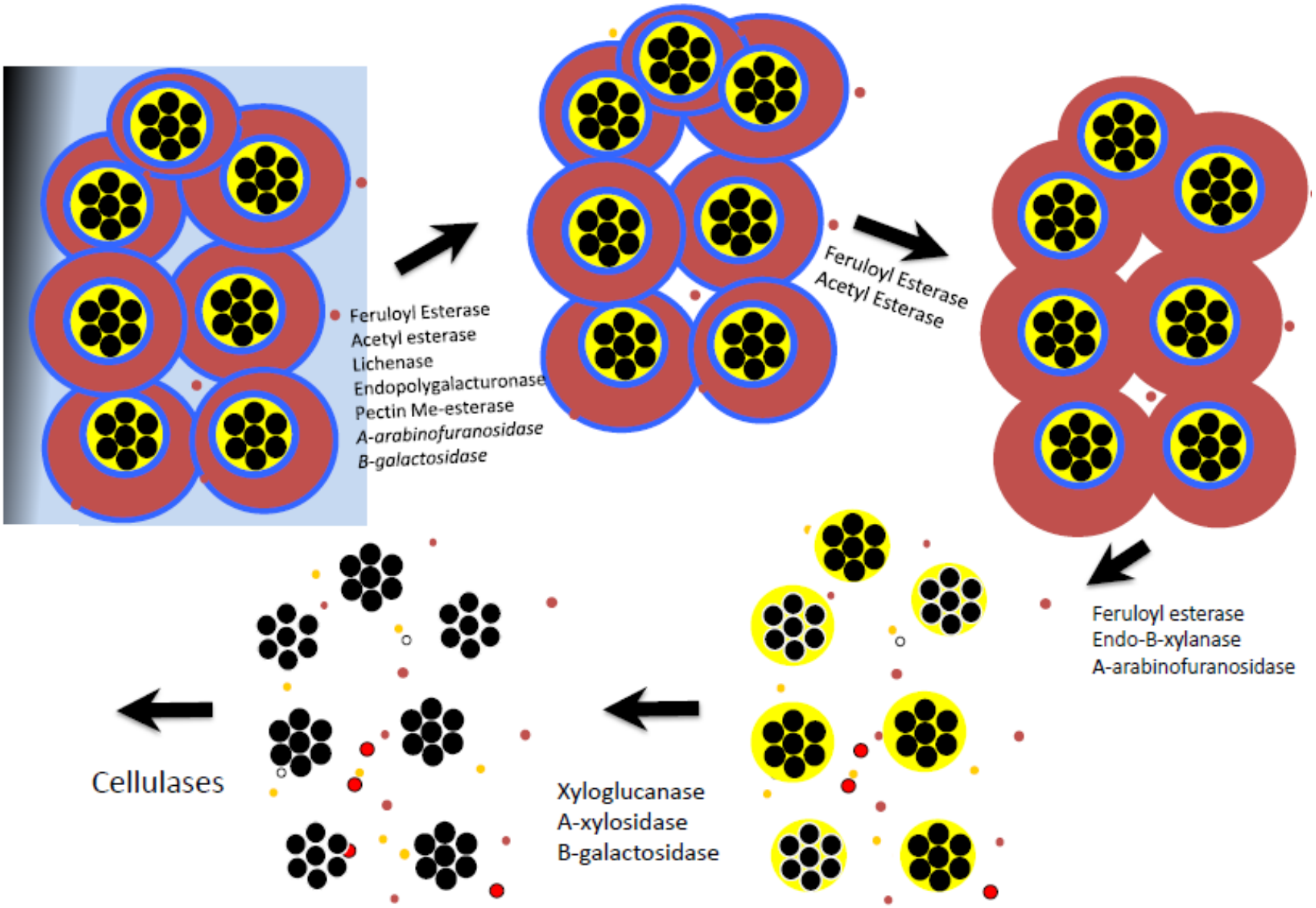
Representation of selected protein families in pathogenic and saprophytic fungi.

	Cochliobolus	*Fusarium*	*Botrytis*	*Neurospora*	*Ashbya*	*Saccharomyces*
Peptide synthetases	30	37	29	7	0	0
Polyketide synthases	40	35	42	7	0	0
ABC transporters	51	54	46	39	17	29
Cytochrome P450s	63	40	33	44	ND	4
Protein kinases	112	94	70	120	ND	117

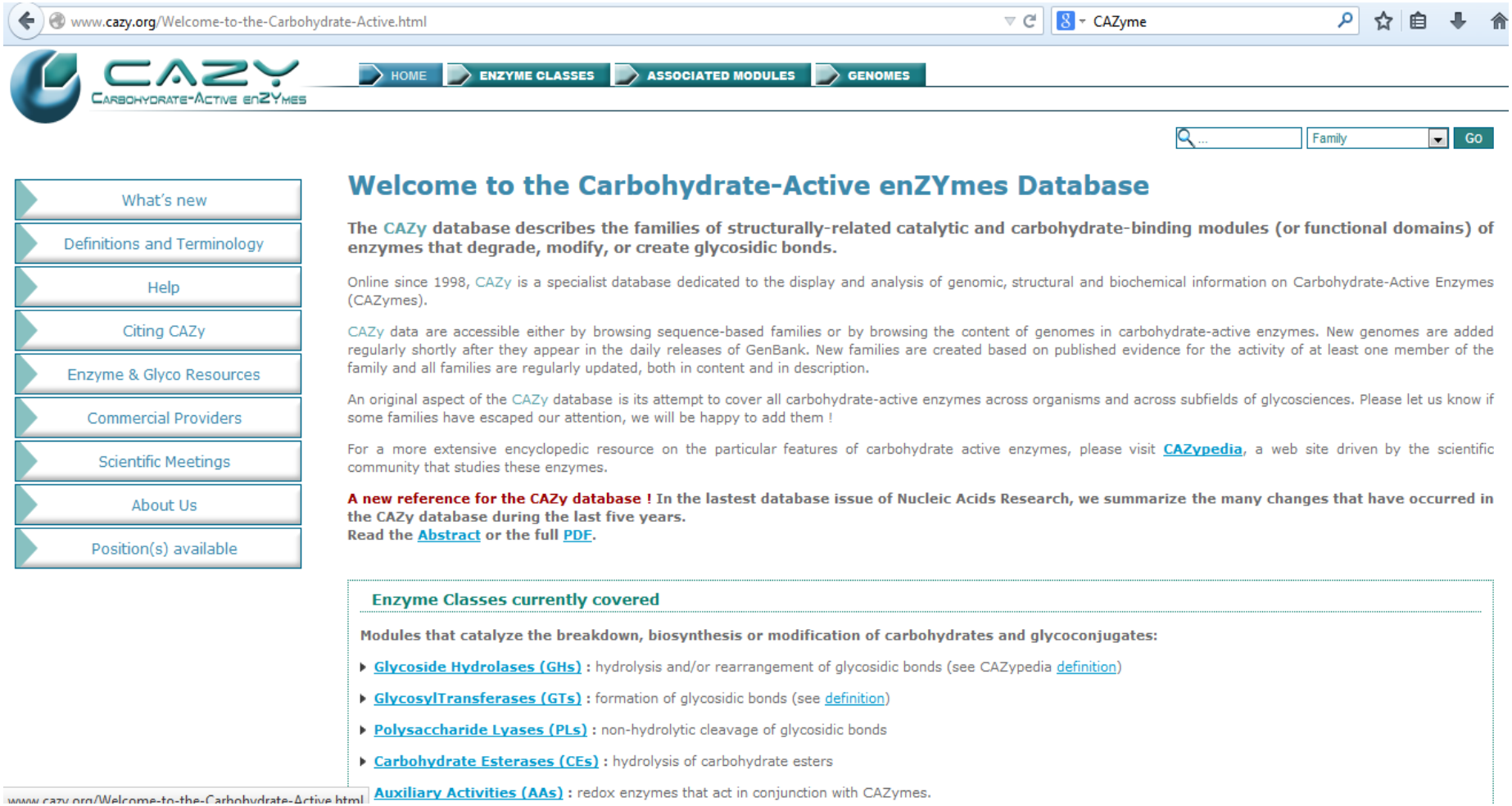
These protein families, compared here for six fungi, were chosen because each has a least one member known to be involved in fungal pathogenesis (the numbers for the filamentous fungi are estimates; they are used to illustrate whether zero, a few, or many members of a particular protein family are encoded by a genome). Examples of virulence factors: nonribosomal peptide synthetase, HC-toxin [39]; polyketide synthase, T-toxin [38]; ABC transporter, ABC1 [53]; cytochrome P450, pisatin demethylase, [54]; protein kinase, PMK1 [55]. ND, not determined.

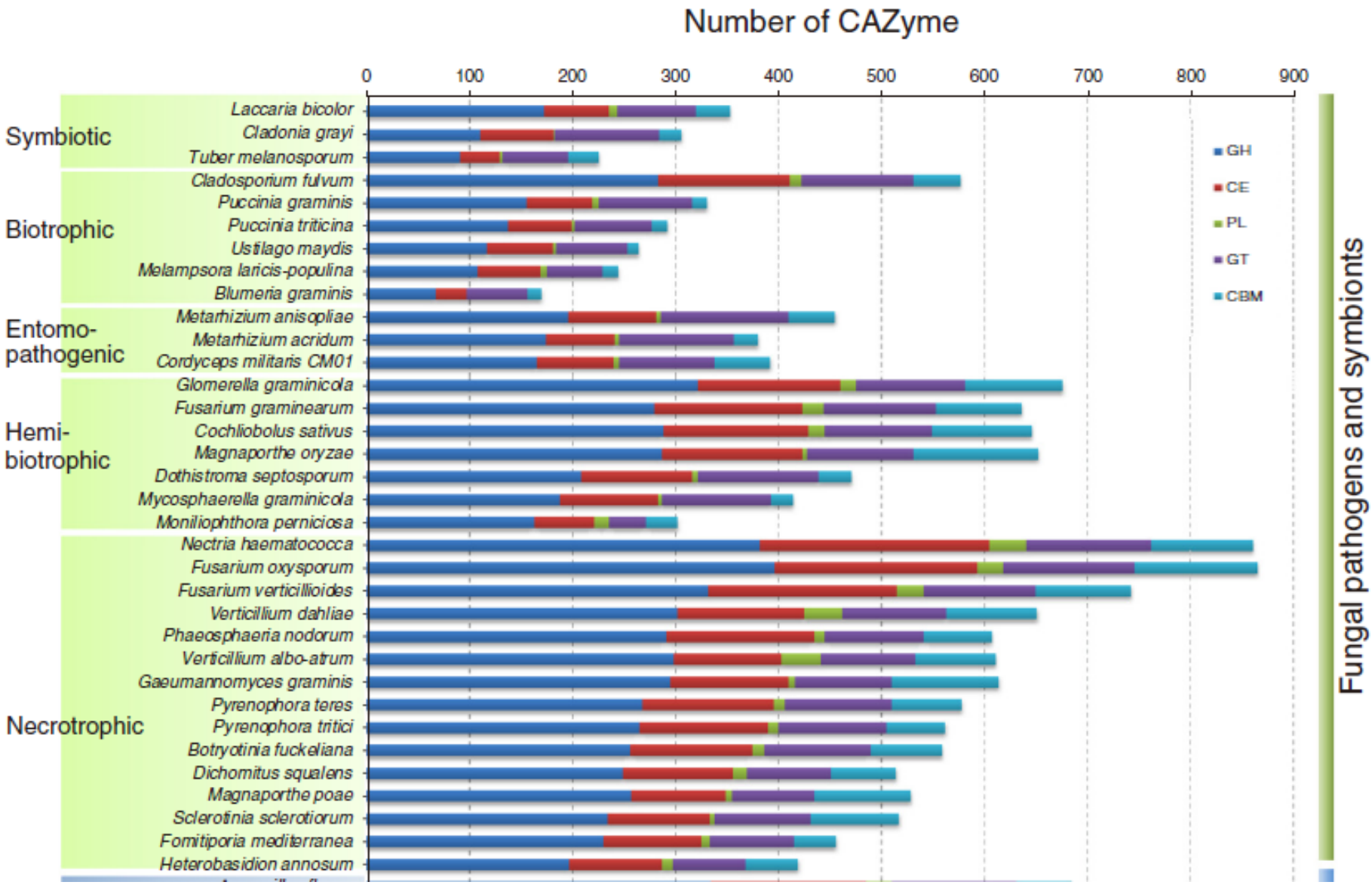
Yoder and Turgeon. Current Opinion in Plant Biology 2001, 4:315–321

Parede Celular e Enzimas de degradação



De Souza et al., 2012


www.cazy.org/Welcome-to-the-Carbohydrate-Active.html
CAZyme
CAZY
Carbohydrate-Active enZYmes
HOME
ENZYME CLASSES
ASSOCIATED MODULES
GENOMES
Family
GO
What's new
Definitions and Terminology
Help
Citing CAZy
Enzyme & Glyco Resources
Commercial Providers
Scientific Meetings
About Us
Position(s) available
Welcome to the Carbohydrate-Active enZYmes Database
The CAZy database describes the families of structurally-related catalytic and carbohydrate-binding modules (or functional domains) of enzymes that degrade, modify, or create glycosidic bonds.
Online since 1998, CAZy is a specialist database dedicated to the display and analysis of genomic, structural and biochemical information on Carbohydrate-Active Enzymes (CAZymes).
CAZy data are accessible either by browsing sequence-based families or by browsing the content of genomes in carbohydrate-active enzymes. New genomes are added regularly shortly after they appear in the daily releases of GenBank. New families are created based on published evidence for the activity of at least one member of the family and all families are regularly updated, both in content and in description.
An original aspect of the CAZy database is its attempt to cover all carbohydrate-active enzymes across organisms and across subfields of glycosciences. Please let us know if some families have escaped our attention, we will be happy to add them !
For a more extensive encyclopedic resource on the particular features of carbohydrate active enzymes, please visit CAZypedia, a web site driven by the scientific community that studies these enzymes.
A new reference for the CAZy database ! In the lastest database issue of Nucleic Acids Research, we summarize the many changes that have occurred in the CAZy database during the last five years.
Read the Abstract or the full PDF.
Enzyme Classes currently covered
Modules that catalyze the breakdown, biosynthesis or modification of carbohydrates and glycoconjugates:
Glycoside Hydrolases (GHs) : hydrolysis and/or rearrangement of glycosidic bonds (see CAZypedia definition)
GlycosylTransferases (GTs) : formation of glycosidic bonds (see definition)
Polysaccharide Lyases (PLs) : non-hydrolytic cleavage of glycosidic bonds
Carbohydrate Esterases (CEs) : hydrolysis of carbohydrate esters
Auxiliary Activities (AAs) : redox enzymes that act in conjunction with CAZymes.
www.cazy.org/Welcome-to-the-Carbohydrate-Active.html



Zhao et al. BMC Genomics 2013, 15:6

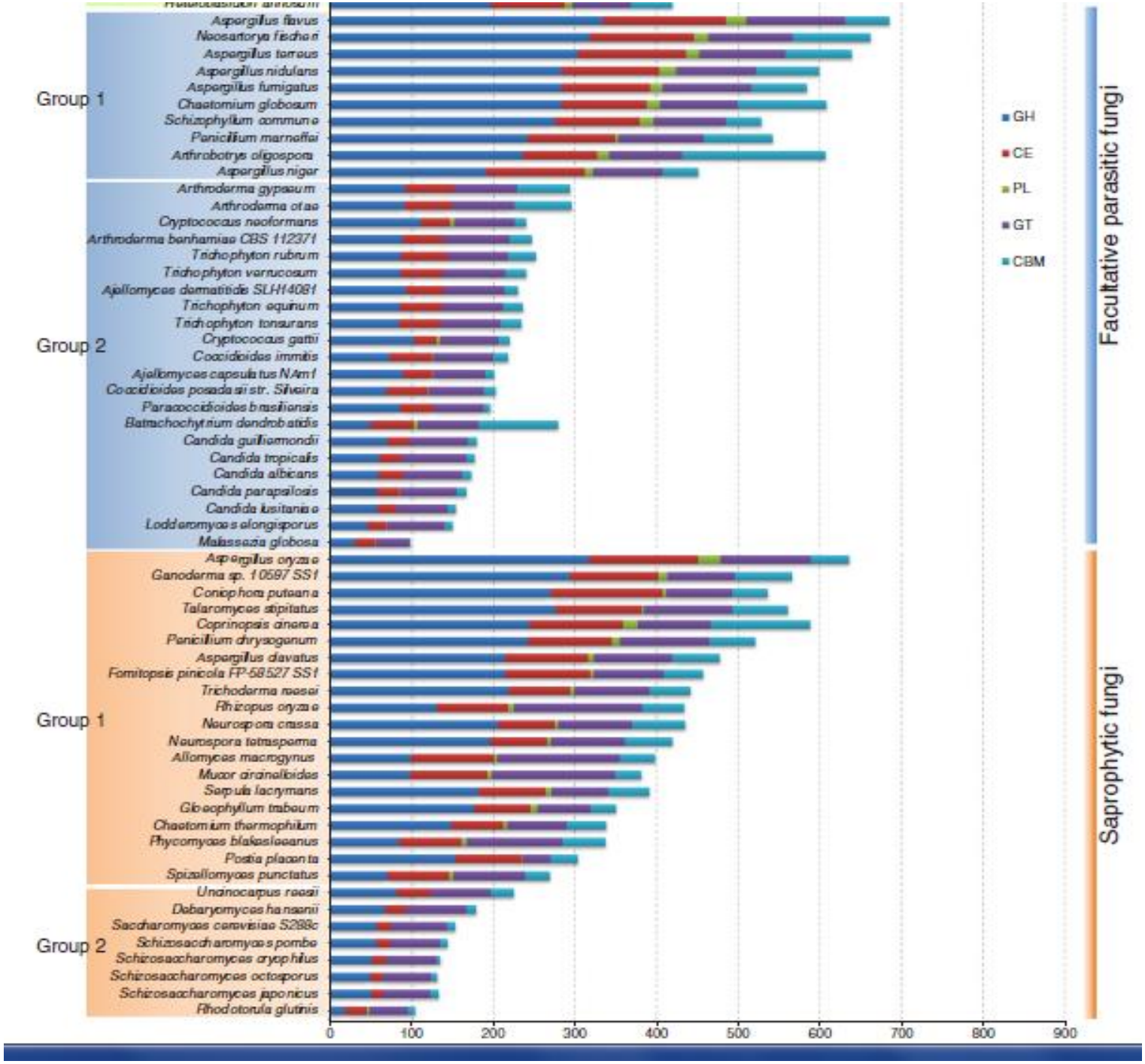

Aspergillus flavus
Neosartorya fischeri
Aspergillus terreus
Aspergillus nidulans
Aspergillus fumigatus
Chaetomium globosum
Schizophyllum commune
Penicillium marneffei
Arthrobotrys oligospora
Aspergillus niger
Group 1
Arthroderma gypseum
Arthroderma otae
Cryptococcus neoformans
Arthroderma benhamiae CBS 112371
Trichophyton rubrum
Trichophyton verrucosum
Ajellomyces dermatitidis SLH14081
Trichophyton equinum
Trichophyton tonsurans
Cryptococcus gattii
Coccidioides immitis
Ajellomyces capsulatus NAm1
Coccidioides posadasii str. Silveira
Paracoccidioides brasiliensis
Batrachochytrium dendrobatidis
Candida guilliermondii
Candida tropicalis
Candida albicans
Candida parapsilosis
Candida lusitaniae
Lodderomyces elongisporus
Malassezia globosa
Group 2
Aspergillus oryzae
Ganoderma sp. 10597 SS1
Coniophora puteana
Talaromyces stipitatus
Coprinopsis cinerea
Penicillium chrysogenum
Aspergillus clavatus
Fomitopsis pinicola FP-58527 SS1
Trichoderma reesei
Rhizopus oryzae
Neurospora crassa
Neurospora tetrasperma
Allomyces macrogynus
Mucor circinelloides
Serpula lacrymans
Gloeophyllum trabeum
Chaetomium thermophilum
Phycomyces blakesleeanus
Postia placenta
Spizellomyces punctatus
Group 1
Uncinocarpus reesii
Debaryomyces hansenii
Saccharomyces cerevisiae S288c
Schizosaccharomyces pombe
Schizosaccharomyces cryophilus
Schizosaccharomyces octosporus
Schizosaccharomyces japonicus
Rhodotorula glutinis
Group 2
GH
CE
PL
GT
CBM
Facultative parasitic fungi
Saprophytic fungi
0
100
200
300
400
500
600
700
800
900

