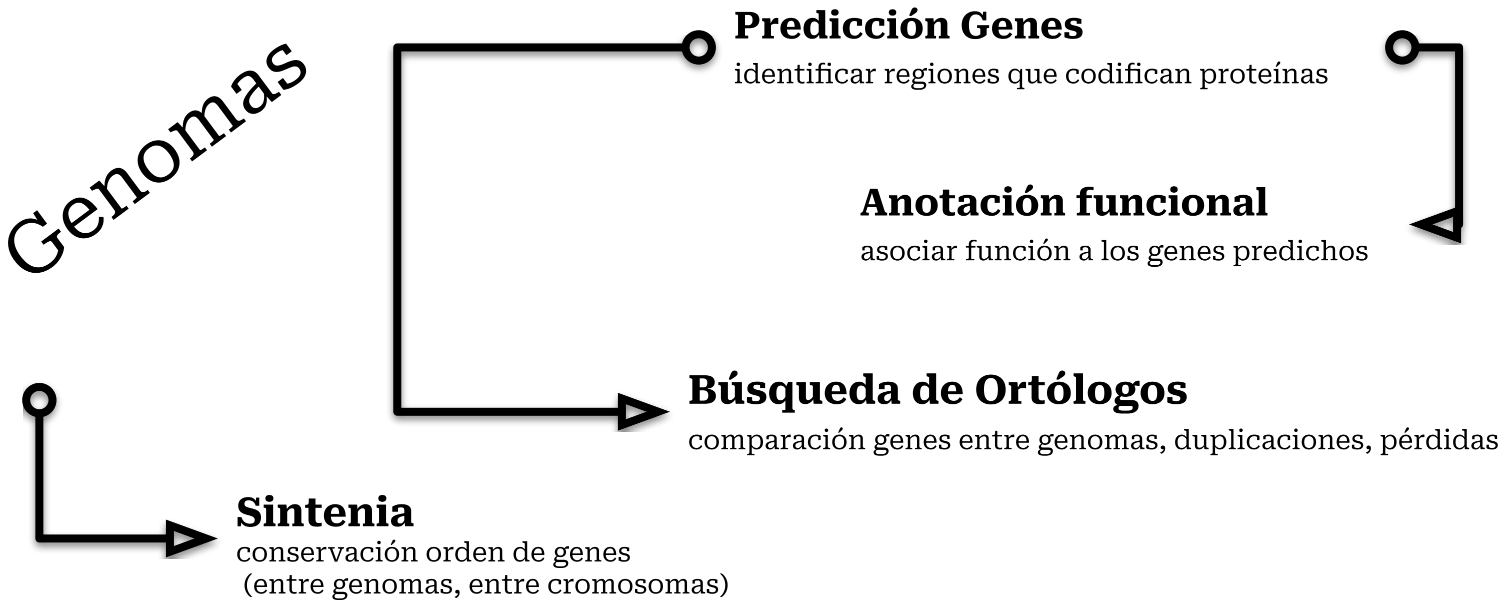
Curso Evolución

Práctico 10 Genómica

Diagrama de pipeline a seguir…**(o que queremos)**



Genomas

Predicción Genes

identificar regiones que codifican proteínas

Anotación funcional

asociar función a los genes predichos

Búsqueda de Ortólogos