Table 2. Sizes of CAZyme (carbohidrate-active enzymes) families, by class, in the 12 fungal genomes analyzed

Lineages		Species	GH	Avg. GH	GT	Avg. GT	CBM	Avg. CBM	CE	Avg. CE	PL	Avg. PL
Ascomycetes	Eurotio.	*A.nid.*	247	265	91	103	36	40	29	28	19	18
		A.fum.	263		103		55		29		13	
		A.ory.	285		114		30		26		21	
	Sordario.	*M.gris.*	231	211	94	96	58	49	47	32	4	8
		N.cra.	171		76		39		21		3	
		T.ree.	**200**		**103**		**36**		**16**		**3**	
		F.gra.	243		110		61		42		20	
	Saccharo.	*C.alb.*	58	47	69	70	4	9	3	3	0	0
		S.cer.	45		67		12		3		0	
		C.gla.	38		73		12		3		0	
	Archiasco.	*S.pom.*	46	46	61	61	5	5	5	5	0	0
Basidio.		*C.neo.*	75		68		10		9		3	

GH: glycoside hydrolase
GT: glycosyltransferase
CBM: carbohydrate-binding module
CE: carbohydrate esterase
PL: polysaccharide lyase

358 genes

Martinez D. et al. Nat Biotechnol. 2008. 26(5):553-60.

Genome Biology

RESEARCH Open Access

Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of *Trichoderma*

Christian P Kubicek[1*], Alfredo Herrera-Estrella[2], Verena Seidl-Seiboth[1], Diego A Martinez[3], Irina S Druzhinina[1],

Table 1 Genome assembly and annotation statistics

	T. atroviride	*T. virens*	*T. reesei*
Genome size, Mbp	36.1	38.8	34.1
Coverage	8.26×	8.05×	9.00×
Assembly gaps, Mbp	0.1 (0.16%)	0.2(0.4%)	0.05 (0.1%)
Number of scaffolds	50	135	89
Number of predicted genes	11865	12518	9143
Gene length, bp	1747.06	1710.05	1793,25
Protein length, amino acids	471.54	478.69	492,27
Exons per gene	2,93	2,98	3,06
Exon length, bp	528.17	506.13	507,81
Intron length, bp	104.20	104.95	119,64
Supported by homology, NR	10,219 (92%)	10,915 (94%)	8409 (92%)
Supported by homology, Swissprot	8,367(75%)	8,773 (75%)	6763 (74%)
Has PFAM domain	5,883 (53%)	6,267 (54%)	5096 (56%)

NR, non-redundant database; PFAM, protein families.

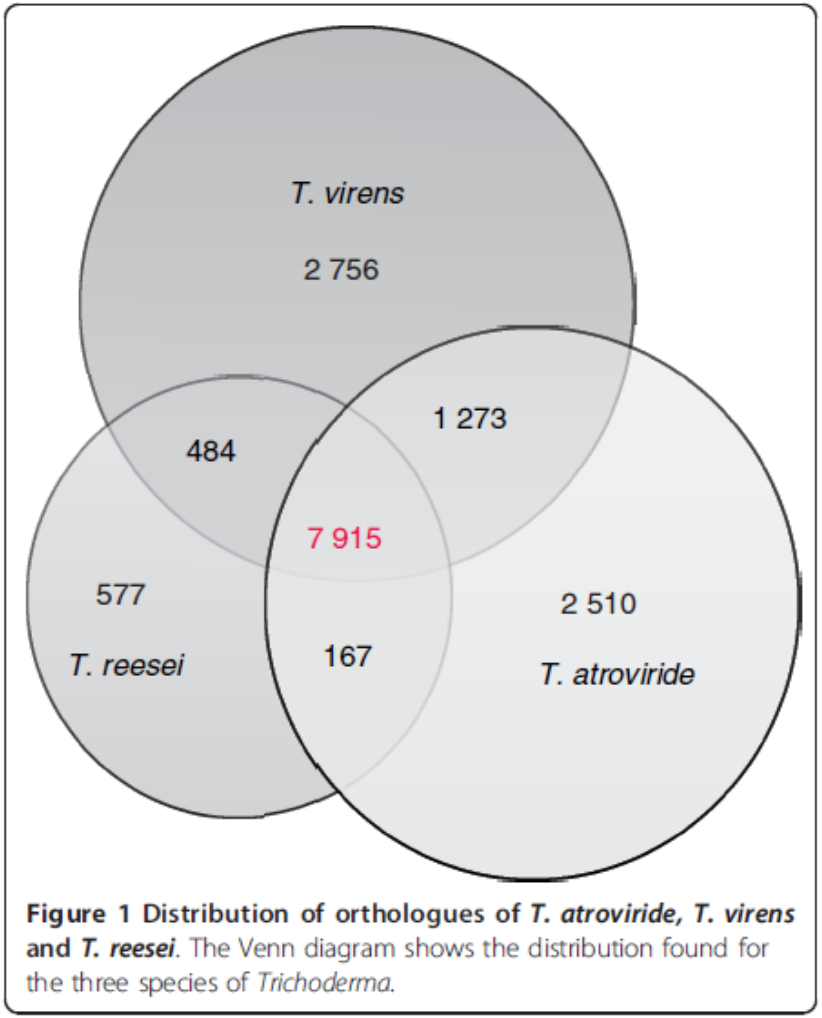


Figure 1 Distribution of orthologues of *T. atroviride*, *T. virens* and *T. reesei*. The Venn diagram shows the distribution found for the three species of *Trichoderma*.

Table 8 The number of polyketide synthases and non-ribosomal peptide synthetases of *Trichoderma* compared to other fungi

Fungal species	PKS	NRPS	PKS-NRPS NRPS-PKS	Total
Trichoderma virens	**18**	**28**	**4**	**50**
Aspergillus oryzae	26	14	4	44
Aspergillus nidulans	26	13	1	40
Cochliobolus heterostrophus	23	11	2	36
Trichoderma atroviride	**18**	**16**	**1**	**35**
Magnaporthe oryzae	20	6	8	34
Fusarium graminearum	14	19	1	34
Gibberella moniliformis	12	16	3	31
Botryotinia fuckeliana	17	10	2	29
Aspergillus fumigatus	13	13	1	27
Nectria haematococca	12	12	1	25
Trichoderma reesei	**11**	**10**	**2**	**23**
Neurospora crassa	7	3	0	10

Table 7 Glycosyl hydrolase families involved in chitin/chitosan and β-1,3 glucan hydrolysis that are expanded in mycoparasitic *Trichoderma* species

		Glycosyl hydrolase family						
		Chitin/chitosan[a]		ß-glucan[a]				Total ß-glucan[b]
	Taxonomy	GH18	GH75	GH17	GH55	GH64	GH81	217
Trichoderma atroviride	S	**29**	**5**	5	**8**	**3**	2	18
Trichoderma virens	S	**36**	**5**	4	**10**	**3**	1	18
Trichoderma reesei	S	**20**	**3**	4	**6**	**3**	2	15
Pezizomycota								
Nectria haematococca	S	*28*	2	6	5	2	1	14
Fusarium graminearum	S	19	1	6	3	2	1	12
Neurospora crassa	S	12	1	4	6	2	1	13
Podospora anserina	S	20	1	4	7	1	1	13
Magnaporthe grisea	S	14	1	7	3	1	2	13
Aspergillus nidulans	E	19	2	5	6	0	1	12
Aspergillus niger	E	14	2	5	3	0	1	9
Penicillium chrysogenum	E	9	1	5	3	2	1	11
Tuber melanosporum	P	5	1	4	2	0	*3*	9
Other ascomycetes								
Saccharomyces cerevisiae	SM	2	0	4	0	0	2	6
Schizosaccharomyces pombe	SS	1	0	1	0	0	1	2
Basidiomycota								
Phanerochaete chrysosporium	A	11	0	2	2	0	0	4
Laccaria bicolor	A	10	0	4	2	0	0	6
Postia placenta	A	20	0	4	6	0	0	10

[a]Main substrates for the respective enzyme families. [b]Number of all enzymes that can act on ß-glucan as a substrate. Taxonomy abbreviations: S, Sordariomycetes; E, Eurotiomycetes; P, Pezizomycetes; S, Saccharomycetes; SS, Schizosaccharomycetes; A, Agaricomycetes. The bold numbers indicate glycosyl hydrolase (GH) families that have a statistically significant expansion in *Trichoderma* ($P < 0.05$) or *Ta* and *Tv* (GH18). This support was obtained only when *N. haematococca* and *T. melanosporum* were not included in the analysis of GH18 and GH81, respectively.

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PLOS ONE

Genomic and Secretomic Analyses Reveal Unique Features of the Lignocellulolytic Enzyme System of *Penicillium decumbens*

Guodong Liu[1☯], Lei Zhang[2☯], Xiaomin Wei[1☯], Gen Zou[2☯], Yuqi Qin[1,3], Liang Ma[2], Jie Li[1], Huajun Zheng[4], Shengyue Wang[4], Chengshu Wang[2], Luying Xun[1,5], Guo-Ping Zhao[2,4], Zhihua Zhou[2*], Yinbo Qu[1,3*]

Table 1. General features of the *P. decumbens* 114-2 genome.

Genomic features	Value
Nuclear genome	
Size of assembled genome (Mbp)	30.2
GC content of assembled genome (%)	50.6
All protein-coding genes	10,013
Protein-coding genes (≥60 aa)	9,823
GC content of protein-coding region (%)	54.4
Average gene length (bp)	1,597
Average number of introns per gene	1.95
Genes with intron	7,766
Average intron size (bp)	118
Average exon size (bp)	463
Number of tRNA genes	176
Mitochondrial genome	
Size (bp)	26,362
GC content (%)	26.4
Protein-coding genes	8
Number of tRNA genes	29

doi:10.1371/journal.pone.0055185.t001

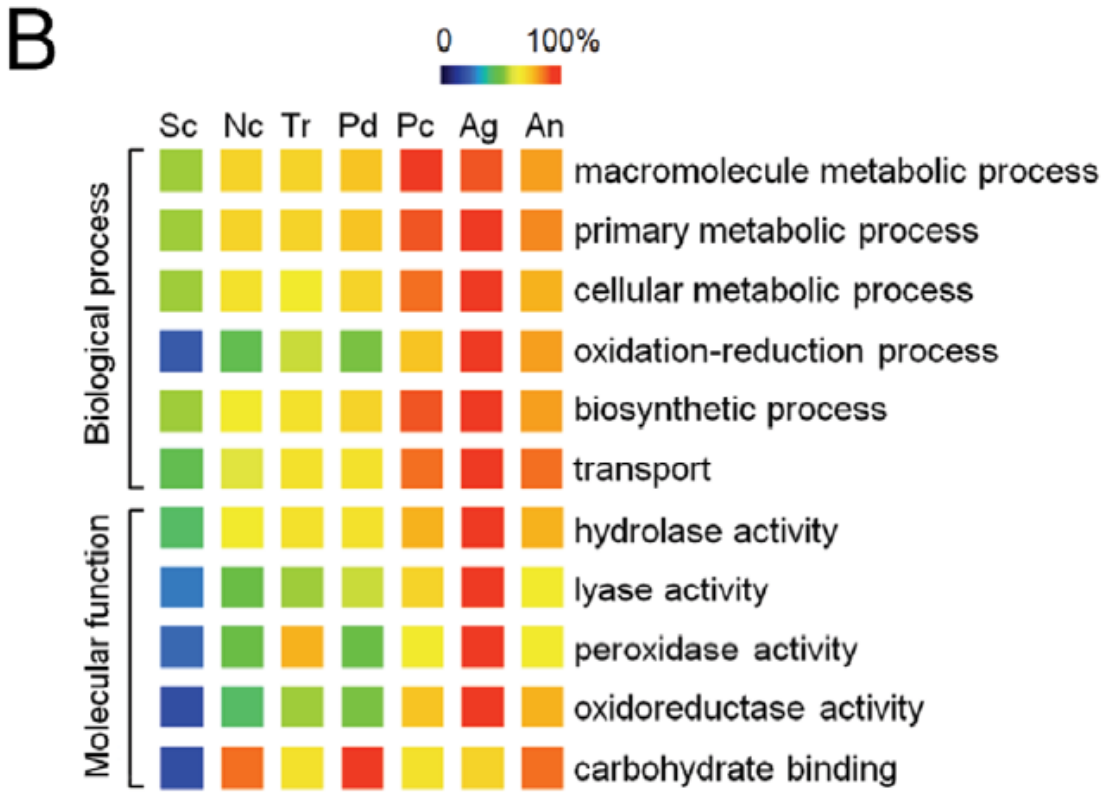


Figure 1. Comparative genomic analysis of *P. decumbens* and other fungal species. (**A**) Maximum-likelihood phylogenetic tree of *P. decumbens* and eleven Ascomycota species. (**B**) Comparison of number of proteins in selected Gene Ontology terms (level 3) involved in carbohydrate utilization and cellular metabolism. The maximum number in each term was set to be 100%. Sc, *Saccharomyces cerevisiae*; Nc, *Neurospora crassa*; Tr, *Trichoderma reesei*; Pd, *P. decumbens*; Pc, *P. chrysogenum*; Ag, *A. niger*; An, *A. nidulans*.
doi:10.1371/journal.pone.0055185.g001

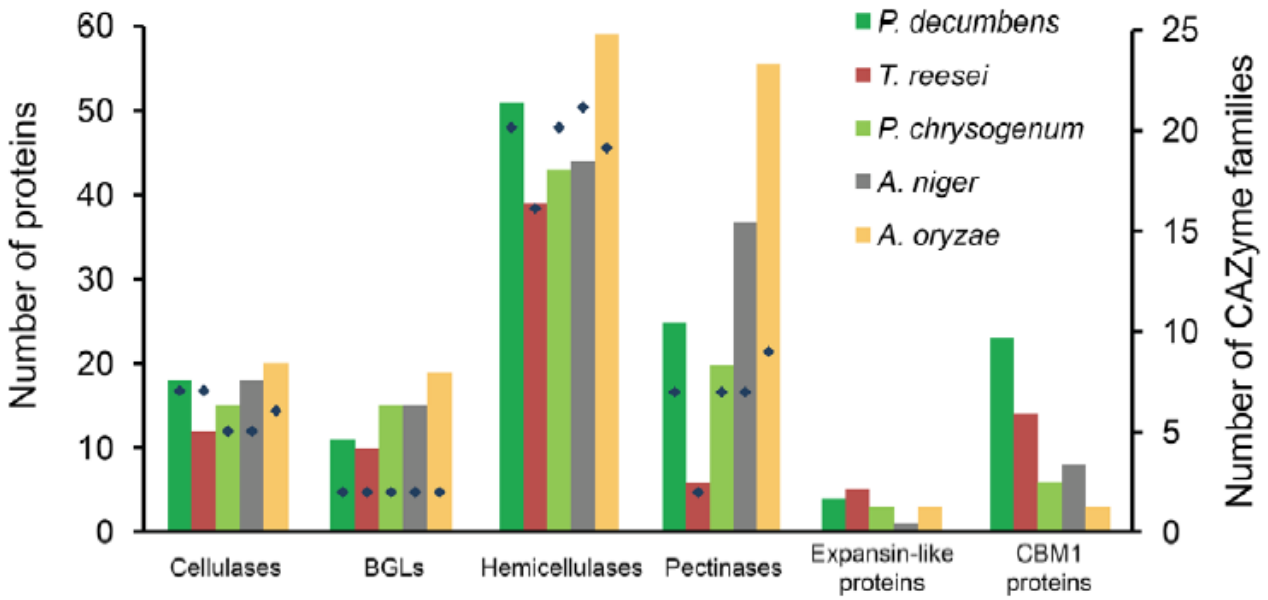
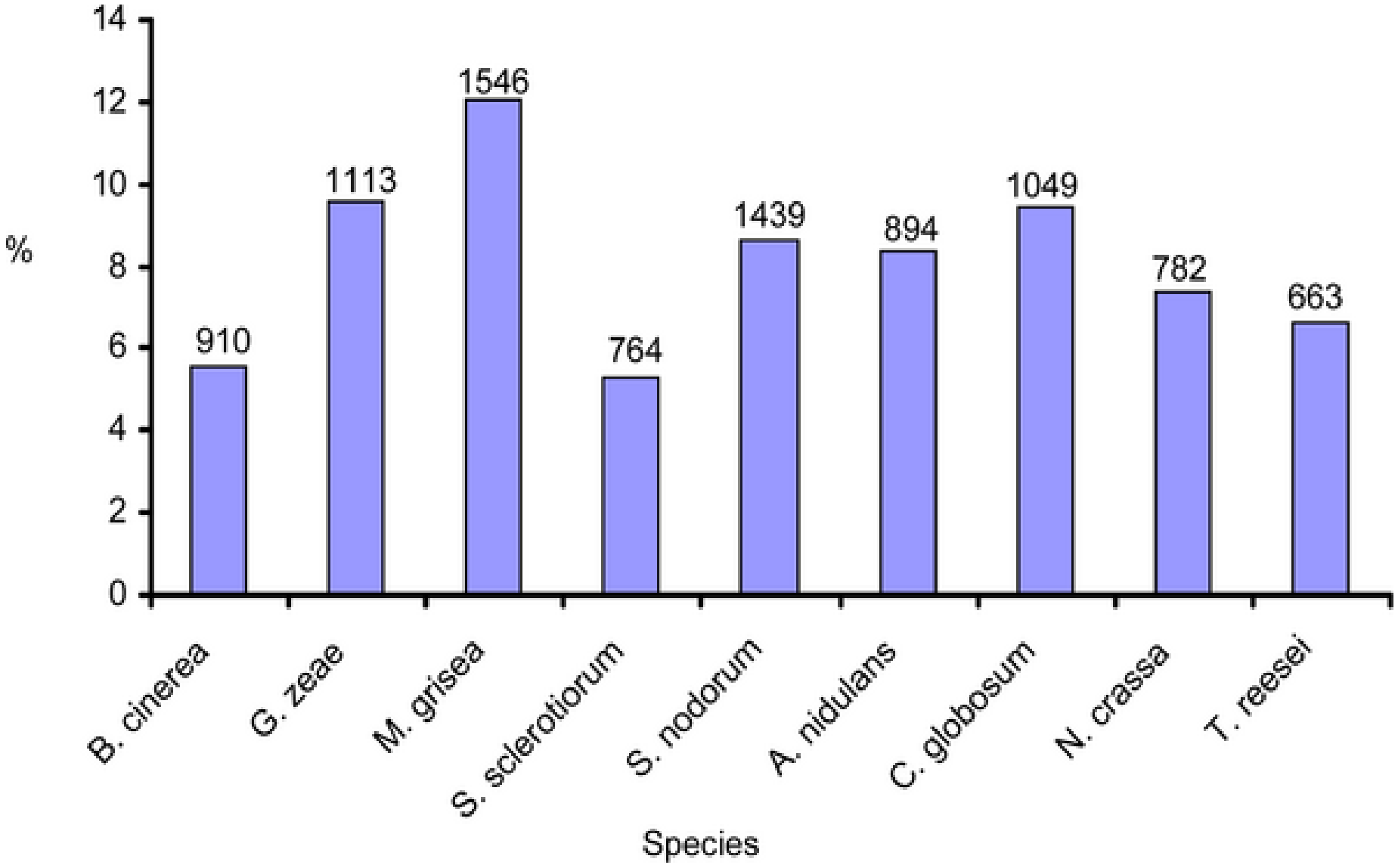


Figure 2. Comparison of numbers of plant cell wall-degrading enzymes among five fungal species. BGLs, β-glucosidases. CBM1 proteins, proteins containing fungal cellulose binding domains. Numbers of proteins (columns) and corresponding CAZyme families (diamonds, only those of cellulases, β-glucosidases, hemicellulases and pectinases) are shown. Tannases, cellobiose dehydrogenases and feruloyl esterases not assigned to CAZy families (see **Table S10**) are not included.

Bar chart showing the percentage of the total proteome that is predicted to be secreted in each fungal species.



Soanes DM, Alam I, Cornell M, Wong HM, et al. (2008) Comparative Genome Analysis of Filamentous Fungi Reveals Gene Family Expansions Associated with Fungal Pathogenesis. PLoS ONE 3(6): e2300.. 2008

Compositions of fungal secretomes indicate a greater impact of phylogenetic history than lifestyle adaptation

Krijger *et al.*

BioMed Central

Krijger *et al. BMC Genomics* 2014, **15**:722
http://www.biomedcentral.com/1471-2164/15/722

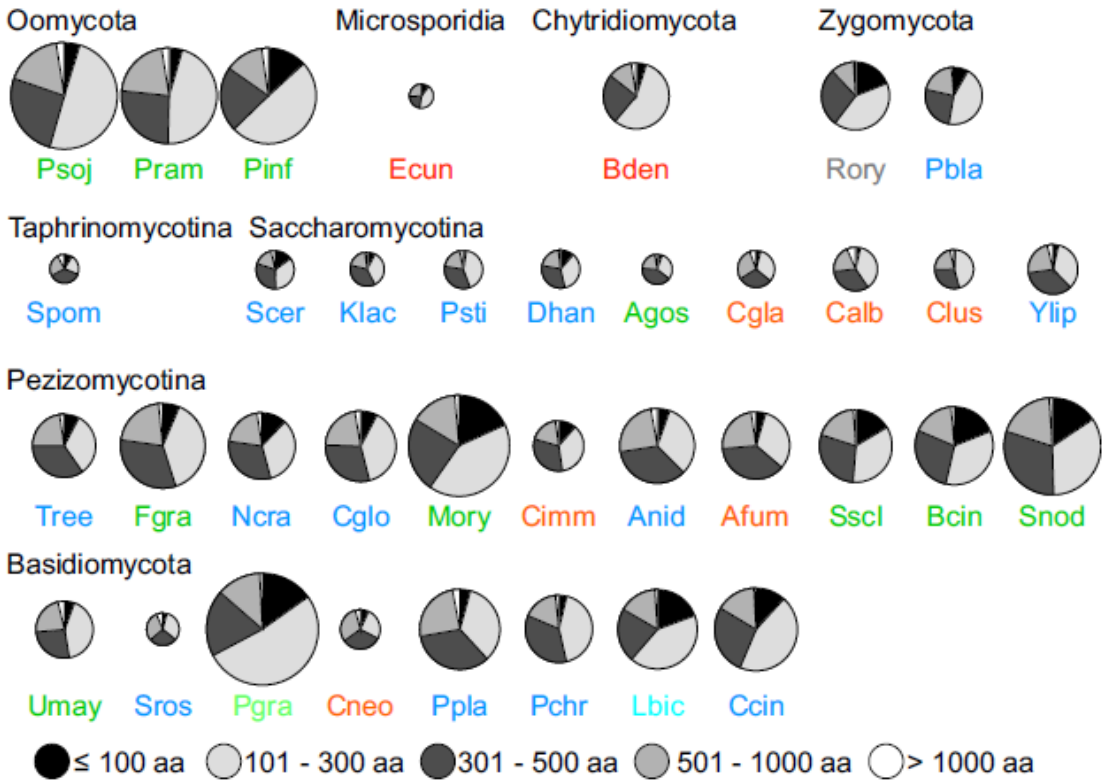
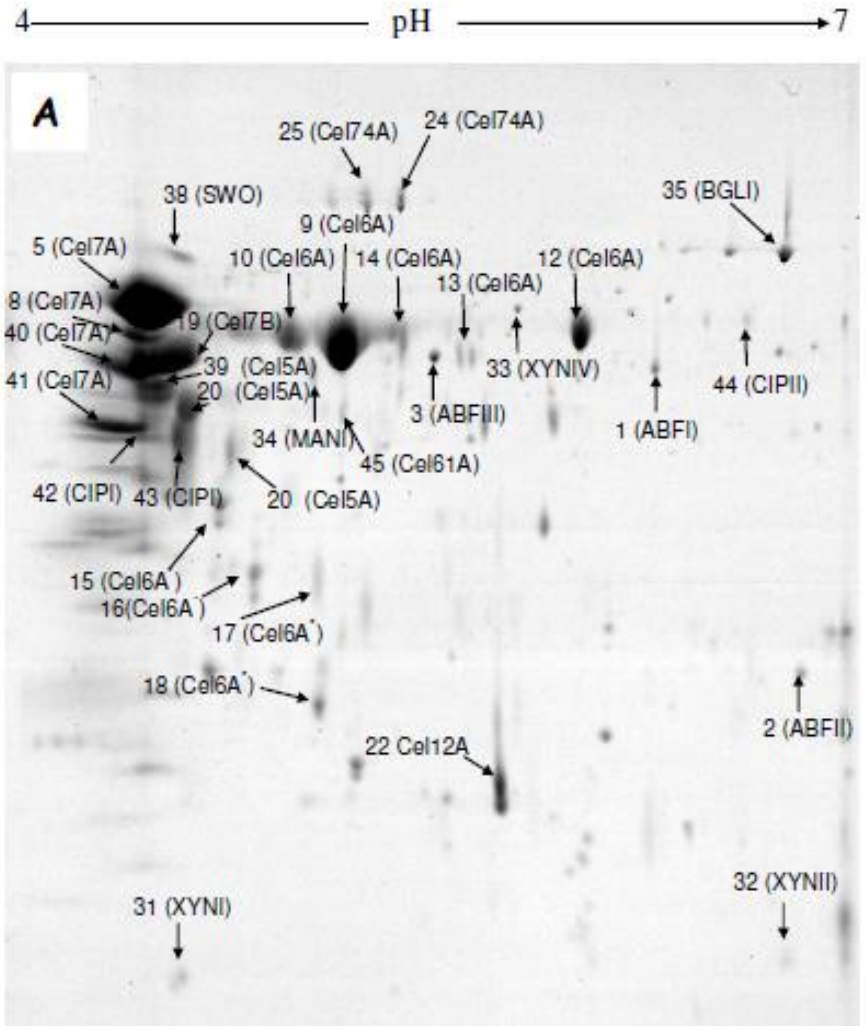
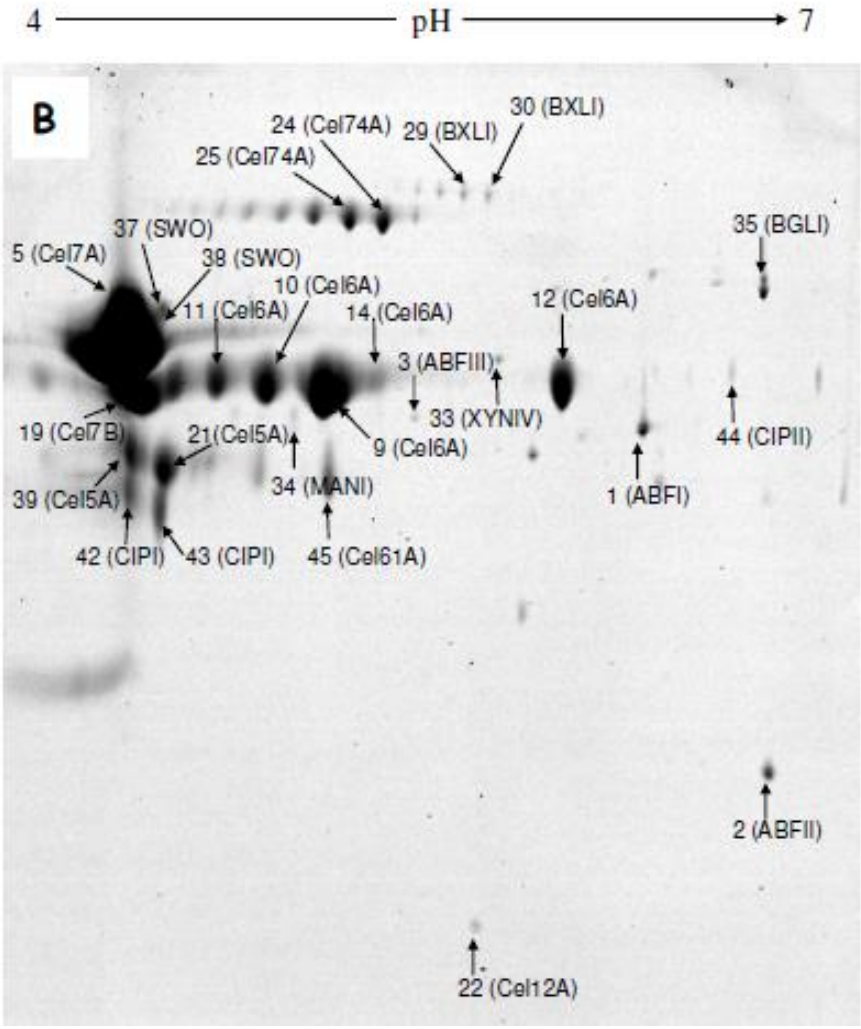


Figure 3 Protein size distributions within soluble secretomes. Number of proteins in five length intervals (≤100 aa, 101-300 aa, 301-500 aa, 501-1000 aa and >1000 aa) as fractions of the total soluble secretomes. Circle areas correspond to the absolute sizes of the soluble secretomes. Species denominators are color-coded by lifestyle: dark blue = saprophytes, dark green = plant pathogens, red = animal pathogens, grey = polyphage (*R. oryzae*), light blue = Ectomycorrhiza (EcM, *L. bicolor*), light green = obligate biotroph (*P. graminis*). Abbreviations for species are given in Table 1.

Herpoël-Gimbert et al. Comparative secretome analyses of two *Trichoderma reesei* CL847 (A) and RUT-C30 (B) hypersecretory strains. Biotechnology for Biofuels 2008, 1:18

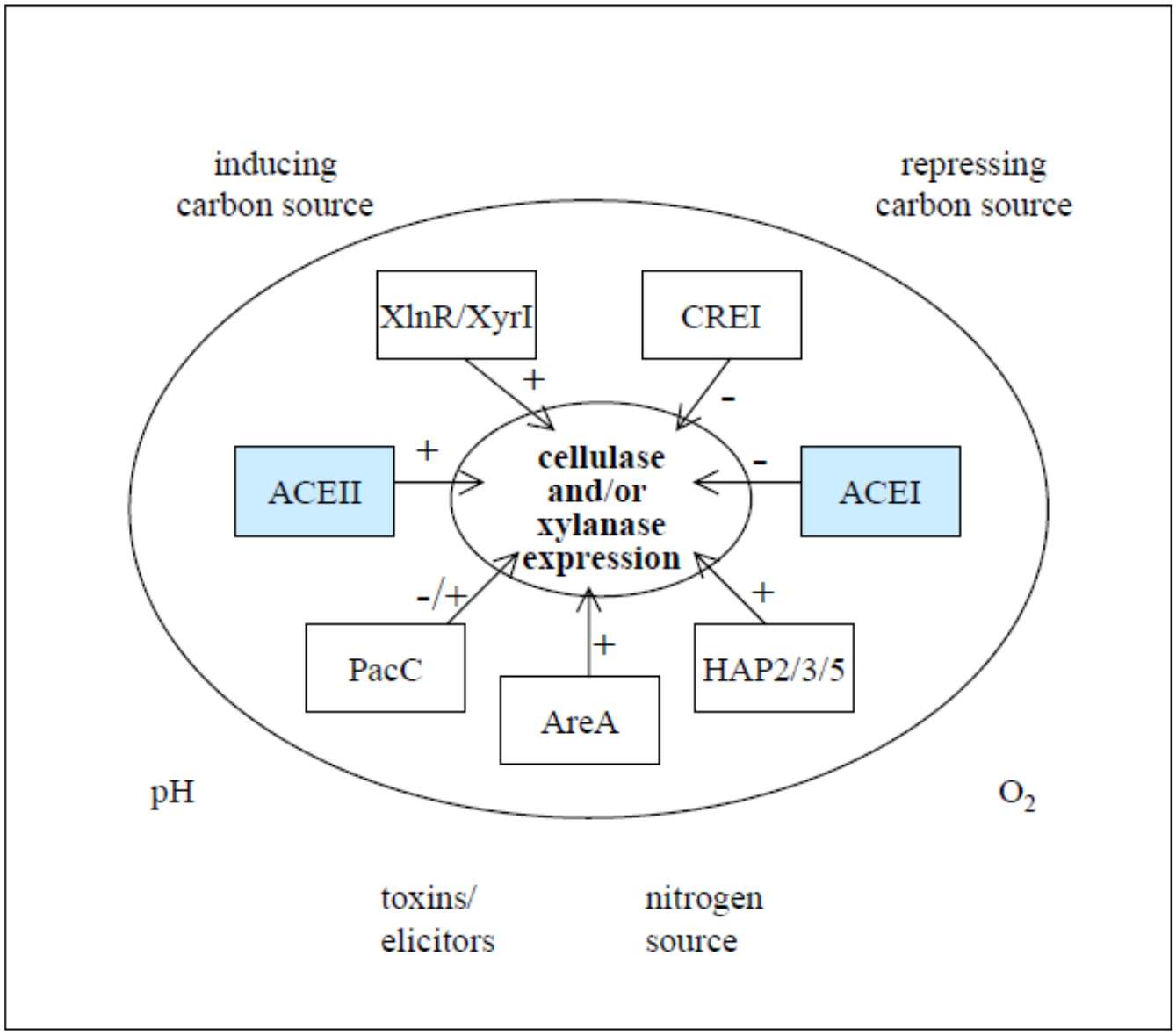




CL847

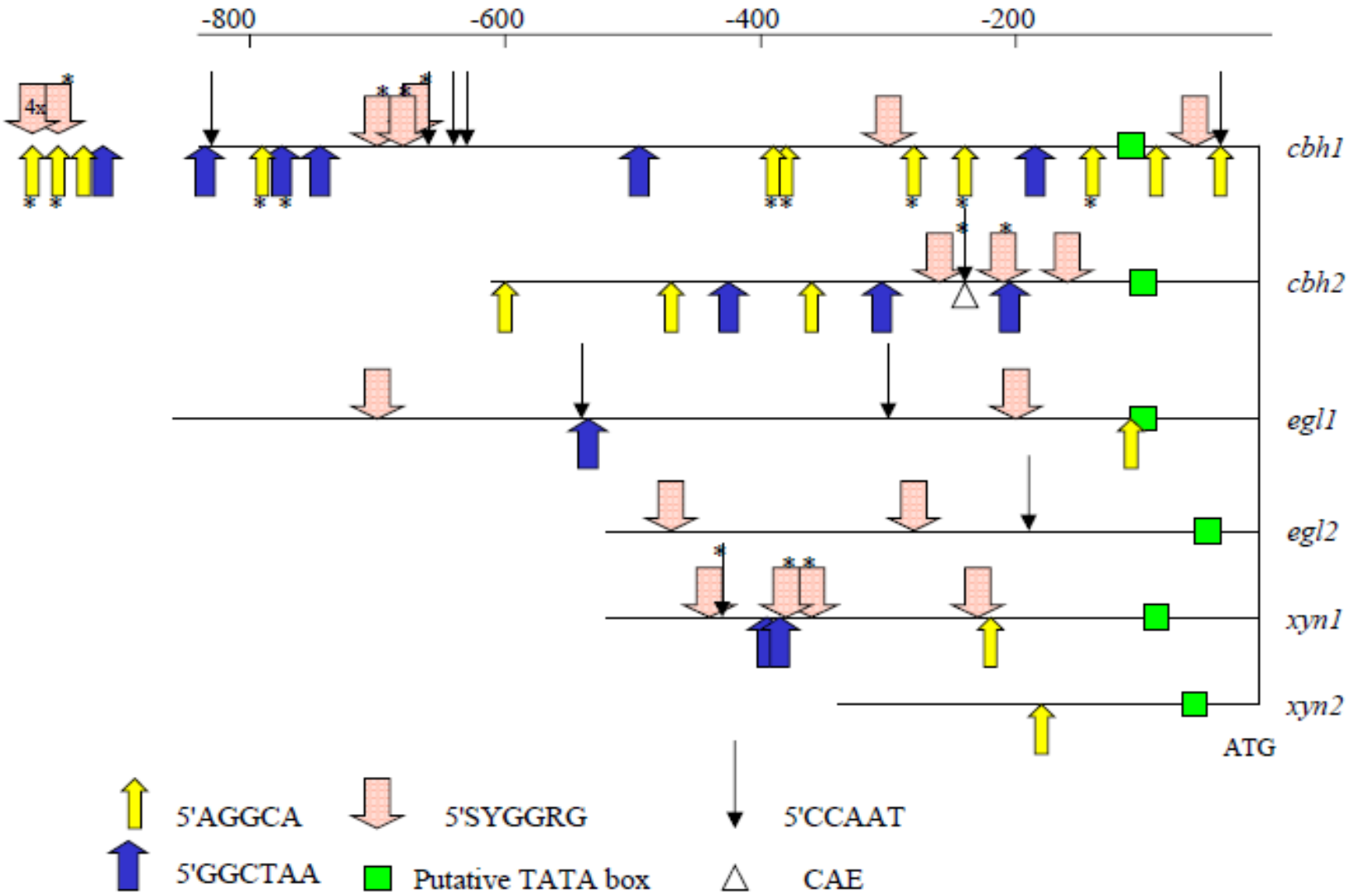
RUT-C30

Reguladores de transcrição de genes Celulases e Xilanases de Fungos



Aro, 2003

Localización del sítio de ligación de putativos factores de transcripción



Aro, 2003

BMC Genomics

RESEARCH ARTICLE Open Access

Sequencing of mitochondrial genomes of nine *Aspergillus* and *Penicillium* species identifies mobile introns and accessory genes as main sources of genome size variability