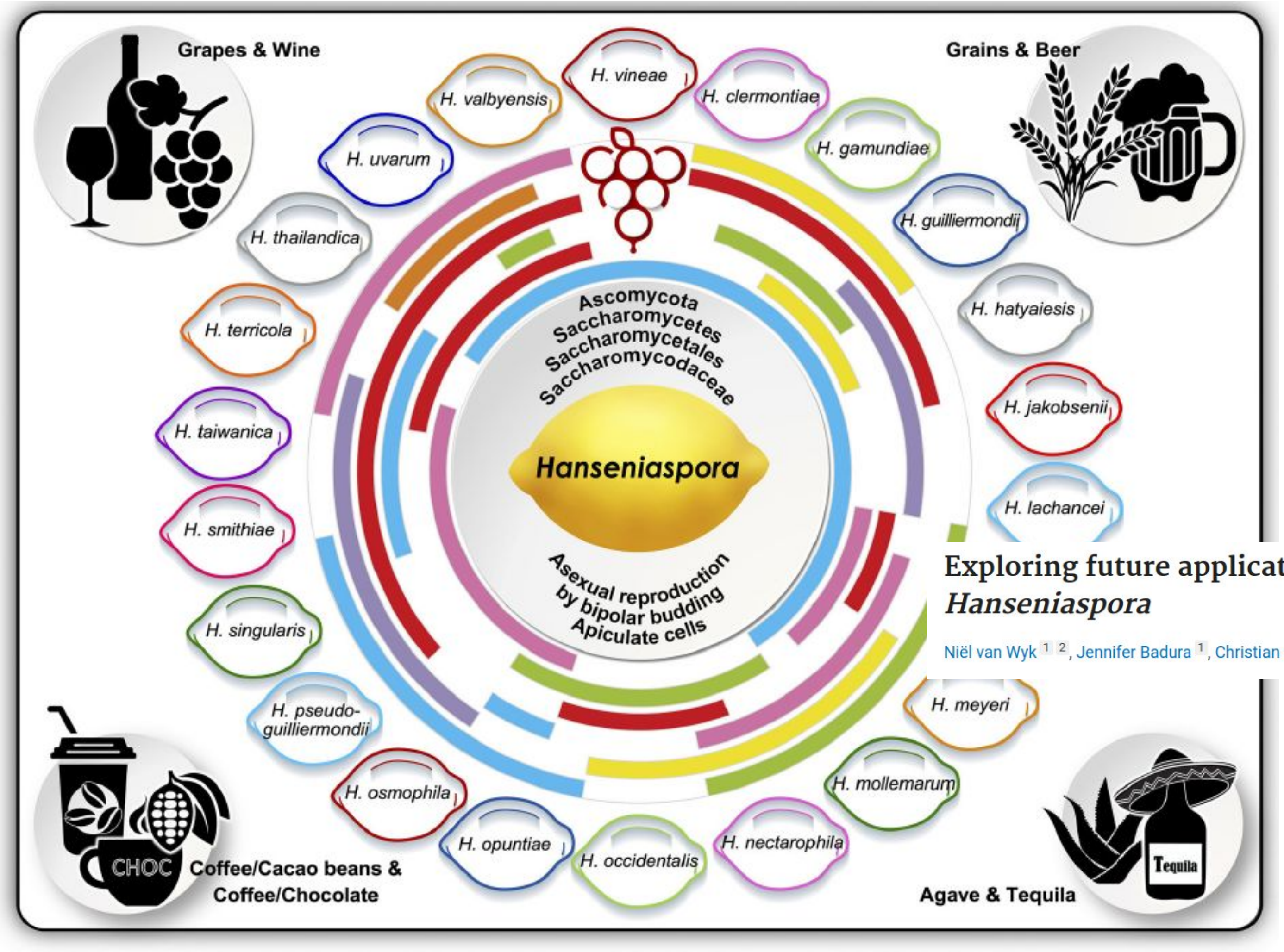
comparación genes entre genomas, duplicaciones, pérdidas

Sintenia

conservación orden de genes
(entre genomas, entre cromosomas)


INSTANT YEAST - LEVURE INSTANTANÉE
LEVADURA INSTANTÁNEA
saf
saf-instant®
NET WEIGHT
POIDS NET
CONTENIDO NETO
16 oz (1 lb) 454 g
LESAFFRE