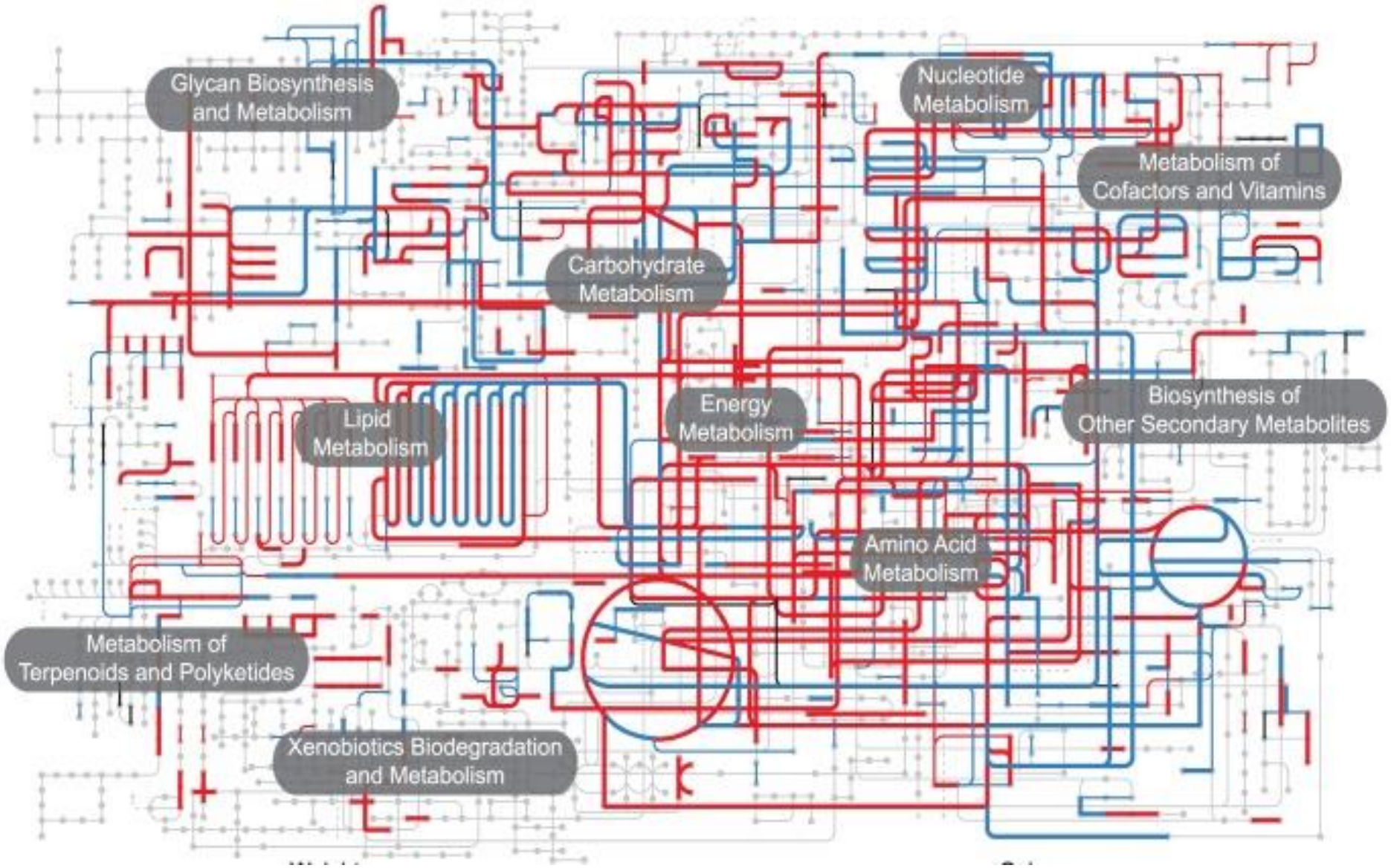
Vinita Joardar[1*], Natalie F Abrams[1], Jessica Hostetler[1], Paul J Paukstelis[2], Suchitra Pakala[1], Suman B Pakala[1], Nikhat Zafar[1], Olukemi O Abolude[3], Gary Payne[4], Alex Andrianopoulos[5], David W Denning[6] and William C Nierman[1]

Table 1 *Aspergillus* and *Penicillium* mitochondrial genome statistics

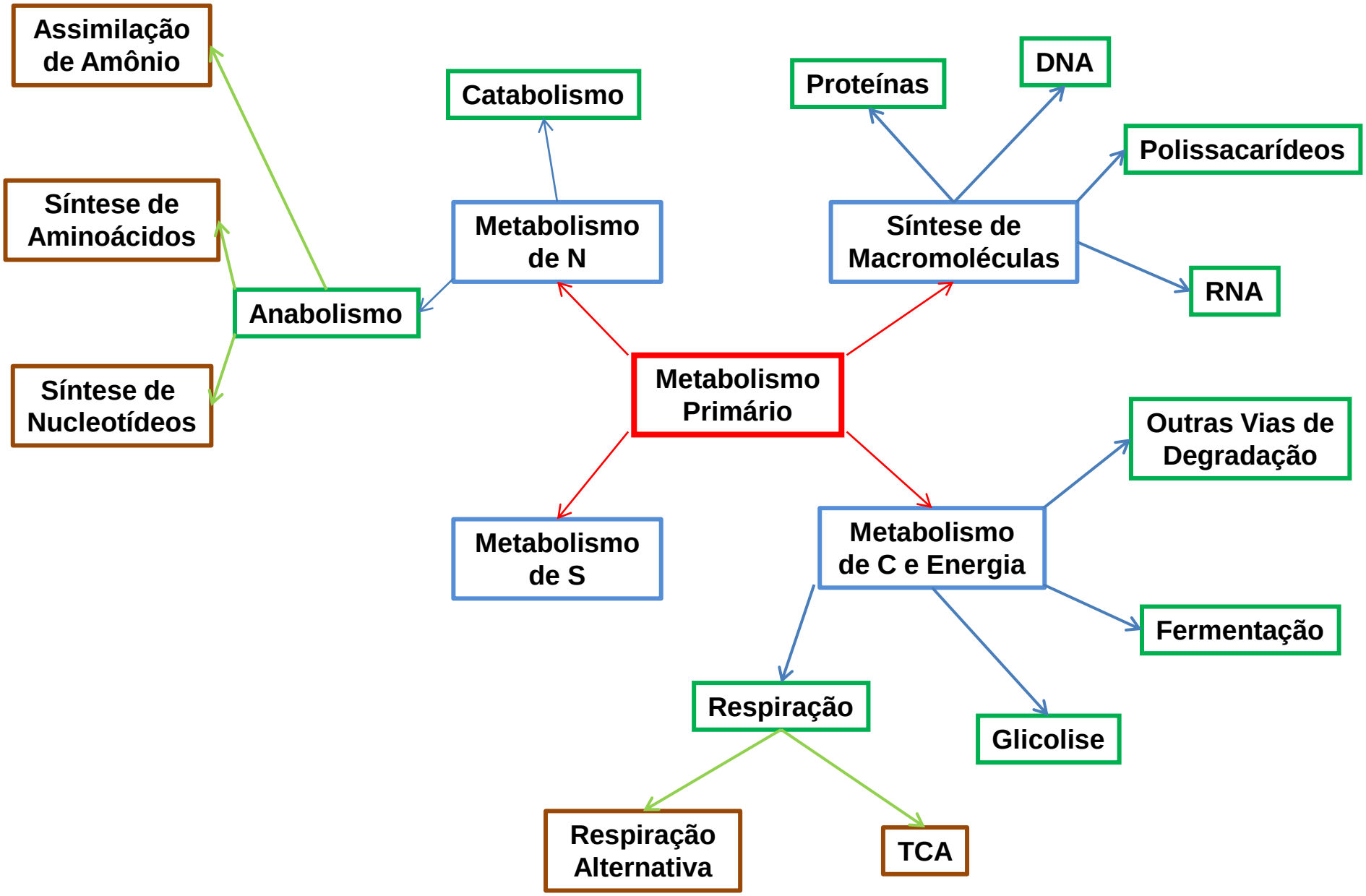
Genome[a]	length of mitochondrial genome (bp)	GC %	Protein-coding genes	Protein-coding genes with introns	Length (and number) of introns in protein-coding genes (bp)	Length of intron in large subunit rRNA (bp)	tRNAs	intronic ORFS	Length (and number) of non-intronic accessory genes (bp)	length of nuclear genome (bp)
A. terreus NIH 2624	24,658	27.1	15	0	0 (0)	1,705	27	1	0 (0)	29,331,195
P. chrysogenum 54-1255	27,017	24.7	16	0	0 (0)	1,678	28	1	1,227 (1)	32,223,735
A. oryzae RIB40[b]	29,202	26.2	17	1	1,780 (1)	1,703	26	2	2,010 (2)	37,088,582
A. flavus NRRL 3357	29,205	26.2	17	1	1,776 (1)	1,703	27	2	2,004 (1)	36,892,344
A. fumigatus A1163	30,696	25.5	19	1	2,020 (1)	1,720	31	3	1,410 (2)	29,205,420
A. niger N909	31,103	26.9	16	2	1,502 (2)	1,800	25	0	1,674 (2)	not available
A. fumigatus AF210	31,762	25.4	20	1	2,020 (1)	1,720	31	3	2,253 (3)	not available
A. fumigatus AF293	31,765	25.4	20	1	2,020 (1)	1,720	31	3	2,253 (3)	29,384,958
A. nidulans FGSC A4	33,227	24.9	20	2	4,108 (5)	1,689	28	4	1,524 (2)	29,828,291
A. tubingensis 0932	33,656	26.8	16	2	3,690 (4)	1,794	25	0	1,647 (2)	not available
N. fischeri NRRL 181	34,373	25.4	22	1	3,429 (2)	1,721	28	4	2,559 (4)	31,770,017
A. clavatus NRRL 1	35,056	25.0	21	2	4,304 (3)	1,719	26	4	4,509 (3)	27,859,441
P. marneffei ATCC 18224	35,432	24.6	26	3	9,775 (9)	1,672	30	10	768 (2)	28,643,865
P. marneffei MP1	35,438	24.6	25	3	9,776 (9)	1,672	30	9	1,647 (2)	not available
T. stipitatus ATCC 10500	36,351	24.9	26	3	12,140 (11)	1,713	27	12	0 (0)	35,685,443

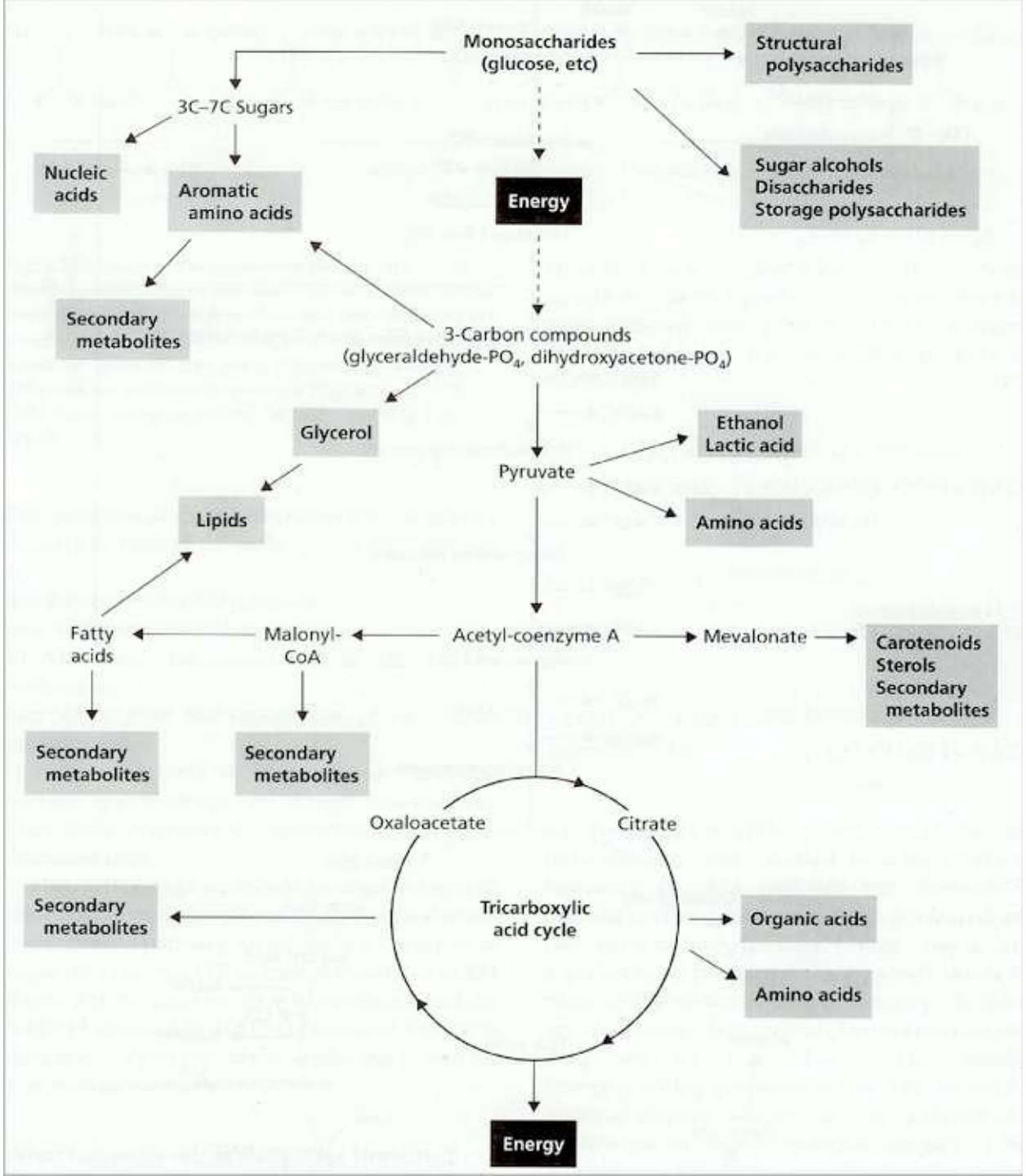
[a]Genomes annotated at JCVI are shown in bold.
[b]Protein coding genes were annotated at JCVI.

Metabolismo Celular



Metabolismo primário em fungos




Monosaccharides (glucose, etc)
Structural polysaccharides
3C–7C Sugars
Nucleic acids
Aromatic amino acids
Energy
Sugar alcohols
Disaccharides
Storage polysaccharides
Secondary metabolites
3-Carbon compounds (glyceraldehyde-PO4, dihydroxyacetone-PO4)
Glycerol
Ethanol
Lactic acid
Pyruvate
Lipids
Amino acids
Fatty acids
Malonyl-CoA
Acetyl-coenzyme A
Mevalonate
Carotenoids
Sterols
Secondary metabolites
Secondary metabolites
Secondary metabolites
Oxaloacetate
Citrate
Secondary metabolites
Tricarboxylic acid cycle
Organic acids
Amino acids
Energy

Key points

- Less than 20% of the genes of *Aspergillus* species are characterized.
- Only a fraction of the characterized genes are within primary metabolism.
- Relatively few new genes within primary metabolism are being characterized.
- Holistic application of metabolic networks is a feasible way of functional genomics for a large number of genes within primary metabolism.

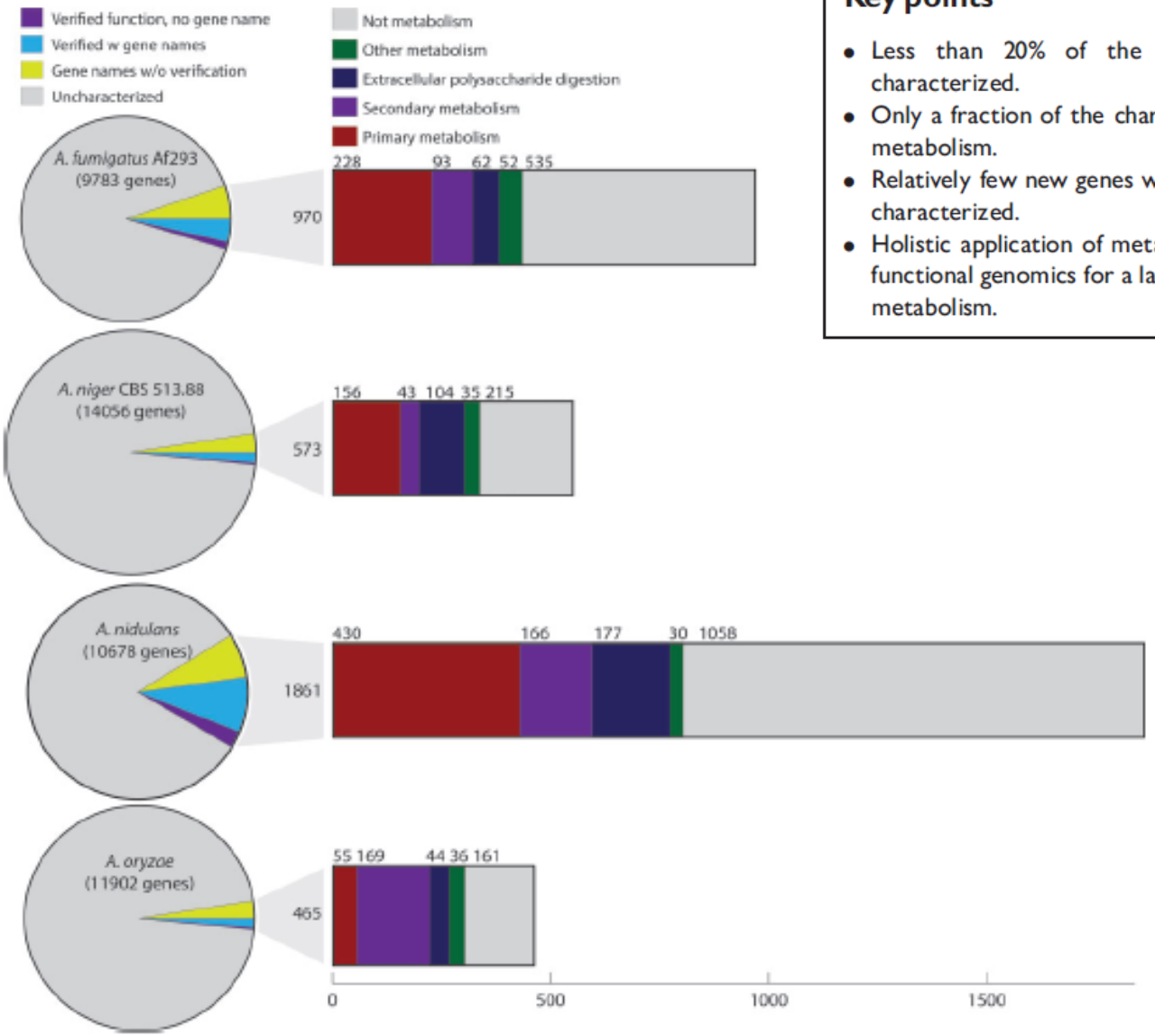


Figure 1: Overview of characterized genes and their function in *A. fumigatus*, *A. niger*, *A. nidulans* and *A. oryzae*. Pie charts show total number of genes; the area of the pie is proportional to the number of annotated genes. Bar charts show the distribution of functions related to different types of metabolism and non-metabolic functions. 'Other metabolism' denotes genes with functions not relevant in the other categories, primarily proteases. Data are summarized from AspGD.org annotation tables [10].

Andersen, MR. Briefings in Functional Genomics, 2014

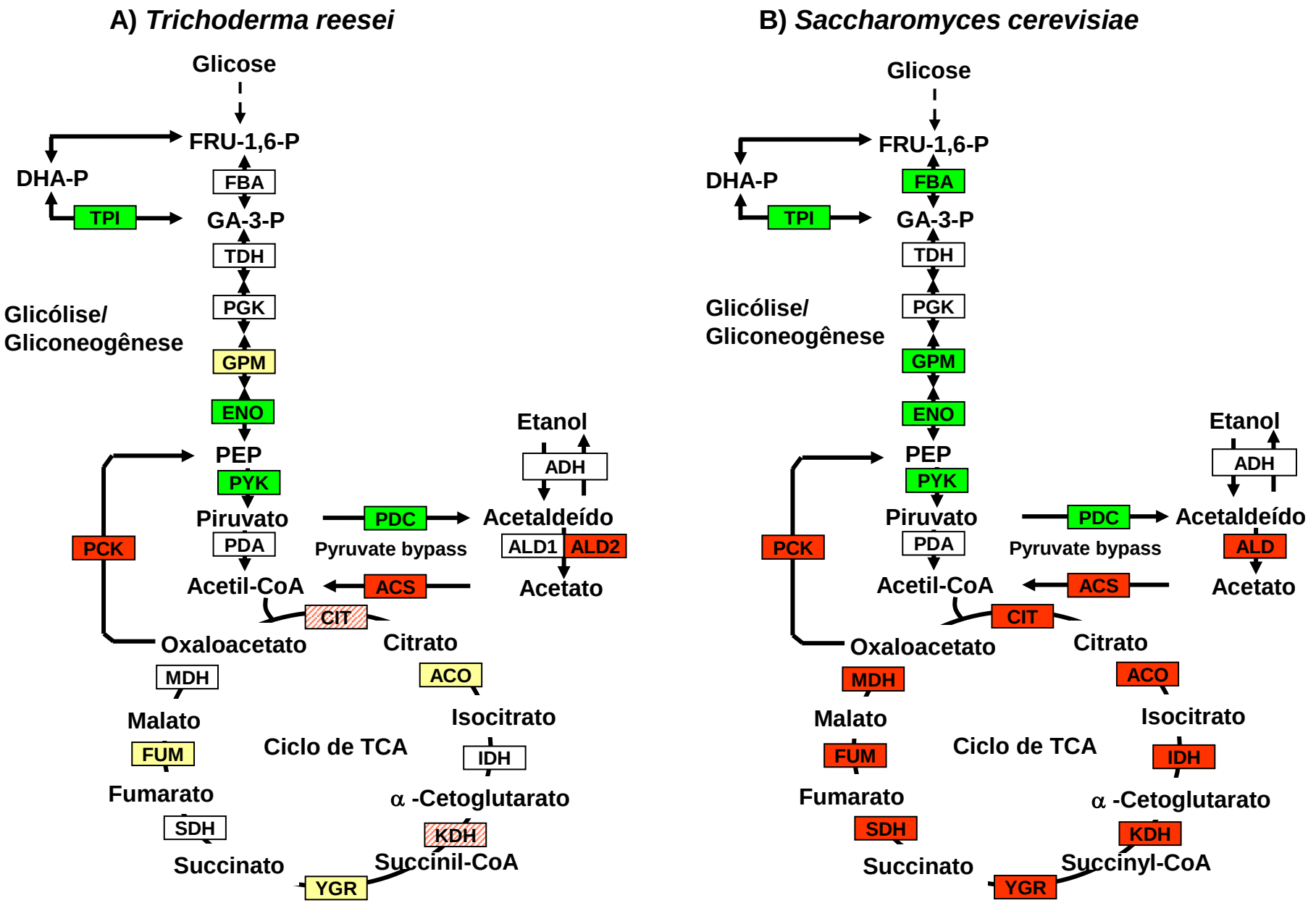


Fig. 22. Comparação do perfil de expressão gênica de genes da glicólise, gliconeogênese, ciclo do TCA e via alternativa de piruvato (piruvate bypass) durante o esgotamento de glicose em *T. reesei* e *S. cerevisiae*. Caixas vermelhas e verdes representam genes cuja expressão aumenta ou diminui, respectivamente, em função do esgotamento de glicose no meio. Caixas brancas indicam que a expressão desses genes não altera. Caixas amarelas representam genes que não foram isolados ainda. O nível de transcrição de PCK foi determinado por Northern blot.

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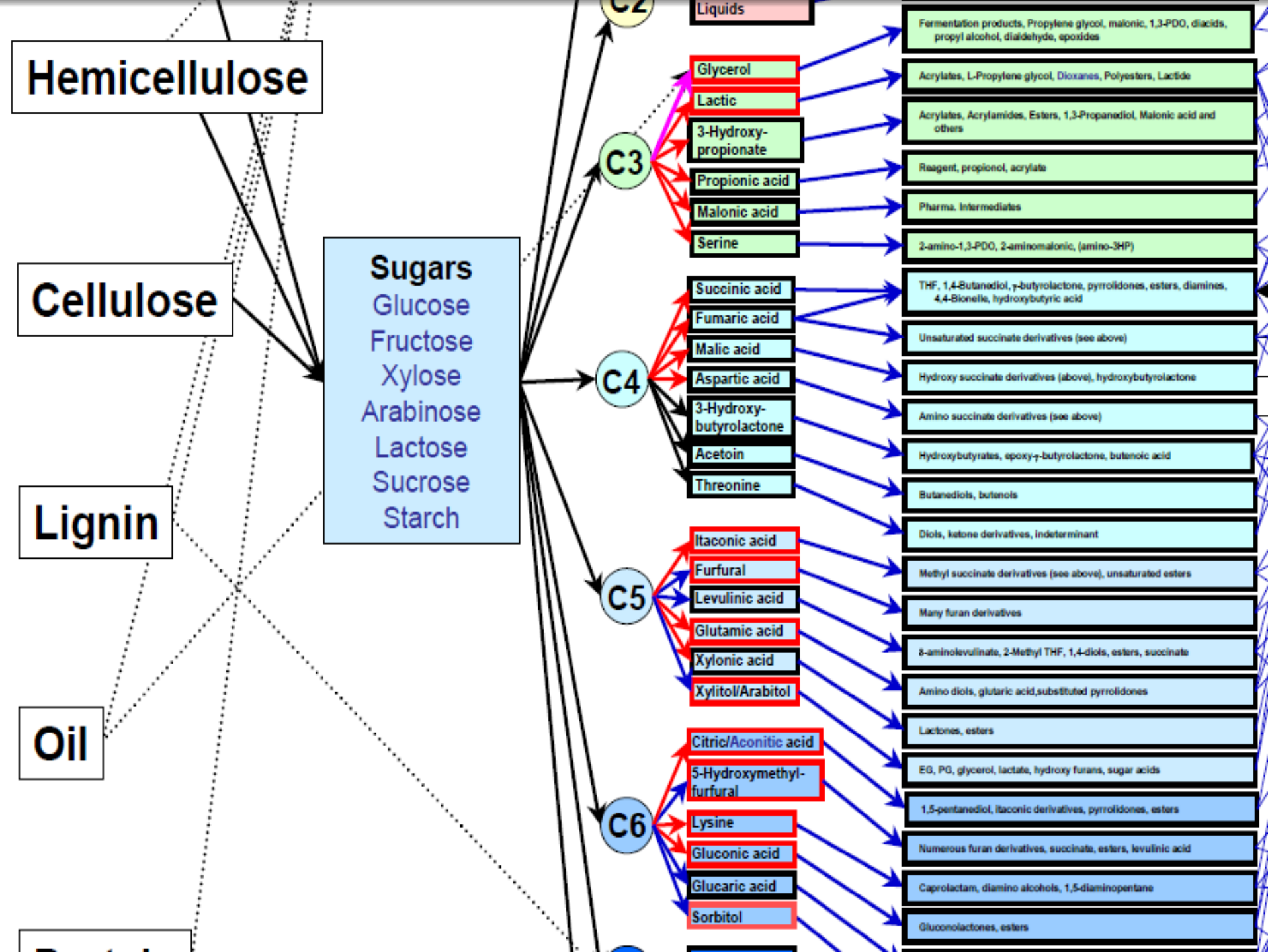
Top Value Added Chemicals from Biomass

Volume I—Results of Screening for Potential Candidates from Sugars and Synthesis Gas

Building Blocks
1,4 succinic, fumaric and malic acids
2,5 furan dicarboxylic acid
3 hydroxy propionic acid
aspartic acid
glucaric acid
glutamic acid
itaconic acid
levulinic acid
3-hydroxybutyrolactone
glycerol
sorbitol
xylitol/arabinitol


Hemicellulose
Cellulose
Lignin
Oil
Sugars
Glucose
Fructose
Xylose
Arabinose
Lactose
Sucrose
Starch
C2
Liquids
C3
Glycerol
Lactic
3-Hydroxy-propionate
Propionic acid
Malonic acid
Serine
C4
Succinic acid
Fumaric acid
Malic acid
Aspartic acid
3-Hydroxy-butyrolactone
Acetoin
Threonine
C5
Itaconic acid
Furfural
Levulinic acid
Glutamic acid
Xylonic acid
Xylitol/Arabitol
C6
Citric/Aconitic acid
5-Hydroxymethyl-furfural
Lysine
Gluconic acid
Glucaric acid
Sorbitol
Fermentation products, Propylene glycol, malonic, 1,3-PDO, diacids, propyl alcohol, dialdehyde, epoxides
Acrylates, L-Propylene glycol, Dioxanes, Polyesters, Lactide
Acrylates, Acrylamides, Esters, 1,3-Propanediol, Malonic acid and others
Reagent, propionol, acrylate
Pharma. Intermediates
2-amino-1,3-PDO, 2-aminomalonic, (amino-3HP)
THF, 1,4-Butanediol, γ-butyrolactone, pyrrolidones, esters, diamines, 4,4-Bionelle, hydroxybutyric acid
Unsaturated succinate derivatives (see above)
Hydroxy succinate derivatives (above), hydroxybutyrolactone
Amino succinate derivatives (see above)
Hydroxybutyrates, epoxy-γ-butyrolactone, butenoic acid
Butanediols, butenols
Diols, ketone derivatives, indeterminant
Methyl succinate derivatives (see above), unsaturated esters
Many furan derivatives
δ-aminolevulinate, 2-Methyl THF, 1,4-diols, esters, succinate
Amino diols, glutaric acid,substituted pyrrolidones
Lactones, esters
EG, PG, glycerol, lactate, hydroxy furans, sugar acids
1,5-pentanediol, Itaconic derivatives, pyrrolidones, esters
Numerous furan derivatives, succinate, esters, levulinic acid
Caprolactam, diamino alcohols, 1,5-diaminopentane
Gluconolactones, esters