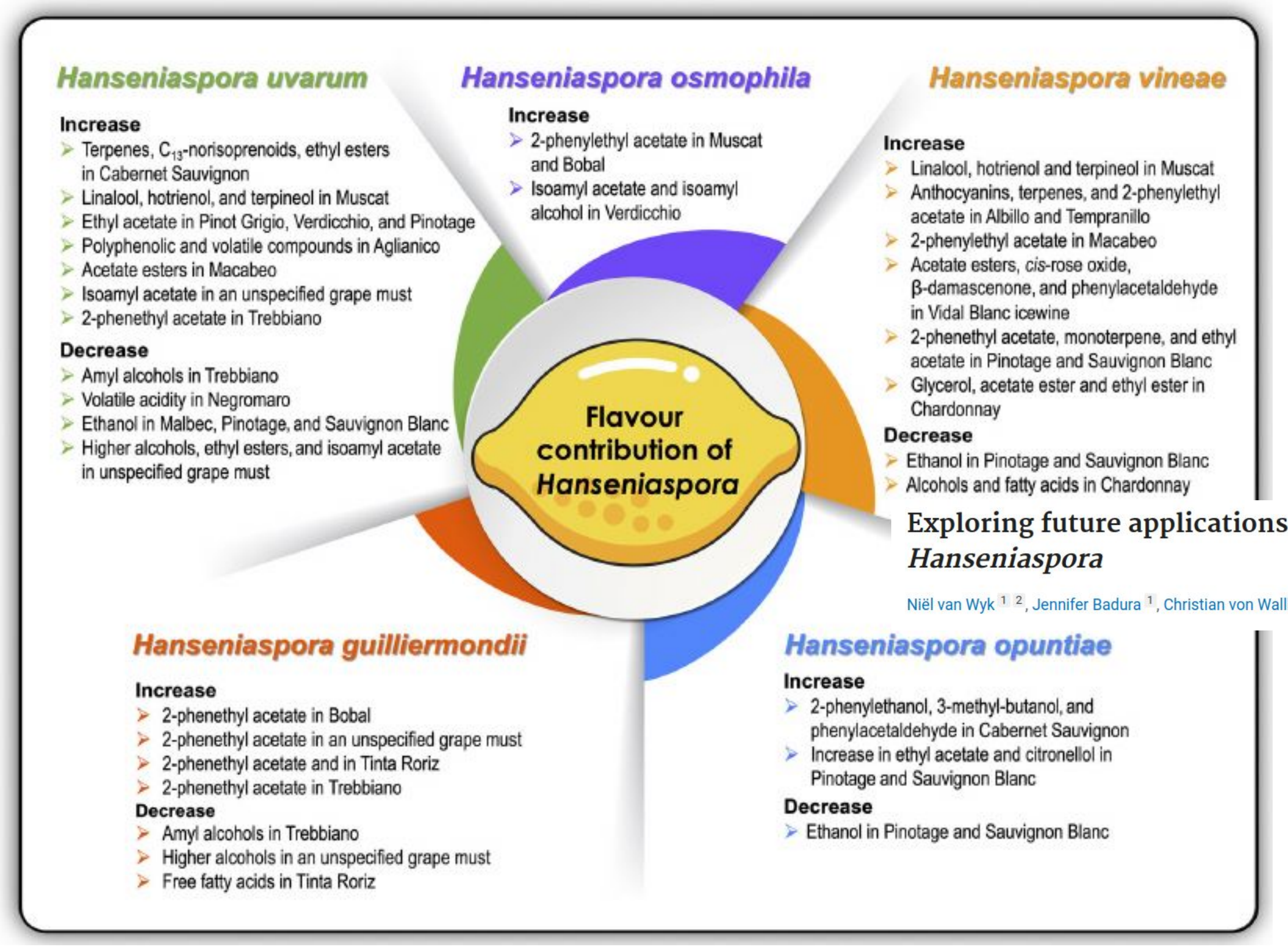
Diversidad, usos, utilidad...



Exploring future applications of the apiculate yeast *Hanseniaspora*

Niël van Wyk [1] [2], Jennifer Badura [1], Christian von Wallbrunn [1], Isak S Pretorius [2]

usos, fermentación



Flavour contribution of *Hanseniaspora*

Hanseniaspora uvarum

Increase
- Terpenes, C_{13}-norisoprenoids, ethyl esters in Cabernet Sauvignon
- Linalool, hotrienol, and terpineol in Muscat
- Ethyl acetate in Pinot Grigio, Verdicchio, and Pinotage
- Polyphenolic and volatile compounds in Aglianico
- Acetate esters in Macabeo
- Isoamyl acetate in an unspecified grape must
- 2-phenethyl acetate in Trebbiano

Decrease
- Amyl alcohols in Trebbiano
- Volatile acidity in Negromaro
- Ethanol in Malbec, Pinotage, and Sauvignon Blanc
- Higher alcohols, ethyl esters, and isoamyl acetate in unspecified grape must

Hanseniaspora osmophila

Increase
- 2-phenylethyl acetate in Muscat and Bobal
- Isoamyl acetate and isoamyl alcohol in Verdicchio

Hanseniaspora vineae

Increase
- Linalool, hotrienol and terpineol in Muscat
- Anthocyanins, terpenes, and 2-phenylethyl acetate in Albillo and Tempranillo
- 2-phenylethyl acetate in Macabeo
- Acetate esters, *cis*-rose oxide, β-damascenone, and phenylacetaldehyde in Vidal Blanc icewine
- 2-phenethyl acetate, monoterpene, and ethyl acetate in Pinotage and Sauvignon Blanc
- Glycerol, acetate ester and ethyl ester in Chardonnay