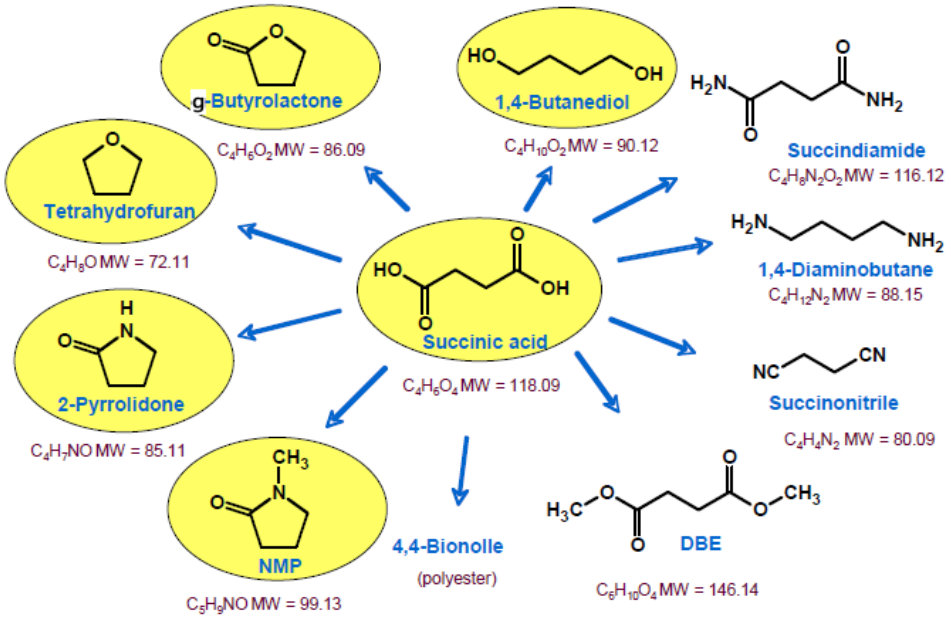


Figure 5 - Succinic Acid Chemistry to Derivatives

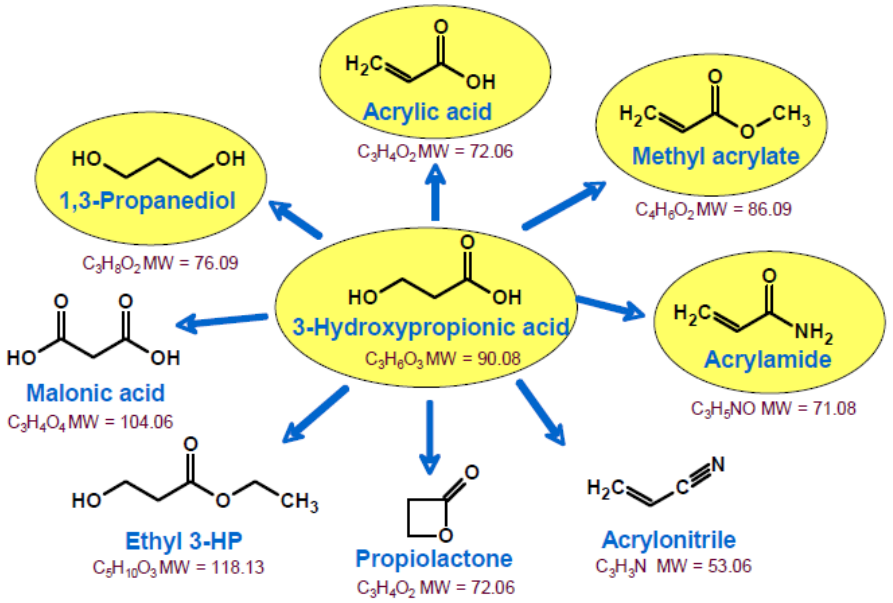


Figure 8 – Derivatives of 3-HPA

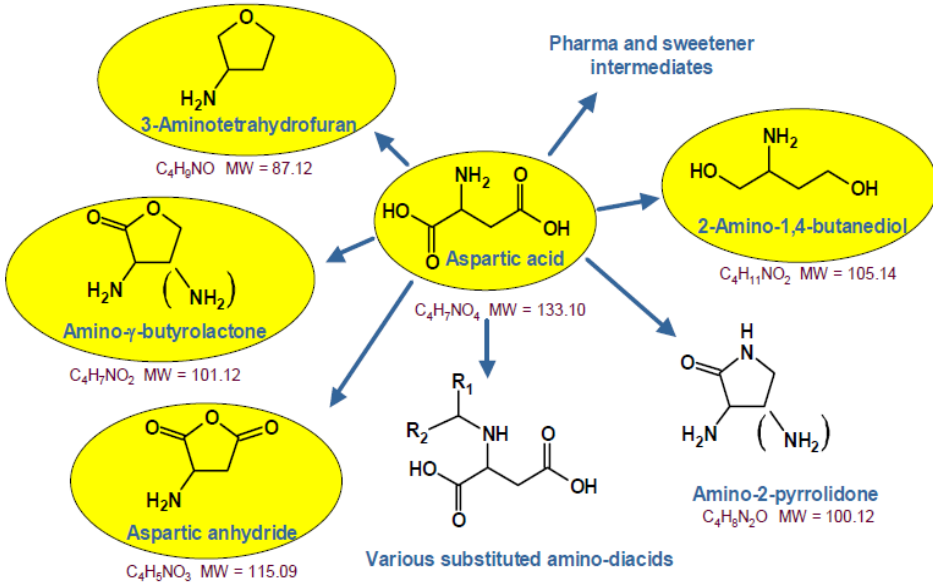


Figure 9 - Aspartic Acid Chemistry to Derivatives

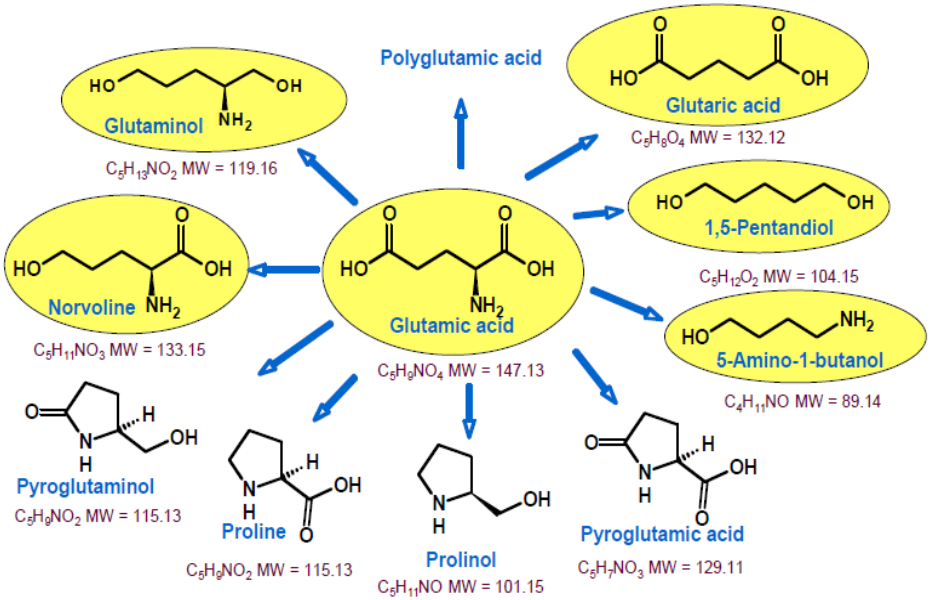
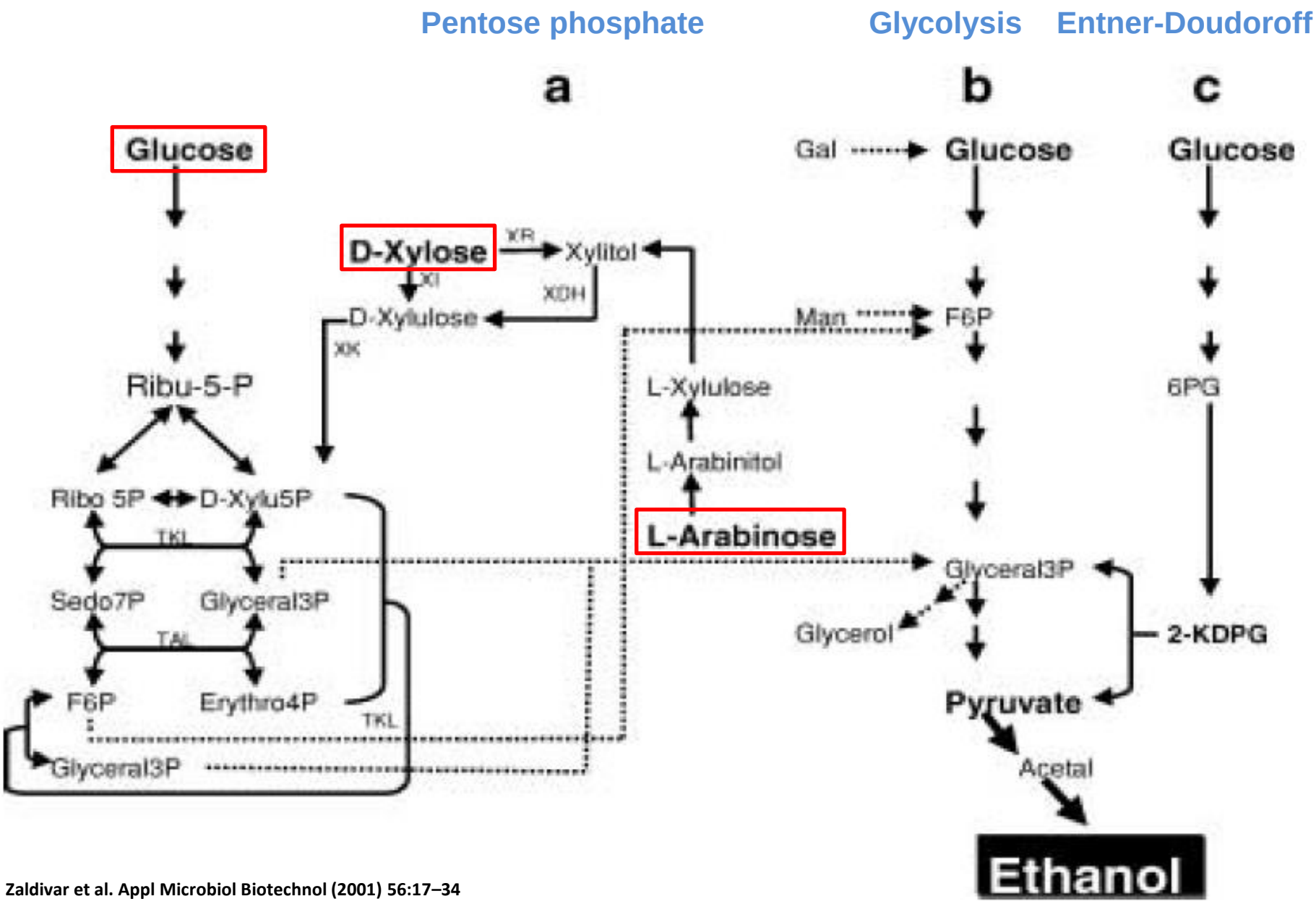


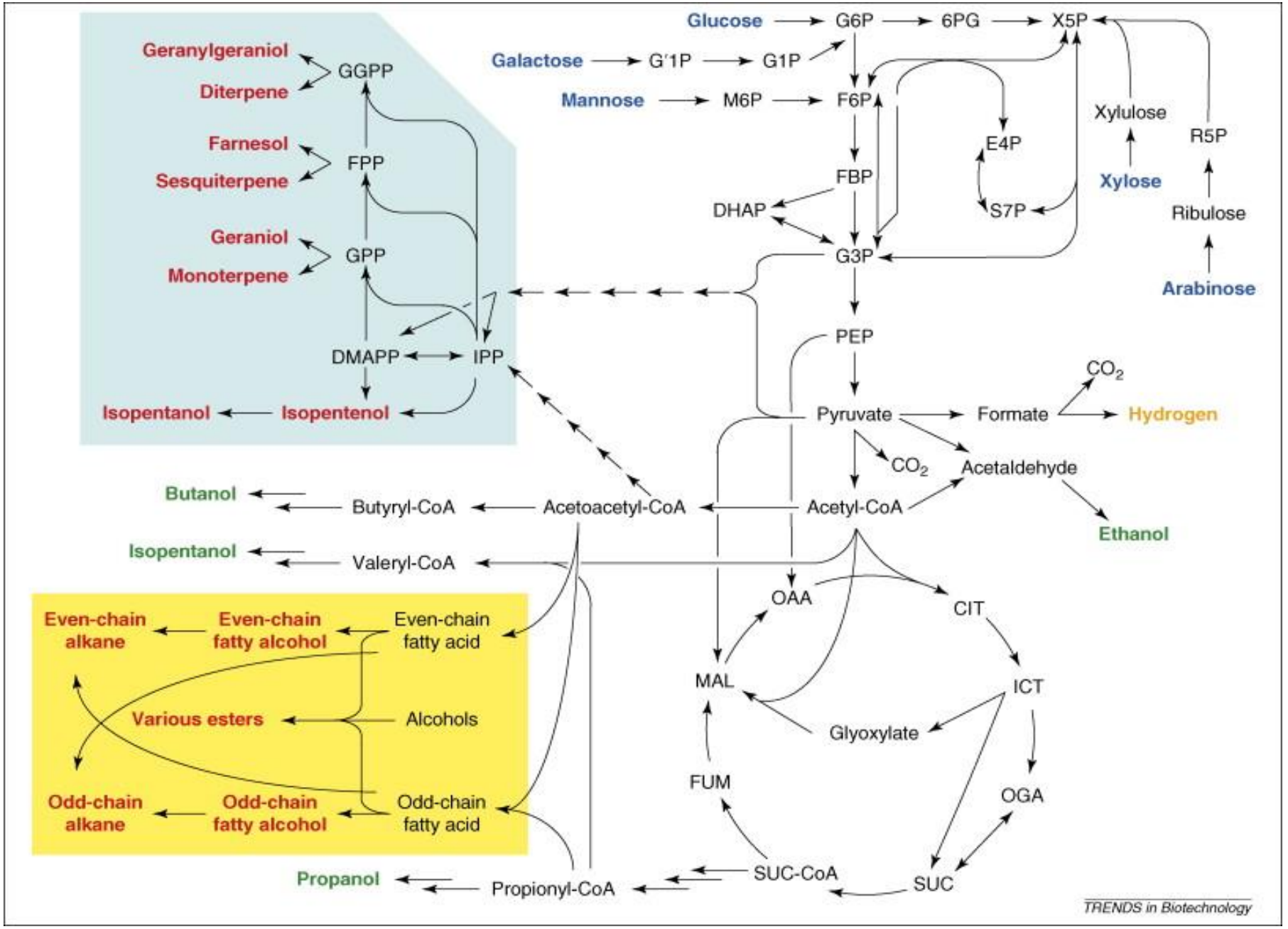
Figure 11 - Glutamic Acid and its Derivatives

Pathways resulting in ethanol production from lignocellulose sugars.



Zaldivar et al. Appl Microbiol Biotechnol (2001) 56:17–34

Biofuel alternatives to ethanol



Fortman et al., 2008. 26(7):375–381

Organic Acid Production by Filamentous Fungi

Jon K. Magnuson and Linda L. Lasure

2. Commercial Successes: Organic Acids from Filamentous Fungi

Although many organic acids are made by living cells, few are produced commercially. Citric, gluconic, itaconic, and lactic acids are manufactured via large-scale bioprocesses. Oxalic, fumaric, and malic acids can be made through fungal bioprocesses, but the market demand is small, since competing chemical conversion routes are currently more economical. A few other organic acids have been explored for the development of novel processes. To date, the largest commercial quantities of fungal organic acids are citric acid and gluconic acid, both of which are prepared by fermentation of glucose or sucrose by *A. niger*. Another *Aspergillus* species, *A. terreus*, is used to make itaconic acid. A significant commercial source of lactic acid at the time of this writing is a bioprocess employing the Zygomycete fungus *Rhizopus oryzae*.

Magnuson, J.K., Lasure, L.L. (2004). Organic Acid Production by Filamentous Fungi. https://doi.org/10.1007/978-1-4419-8859-1_12

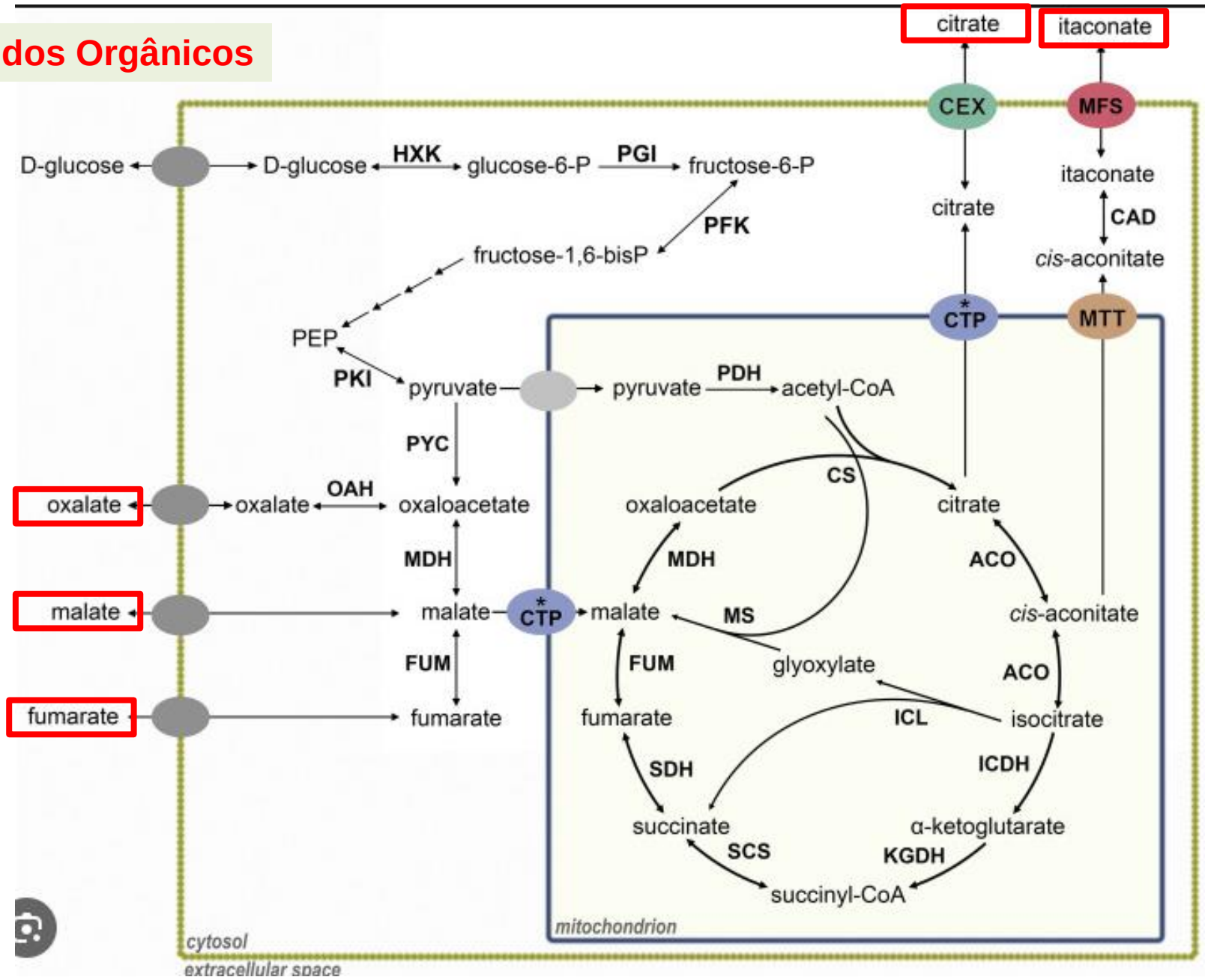
Organic acid	Filamentous fungi	Applications
Citric acid	*Aspergillus niger* *Yarrowia lipolytica*	Preservative, pH adjustment in food, beverage, pharmaceutical and cosmetic industries
Gluconic acid	*Aspergillus niger* *Penicillium spp.*	Food additive Glass and metal cleaning
Itaconic acid	*Aspergillus terreus* *Aspergillus itaconicus* *Ustilago maydis*	Co-polymer and detergents
Oxalic acid	*Aspergillus niger*	Cleaning and bleaching
Kojic acid	*Aspergillus oryzae* *Aspergillus flavus*	Precursor for food additives and cosmetic industry
Succinic acid	*Aspergillus flavipes*	Food additive Precursor of polymers, resins and solvents
Malic acid	*Aspergillus spp.*	Food additive Synthesis of polymers
Fumaric acid	*Aspergillus niger* *Rhizopus delemar*	Food additive Synthesis of polymers

Table 1.1. Organic acid production by filamentous fungi (Goldberg et al., 2006; Kubicek et al., 2010; Liaud et al., 2014).

Published in 2018

Transport processes in the production of organic acids from lignocellulosic feedstocks by Aspergillus niger

Ácidos Orgânicos



Biotechnology Advances Volume 43, 1 November 2020, 107551
https://doi.org/10.1016/j.biotechadv.2020.107551

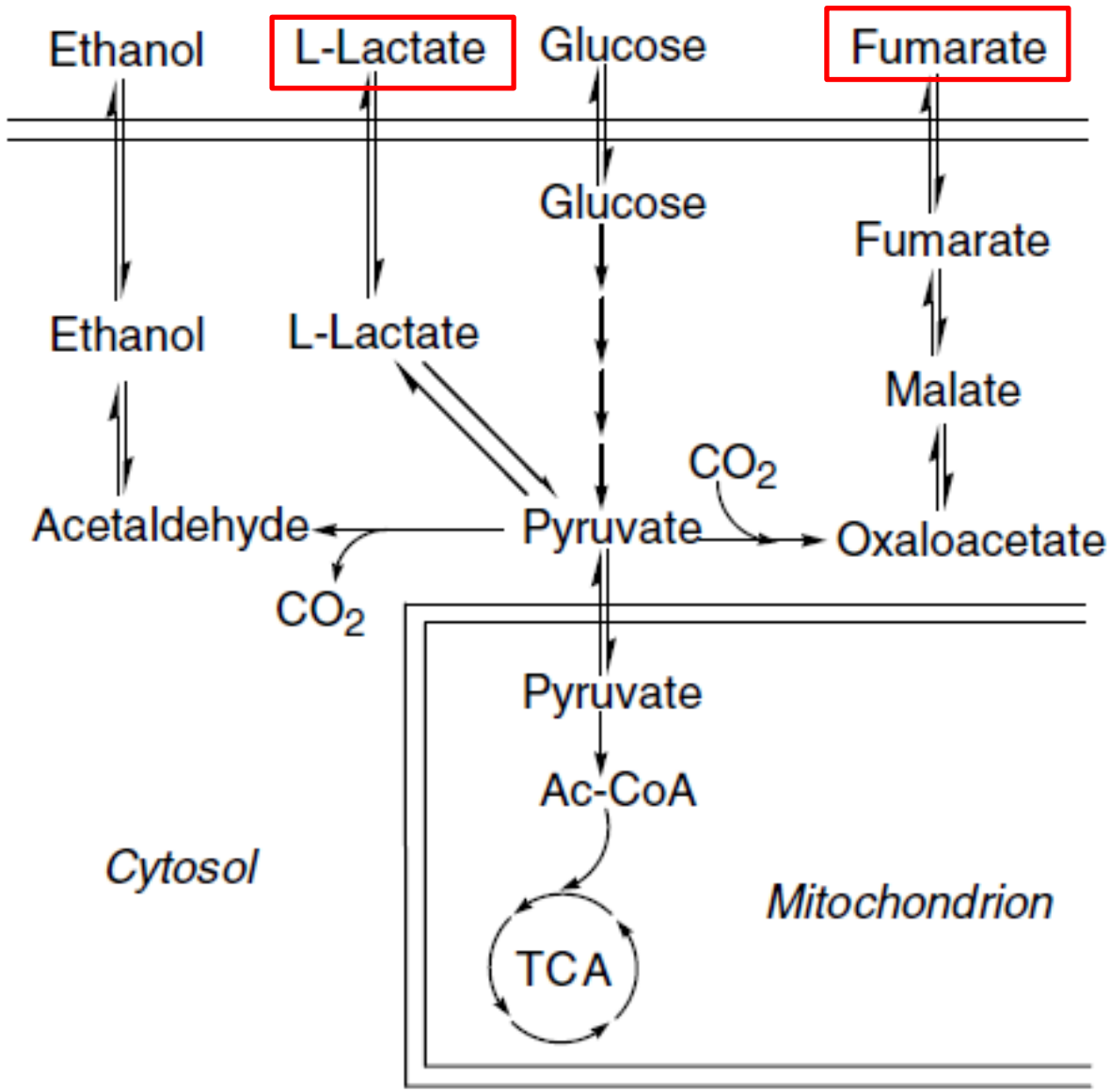


Figure 12.4. Critical pathways for organic acid synthesis in *Rhizopus oryzae*.

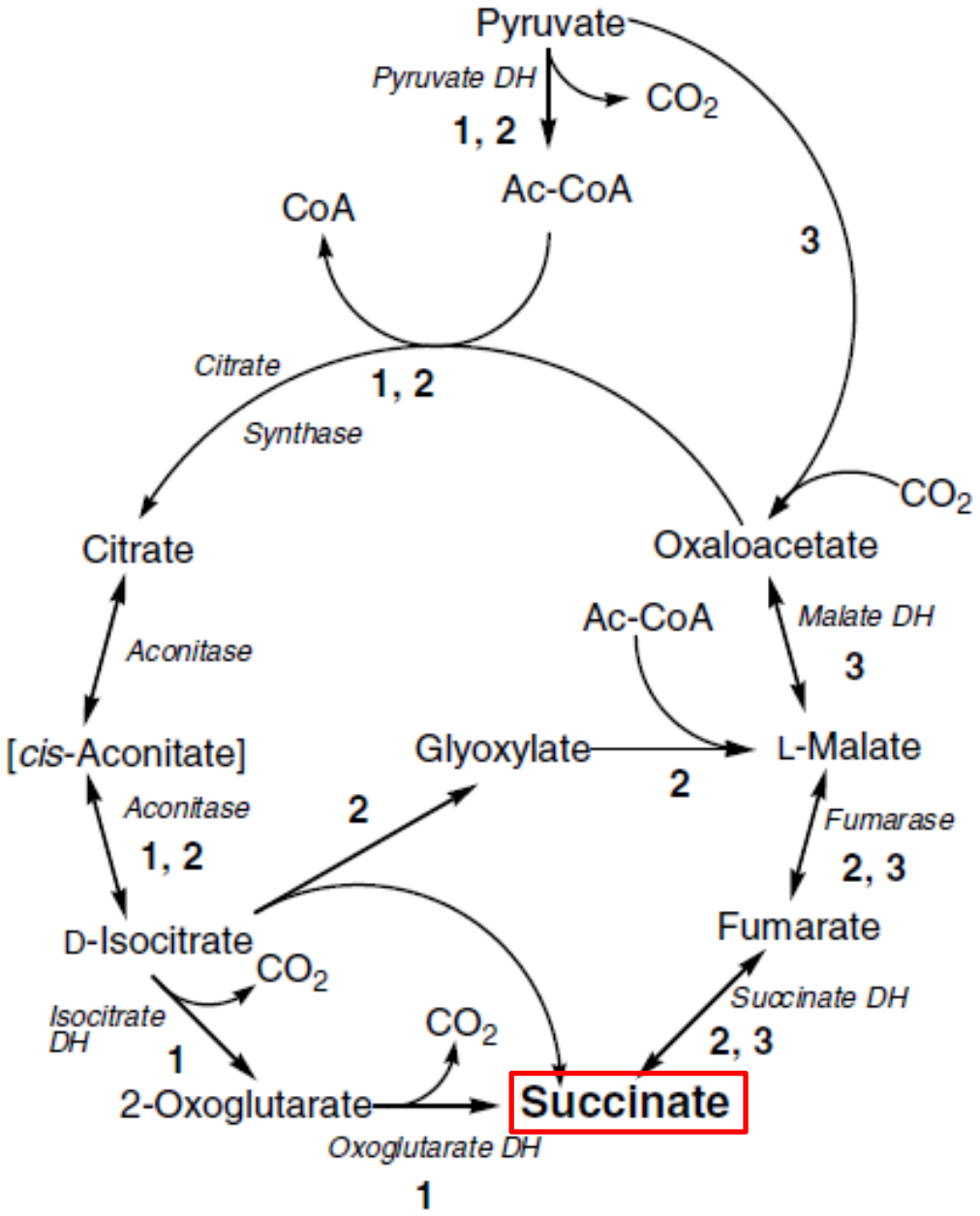
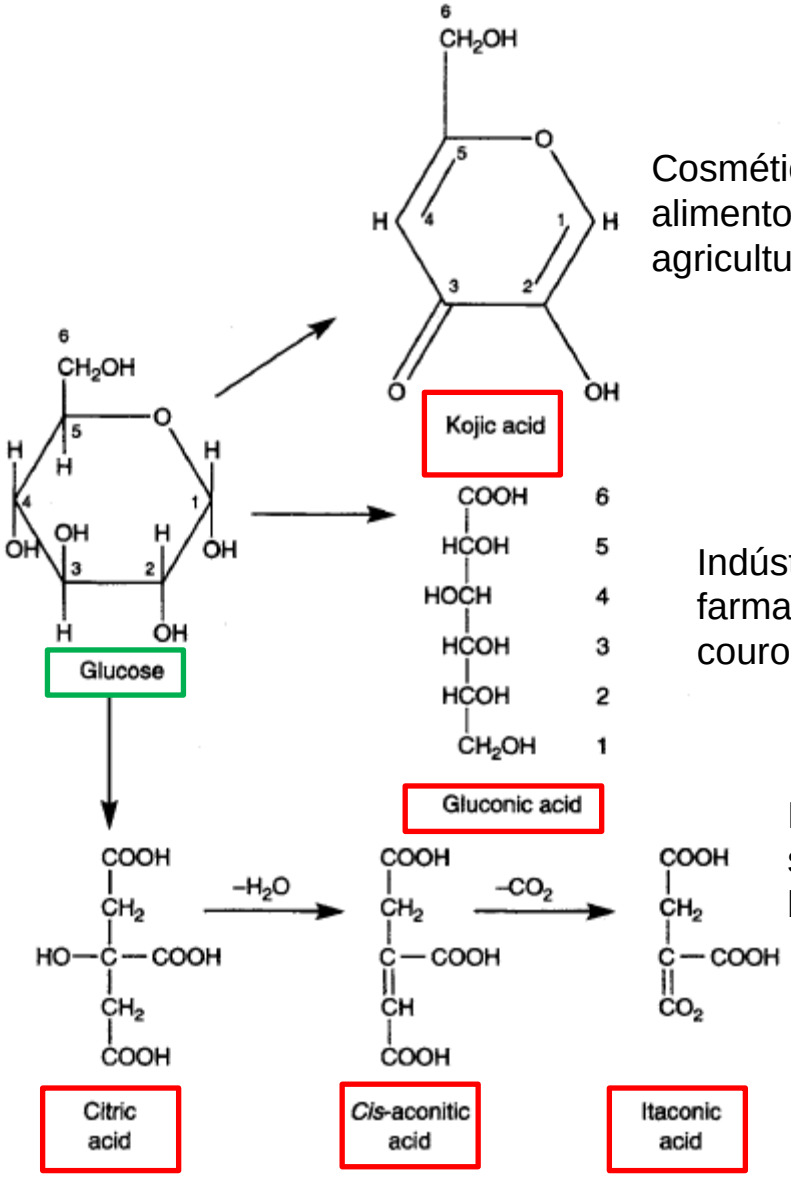


Figure 12.5. Three potential succinate biosynthetic pathways. 1. Oxidative TCA pathway. 2. Glyoxylate bypass pathway. 3. Reductive TCA pathway.

Ácidos orgânicos de importância econômica, produzidos por fungos



Cosméticos, medicina, alimentos, indústria química, agricultura

Indústrias alimentar, farmacêutica, têxtil, de couro e outras.

Agente acidulante, conservante, emulsionante, saborizante, sequestrante e tampão, utilizado em indústrias de alimentos, bebidas, armacêuticos, nutracêuticos e cosméticos

Resinas sintéticas, fibras sintéticas, plásticos, borrachas e aditivos de óleo

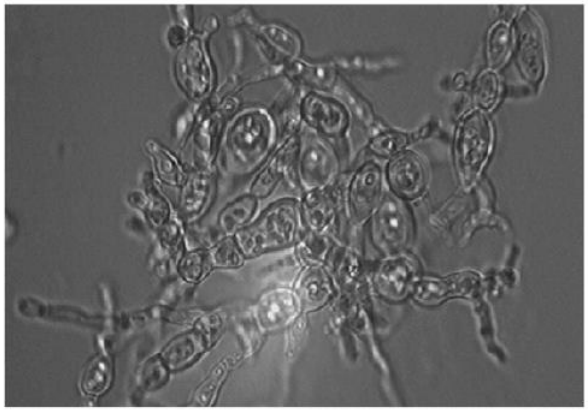
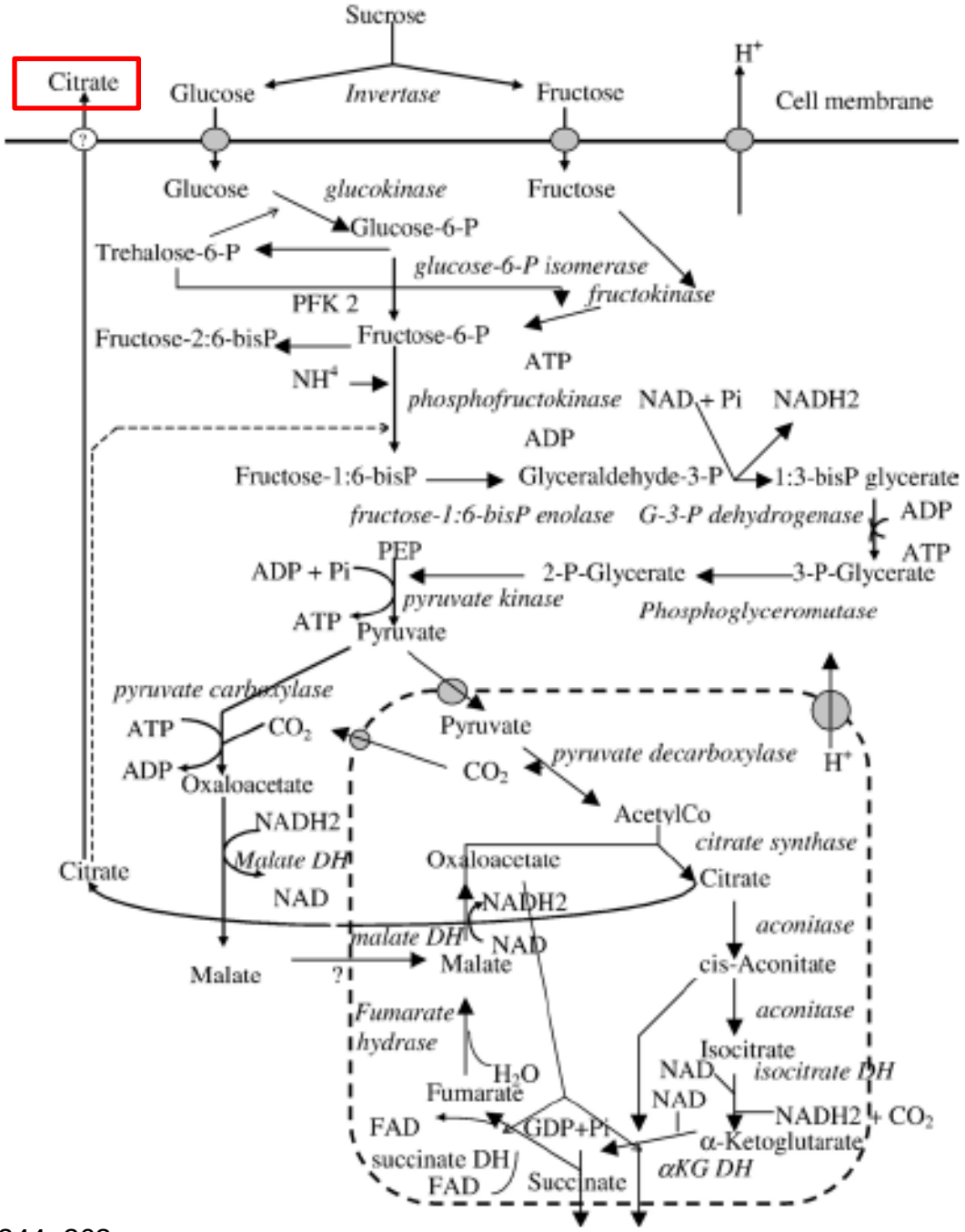


Fig. 2. Typical acidogenic mycelium of *A. niger* grown in manganese deficient medium in a stirred tank bioreactor under intensive agitation conditions (i.e. the average value of impeller power levels, expressed as energy dissipation/circulation function, was 29.0 ± 1.0 $kW \cdot m^{-3} s^{-1}$) and pH controlled at 2.0.

Citric acid overproduction requires a unique combination of several unusual nutrient conditions, i.e. excessive concentrations of carbon source, hydrogen ions, and dissolved oxygen, and suboptimal concentrations of certain trace metals and phosphate, that synergistically influence the yield of citric acid.



Papagianni, M. Biotechnology Advances 25 (2007) 244–263

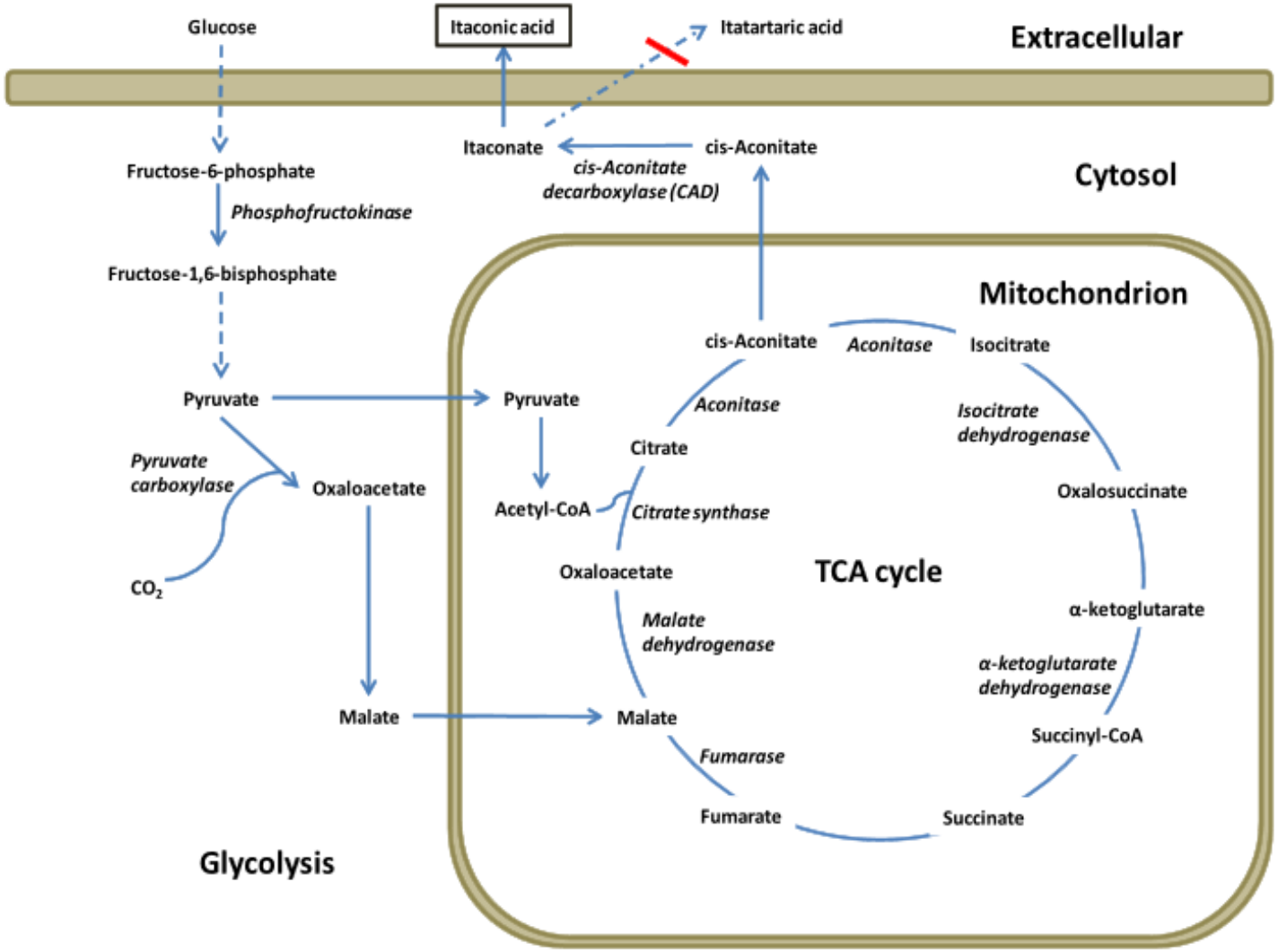


Fig. 1. Biosynthesis pathway of itaconic acid in *Aspergillus terreus*. Metabolites are given in normal font, enzymes are given in italic. The information was obtained from the studies of Jaklitsch et al. (1991), Bonnarme et al. (1995) and Li et al. (2011).

Table 4 Application of itaconic acid

Materials	Application	Reference
Vinylidene chloride containing below 2% IA	Improved adhesion to paper, cellophane	(Pitzl 1951)
Alkali salt of poly IA	detergent	(Lancashire 1969)
Rubber-like resin (Copolymer of IA)	Electrical insulation	(Smith et al. 1974)
N-substituted pyrrolidones (IA with amines)	Thickeners in lubricating grease, detergents, shampoos	(Gordon and Coupland 1980)
Imidazoline derivative	shampoos	(Christiansen 1980)
Polyacrylonitrile copolymer incorporating low level of IA	Efficient dying and deep shade in textile industry	(Tate 1981)
Copolymer of acrylic acid and IA	Scale inhibitor in boiler	(Walinsky 1984)
IA monoester compounds	Dental adhesives, dental fillers	(Saitoh et al. 1993)
Hardening agent	Contact lens	(Ellis et al. 1994)
Pigmented dispersion resins containing 0.1-1.5% IA	Wet abrasion resistance	(Zhao et al. 1999)
Styrene butadiene lattices containing 1-5% IA	Carpet backing or paper coating	(Willke and Vorlop, 2001)
Acrylic lattices supplemented with IA	Nonwoven fabric binder	(Willke and Vorlop, 2001)
Sulfonated poly IA	Industrial cleaner	(Willke and Vorlop, 2001)
N-vinyl 2-pyrrolidone/IA hydrogels	Antifungal drug	(Sen and Yakar 2001)
Poly(acrylamide-co-monomethyl itaconate) hydrogels	Transdermal therapy	(Blanco et al. 2003)
IA	Inhibitor of fructose 2,6-bisphosphate synthesis	(Sakai et al. 2004)
N-isopropylacrylamide/IA copolymeric hydrogels	Drug release	(Tasdelen et al. 2004)
Polycarboxylic acid nanoparticles	Ophthalmic drug delivery	(De et al. 2004)
Poly(acrylamide-co-IA) hydrogels	Drug delivery	(Stanojević et al., 2006)
Poly(acrylic acid-co-IA)	Glass-ionomer cements	(Culbertson 2006)
N-vinylcaprolactam-containing copolymer of acrylic-IA	Glass-ionomer dental cements	(Moshaverinia et al. 2009)

IA is an important intermediate in polymer production. It is extremely useful in the industrial production of synthetic resins, synthetic fibers, pesticides, plastic, rubbers, surfac-tants, ion-exchange agents, and lubricating oil additives.