Decrease
- Ethanol in Pinotage and Sauvignon Blanc
- Alcohols and fatty acids in Chardonnay

Hanseniaspora guilliermondii

Increase
- 2-phenethyl acetate in Bobal
- 2-phenethyl acetate in an unspecified grape must
- 2-phenethyl acetate and in Tinta Roriz
- 2-phenethyl acetate in Trebbiano

Decrease
- Amyl alcohols in Trebbiano
- Higher alcohols in an unspecified grape must
- Free fatty acids in Tinta Roriz

Hanseniaspora opuntiae

Increase
- 2-phenylethanol, 3-methyl-butanol, and phenylacetaldehyde in Cabernet Sauvignon
- Increase in ethyl acetate and citronellol in Pinotage and Sauvignon Blanc

Decrease
- Ethanol in Pinotage and Sauvignon Blanc

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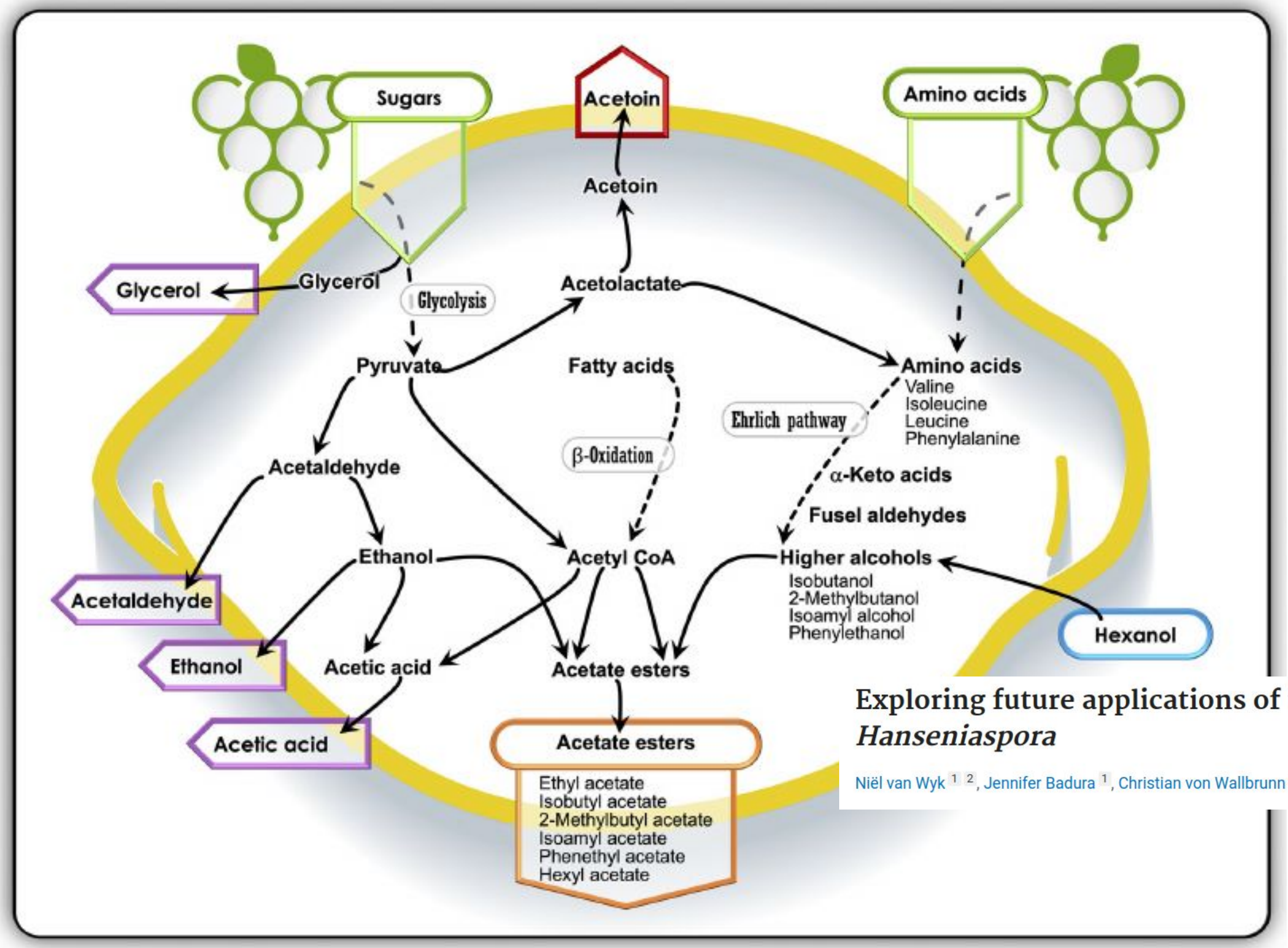
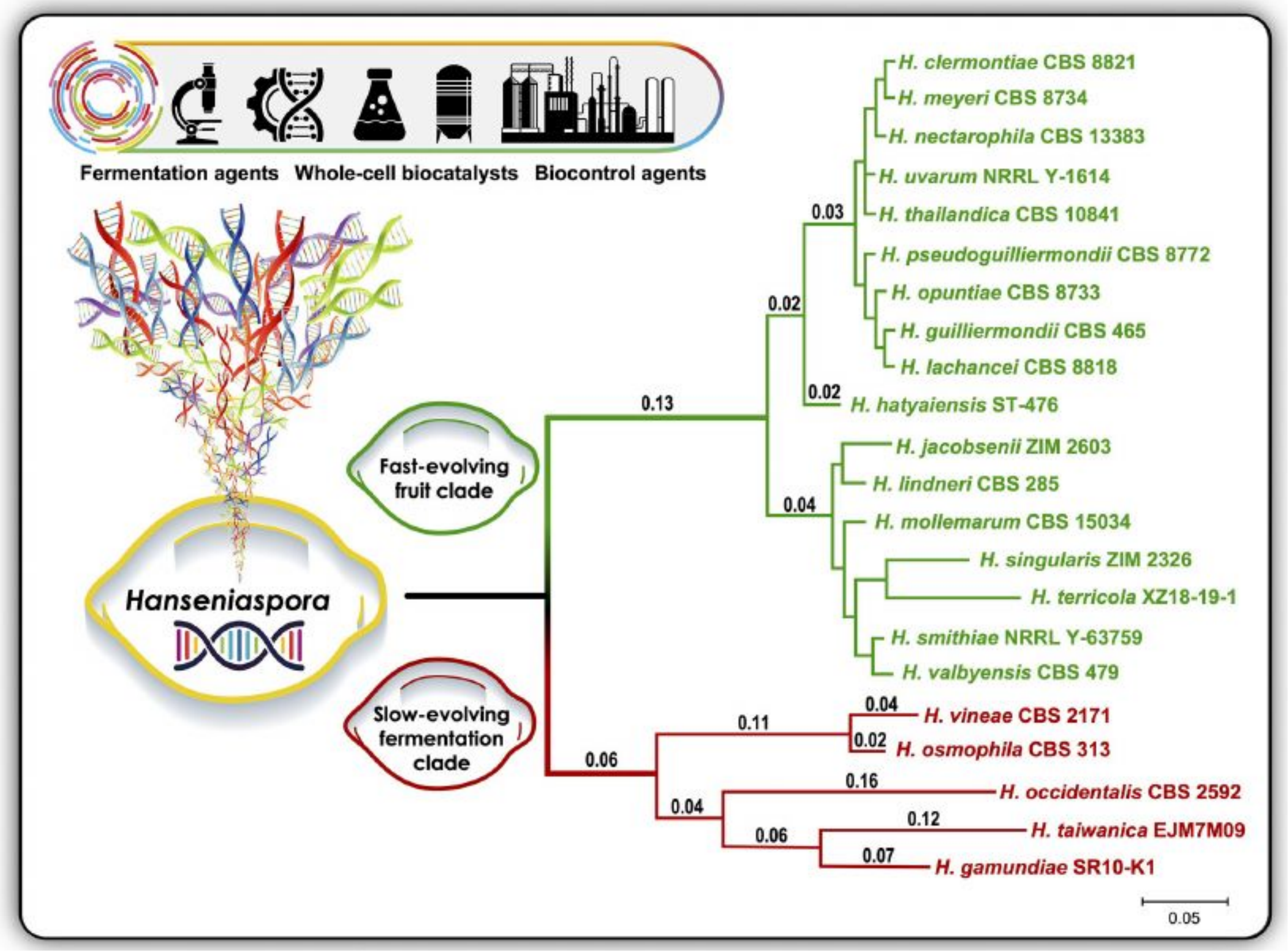
Aromas...metabolismo... arsenal químico



Exploring future applications of the apiculate yeast *Hanseniaspora*

Niël van Wyk [1] [2], Jennifer Badura [1], Christian von Wallbrunn [1], Isak S Pretorius [2]

divergencia enorme en el grupo



algo más local...