Okabe, M. Appl Microbiol Biotechnol (2009) 84:597-606

Table 5 Supply of IA

Company	Location	Since	Capacity (tons/year)
Pfizer Food Science	New York, USA; Sandwick, UK	1945–1995	5,000–7,000[a]
Iwata Chemicals	Kyogyo, Japan	1970	10,000[b]
Tianli Biological Fermentation Factor	Yunnan, China	1988	2,000[c]
Gansu Feipeng Biochemical Co. Ltd.	Gansu, China	1989	1,000[c]
Chengdu Lake Biology Engineering Industry	Sichuan, China	1993	4,000[c]
Nanjing Huajin Biologicals Co. Ltd.	Nanjing, China	1994	1,000[c]
Jiangsu Binhai Sanai Biological Co. Ltd.	Jiangsu, China	1994	1,200[c]
Rhodia	Melle, France	1995	10,000[b]
Zhejiang Guoguang Biochemical Co. Ltd.	Zhejiang, China	1995	1,000[c]
Cargill/Cultor Food Science	Eddyville, USA	1996	30,000[b]
Shandong Zibo Zhongshun	Shandong, China	1999	1,200[c]
Science & Technology Co. Ltd. Diversified Co. of Zibo Mineral Bureau	Zibo, China	1999	3,000[c]
Guangdong Leizhou Yueli IA Co. Ltd.	Guangdong, China	1999	1,500[c]
Qingdao Langyatai Group	Qingdao, China	2000	4,500[c]

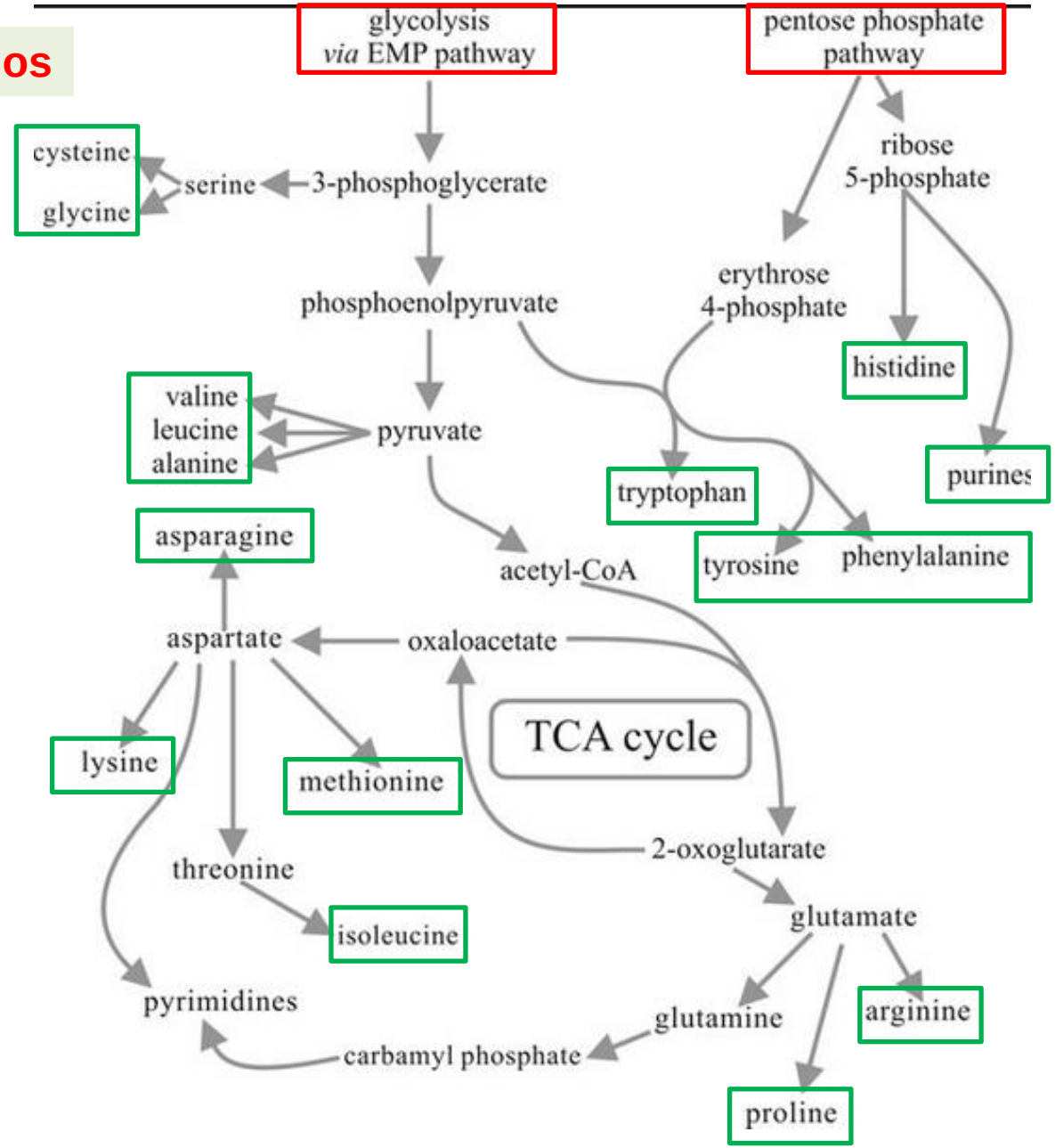
[a] Stop IA production from 1996

[b] T. Udagawa, 2009, private communication

[c] Source: http://www.thefreelibrary.com/Itaconic+acid+supply+exceeds+demand.+(Market+Report).-a091473938

Okabe, M. Appl Microbiol Biotechnol (2009) 84:597-606

Aminoácidos



https://www.davidmoore.org.uk/21st_century_guidebook_to_fungi_platinum/Ch10_12.htm

Recent advancements in the role of volatile organic compounds from fungi

Lourdes Macías-Rodríguez[1], Hexon Ángel Contreras-Cornejo[1], Jesús Salvador López-Bucio[2] and José López-Bucio[1]

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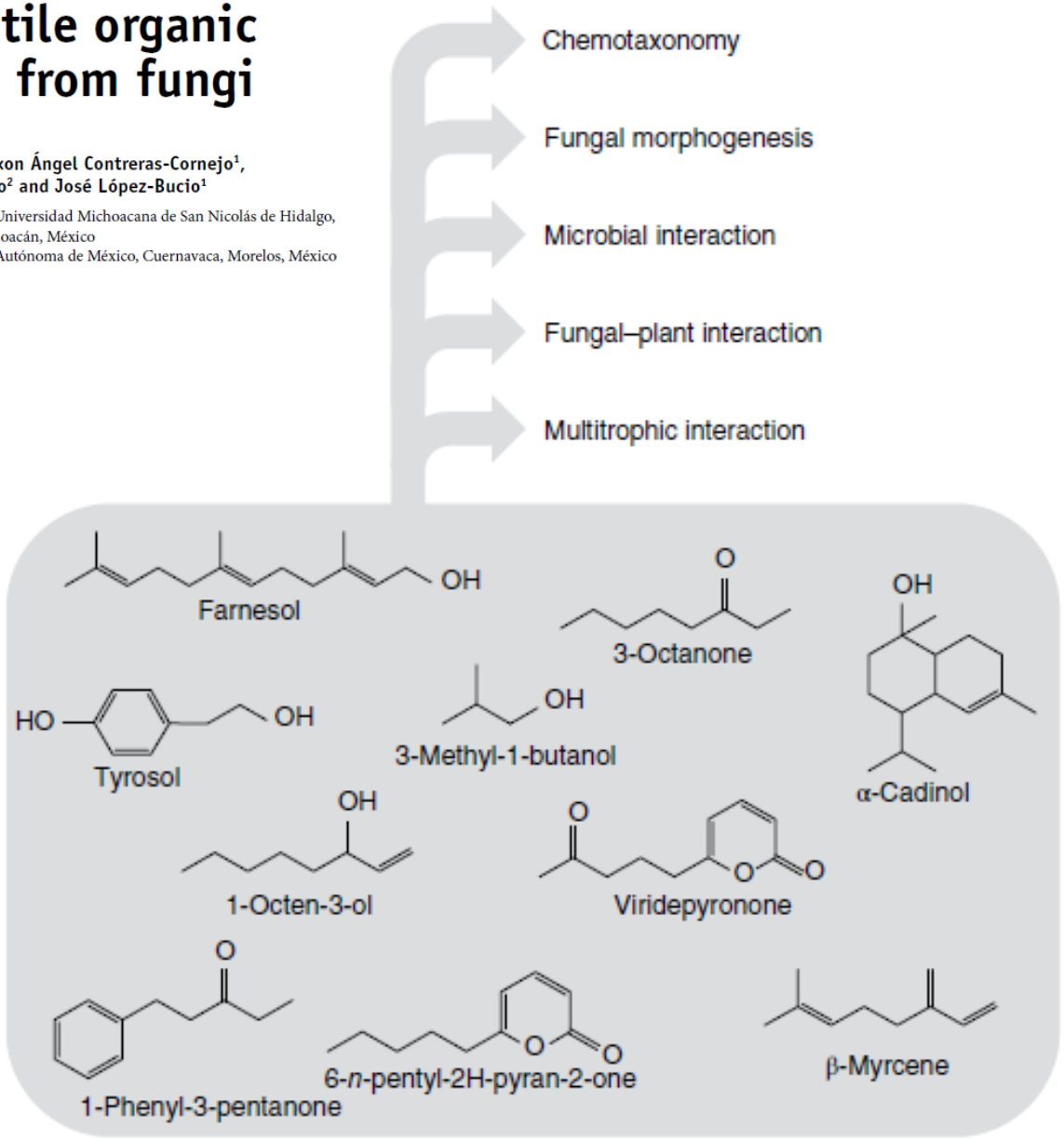
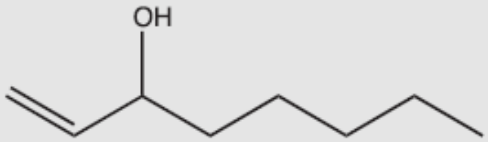
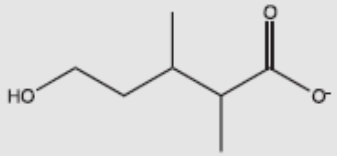
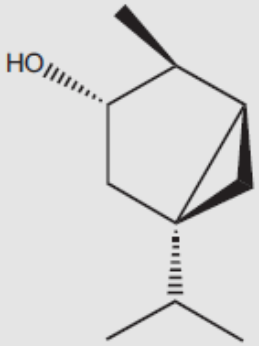
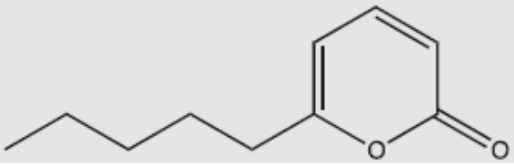
[2]Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México

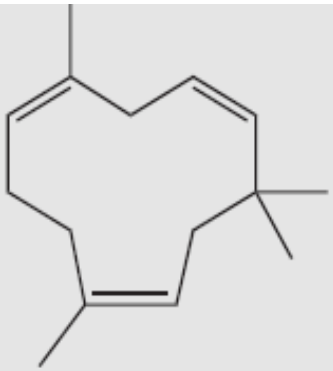
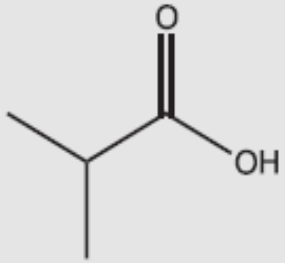
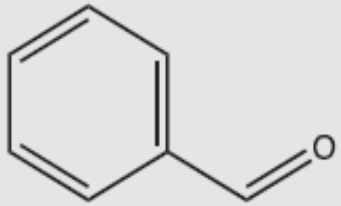
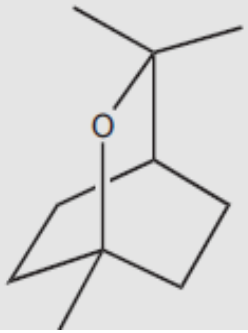


Fungal volatile organic compounds: A review with emphasis on their biotechnological potential

*Shannon U. MORATH, Richard HUNG, Joan W. BENNETT**

Table 1 — Structures, functions and odors of selected common volatile compounds produced by fungi.

Molecule	Structure	Potential Function(s); odors
1-Octen-3-ol		Semiochemical; earthy, "mushroomy" odor
1-Butanol-3-, methyl-, acetate		Antifungal; banana odor
Sabinene		Unknown; peppery odor
6-Pentyl-α-pyrone		Antibiotic; coconut odor

β-Caryophyllene		Plant-growth promoting; woody-spicy odor
Isobutyric acid		Antifungal; rancid cheese-like odor
Benzyl aldehyde		Anti-microbial; almond odor
1,8-Cineole		Antifungal; camphor-like odor

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2014

The story of mycodiesel

Gary Strobel

A identificação de uma série completa de derivados de alcano de cadeia linear de menor massa sendo produzida por um fungo endofítico sugeriu, pela primeira vez, que os micróbios possam ter a capacidade de produzir os esqueletos de carbono básicos que compõem o combustível para motores diesel e a mistura de VOC deste fungo foi denominada: Mycodiesel. Gliocladium roseum (NRRL 50072)

Time (min)	Relative area	Stds*†‡	Possible compound§	Mol. mass (Da)
1.603	5.4	‡	Oxirane, ethyl-	72.06
2.081	3.4	*†	Heptane, 2-methyl-§	114.14
2.666	14.1	*†	Octane§	114.14
3.138	15.5	*†	1-Octene§	112.13
4.598	24.5	*	Ethanol	46.04
4.872	1.2	*	Cyclohexene, 4-methyl-	96.09
5.204	13.5	‡	Hexane, 2,4-dimethyl- (possible isomer)	114.14
5.378	10.8		Undecane, 2,6-dimethyl-	184.22
5.533	13.5	‡	Hexadecane§ (possible isomer)	226.27
5.941	10.5		Heptane, 5-ethyl-2,2,3-trimethyl- (or isomer)	170.20
6.365	8.7	†	Undecane, 4-methyl-§	170.20
6.418	5.4		Heptane, 5-ethyl-2,2,3-trimethyl- (or isomer)	170.20
6.668	6.1		Octane, 3-ethyl-2,7-dimethyl-	170.20
6.768	12.1		Decane, 2,2,6-trimethyl-	184.22
6.931	6.8	*†	Undecane§	156.19
7.112	5.4		Decane, 3,3,5-trimethyl-	184.22
7.173	6.4	*	Nonane, 3-methyl-§	142.17
7.232	7.3	*	1-Propanol, 2-methyl-	74.07
7.325	10.0		Furan, 4-methyl-2-propyl-	124.09
7.481	6.7		Undecane, 4,4,-dimethyl-	184.22
7.648	13.3	*	1-Butanol, 3-methyl-, acetate	130.10
7.836	18.3	*	2-n-Butyl furan	124.09
8.026	10.8	†	Benzene, 1,3-dimethyl-§	106.08
8.114	12.2		Decane, 3,3,5-trimethyl-	184.22
8.303	11.4	*	Pentane, 1-iodo-	197.99
8.364	8.7	*	2-Hexanol	102.10
8.498	7.4	*	Acetic acid, pentyl ester	130.10
8.735	14.9	*	Hexanoic acid, methyl ester	130.10
9.066	11.5	*	1-Butanol, 3-methyl-	88.09

this organism produced an extensive series of the acetic acid esters of straight-chained alkanes including those of pentyl, hexyl, heptyl, octyl, sec-octyl and decyl alcohols. Other hydrocarbons: undecane, 2,6-dimethyl; decane, 3,3,5-trimethyl; cyclohexene, 4-methyl; decane, 3,3,6-trimethyl; and undecane, 4,4-dimethyl.

Lipids of Filamentous Fungi as a Material for Producing Biodiesel Fuel

Ya. E. Sergeeva, L. A. Galanina, D. A. Andrianova, and E. P. Feofilova

Fungal strains under study and their ability to produce lipids

Strain	Biomass, g/l	Lipids	
		%	g/l
Zygomycetes			
Absidia cerulea VKM F-858(+)	6.2	12.8	0.79
Cunninghamella echinulata F-470(–)	7.1	43.0	3.05
C.echinulata F-626(–)	6.9	47.1	3.23
C.echinulata F-657(–)	6.5	48.6	3.15
C.japonica VKM F-1204(–)	10.5	50.7	5.32
Ascomycetes			
Aspergillus niger VKM F-33	10.0	11.2	1.12
A.japonicus VKM F-2632D	8.6	13.5	1.16
Penicillium chrysogenum, strain from the Chair of Mycology, Moscow University	15.3	5.3	0.81
P.expansum, strain from the Winogradsky Institute	1.57	3.91	0.06
P. lanosum VKM F-297	6.96	22.78	1.56
P. lanosum VKM F-304	2.14	8.62	0.18
P. lanosum VKM F-1556	6.5	19.9	1.29
P.lanosum VKM F-1956	6.3	14.18	0.89
P.luteum VKM F-307	2.87	5.8	0.17
Basidiomycetes			
Aqaricua bisporus	–	4.0	–
Pleurotus ostreatus	–	5.0	–

Fungal biotechnology: From yesterday to tomorrow

Mitchell G. Roth[1], Nathaniel M. Westrick[2] and Thomas T. Baldwin[3*]

3.3 Fungal batteries

The future of fungal applications is electric! Though passionate mycologists are likely to agree figuratively, this can also be taken quite literally. The porous structure of mushroom flesh can be processed into carbon-rich, porous nano-ribbons, providing unique qualities and abilities to hold and release electrical currents, providing great potential to improve ion flow in Lithium-sulfur batteries (Campbell et al., 2015; Wu et al., 2016). Further, the classic "toadstool" mushroom, *Amanita muscaria*, and others in the *Amanita* genus frequently produce a compound called Amavadin, which has a vanadium ion in its core. Vanadium is relatively rare in nature, but has tremendous potential to contribute to the next generation of battery production *via* redox flow batteries (Kim et al., 2015; Egitto et al., 2022). Investigating ways to promote vanadium accumulation in mushrooms provides a promising avenue for producing more efficient and sustainable batteries in a world that is becoming more dependent upon electricity and the storage of electrical power.

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