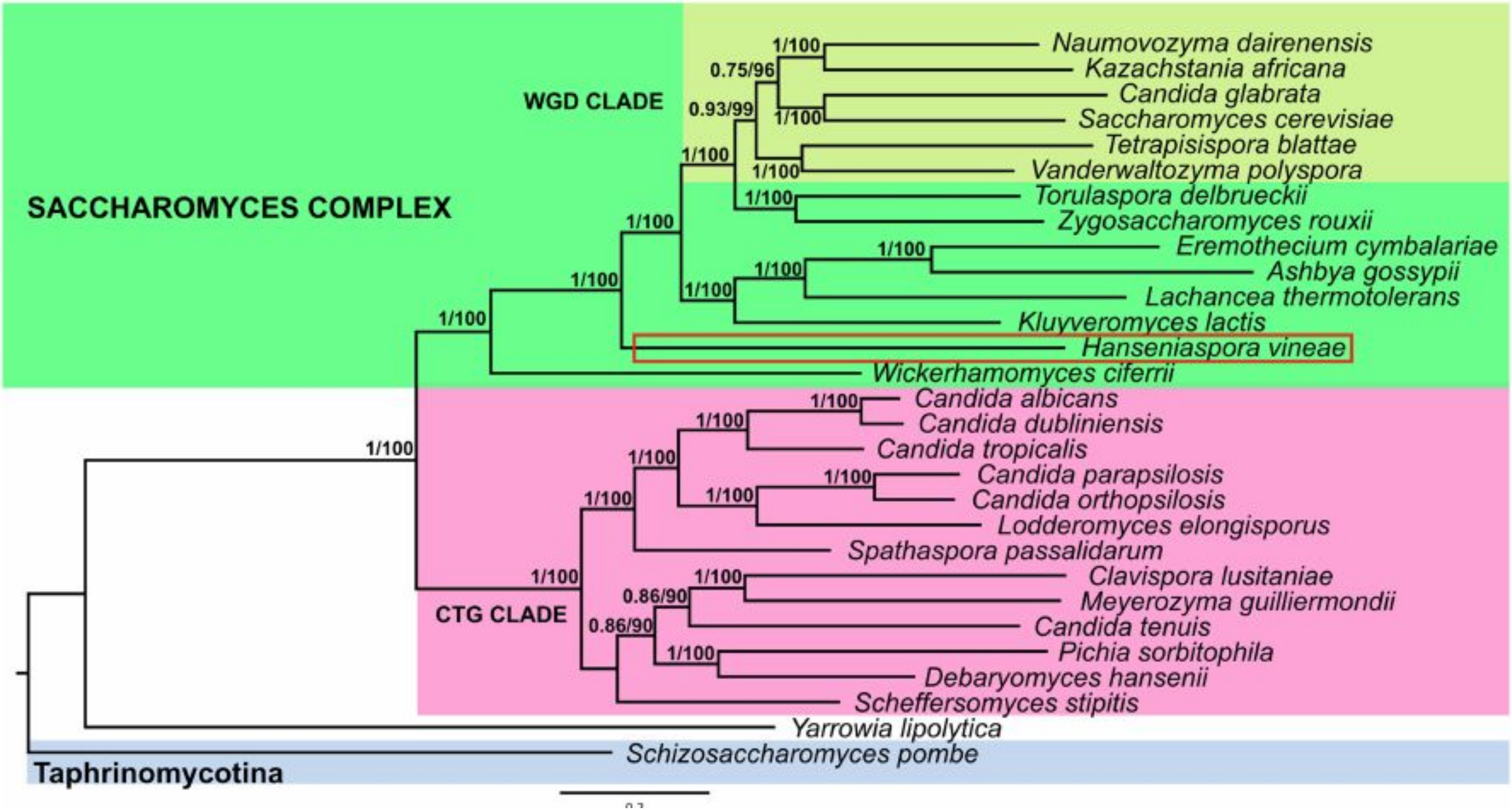
GENETICS AND MOLECULAR BIOLOGY

Genomic and Transcriptomic Basis of *Hanseniaspora vineae*'s Impact on Flavor Diversity and Wine Quality

Facundo Giorello,[a,b] Maria Jose Valera,[b] Valentina Martin,[b] Andres Parada,[c] Valentina Salzman,[d] Laura Camesasca,[e] Laura Fariña,[b] Eduardo Boido,[b] Karina Medina,[b] Eduardo Dellacassa,[f] Luisa Berna,[d] Pablo S. Aguilar,[d,g] Albert Mas,[h] Carina Gaggero,[e] Francisco Carrau[b] algo más local...

ABSTRACT *Hanseniaspora* is the main genus of the apiculate yeast group that represents approximately 70% of the grape-associated microflora. *Hanseniaspora vineae* is emerging as a promising species for quality wine production compared to other non-Saccharomyces species. Wines produced by *H. vineae* with *Saccharomyces cerevisiae* consistently exhibit more intense fruity flavors and complexity than wines produced by *S. cerevisiae* alone. In this work, genome sequencing, assembling, and phylogenetic analysis of two strains of *H. vineae* showed that it is a member of the *Saccharomyces* complex and it diverged before the whole-genome duplication (WGD) event from this clade. Specific flavor gene duplications and absences were identified in the *H. vineae* genome compared to 14 fully sequenced industrial *S. cerevisiae* genomes. The increased formation of 2-phenylethyl acetate and phenyl-propanoids such as 2-phenylethyl and benzyl alcohols might be explained by gene duplications of H. vineae aromatic amino acid aminotransferases (ARO8 and ARO9) and phenylpyruvate decarboxylases (ARO10). Transcriptome and aroma profiles under fermentation conditions confirmed these genes were highly expressed at the beginning of stationary phase coupled to the production of their related compounds. The extremely high level of acetate esters produced by *H. vineae* compared to that by *S. cerevisiae* is consistent with the identification of six novel proteins with alcohol acetyltransferase (AATase) domains. The absence of the branched-chain amino acid transaminases (BAT2) and acyl coenzyme A (acyl-CoA)/ethanol O-acyltransferases (EEB1) genes correlates with *H. vineae*'s reduced production of branched-chain higher alcohols, fatty acids, and ethyl esters, respectively. Our study provides sustenance for understanding and potentially utilizing genes that determine fermentation aromas.

Paper Giorello et al.



Posición filogenética de H. vineae (Giorello et al. 2019)

Paper Giorello et al.

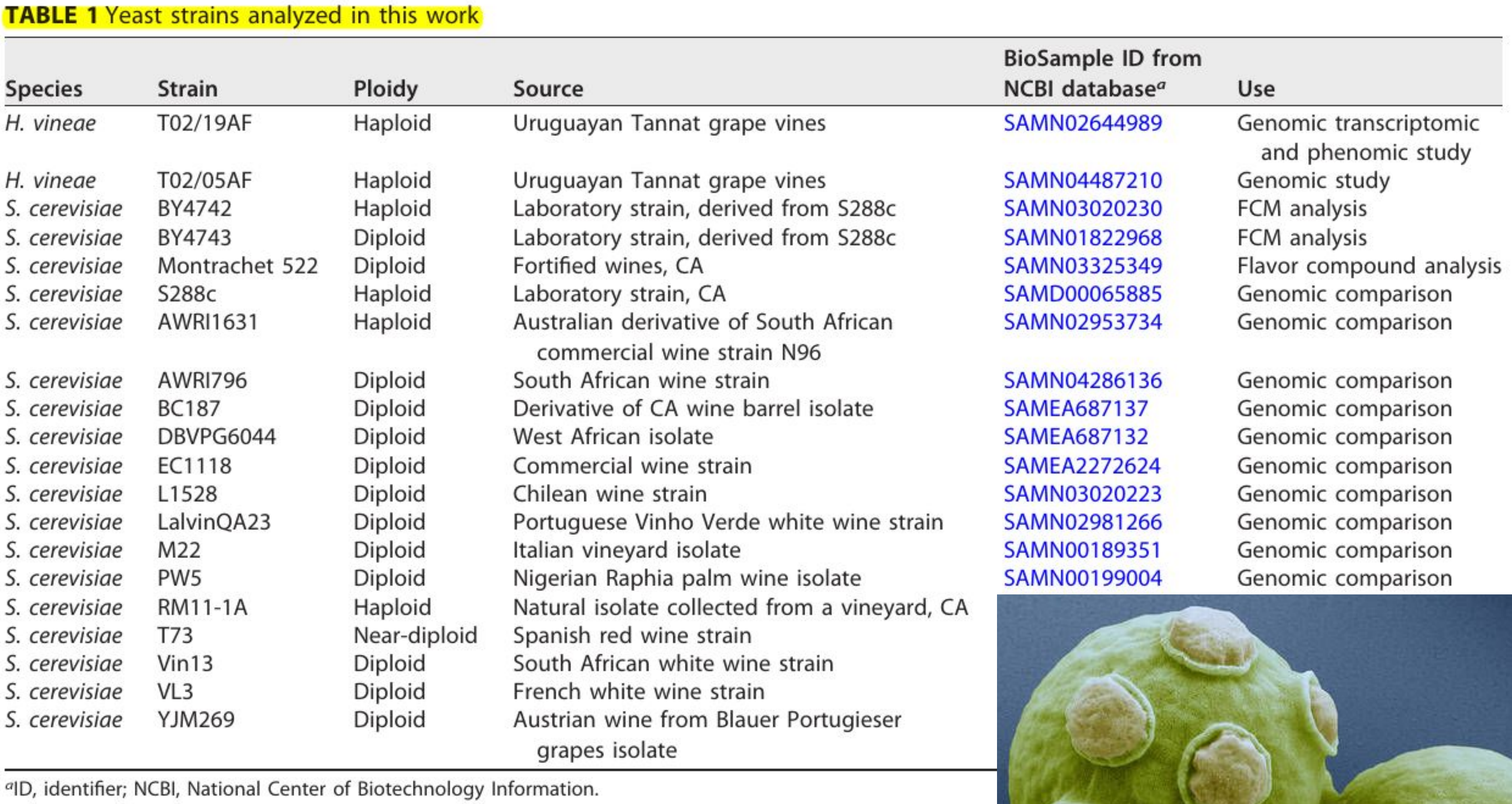


TABLE 1 Yeast strains analyzed in this work

Species	Strain	Ploidy	Source	BioSample ID from NCBI database[a]	Use
H. vineae	T02/19AF	Haploid	Uruguayan Tannat grape vines	SAMN02644989	Genomic transcriptomic and phenomic study
H. vineae	T02/05AF	Haploid	Uruguayan Tannat grape vines	SAMN04487210	Genomic study
S. cerevisiae	BY4742	Haploid	Laboratory strain, derived from S288c	SAMN03020230	FCM analysis
S. cerevisiae	BY4743	Diploid	Laboratory strain, derived from S288c	SAMN01822968	FCM analysis
S. cerevisiae	Montrachet 522	Diploid	Fortified wines, CA	SAMN03325349	Flavor compound analysis
S. cerevisiae	S288c	Haploid	Laboratory strain, CA	SAMD00065885	Genomic comparison
S. cerevisiae	AWRI1631	Haploid	Australian derivative of South African commercial wine strain N96	SAMN02953734	Genomic comparison
S. cerevisiae	AWRI796	Diploid	South African wine strain	SAMN04286136	Genomic comparison
S. cerevisiae	BC187	Diploid	Derivative of CA wine barrel isolate	SAMEA687137	Genomic comparison
S. cerevisiae	DBVPG6044	Diploid	West African isolate	SAMEA687132	Genomic comparison
S. cerevisiae	EC1118	Diploid	Commercial wine strain	SAMEA2272624	Genomic comparison
S. cerevisiae	L1528	Diploid	Chilean wine strain	SAMN03020223	Genomic comparison
S. cerevisiae	LalvinQA23	Diploid	Portuguese Vinho Verde white wine strain	SAMN02981266	Genomic comparison
S. cerevisiae	M22	Diploid	Italian vineyard isolate	SAMN00189351	Genomic comparison
S. cerevisiae	PW5	Diploid	Nigerian Raphia palm wine isolate	SAMN00199004	Genomic comparison
S. cerevisiae	RM11-1A	Haploid	Natural isolate collected from a vineyard, CA		
S. cerevisiae	T73	Near-diploid	Spanish red wine strain		
S. cerevisiae	Vin13	Diploid	South African white wine strain		
S. cerevisiae	VL3	Diploid	French white wine strain		
S. cerevisiae	YJM269	Diploid	Austrian wine from Blauer Portugieser grapes isolate		

[a] ID, identifier; NCBI, National Center of Biotechnology Information.

Genomas de levaduras

Genes asociados a fermentación y sabor

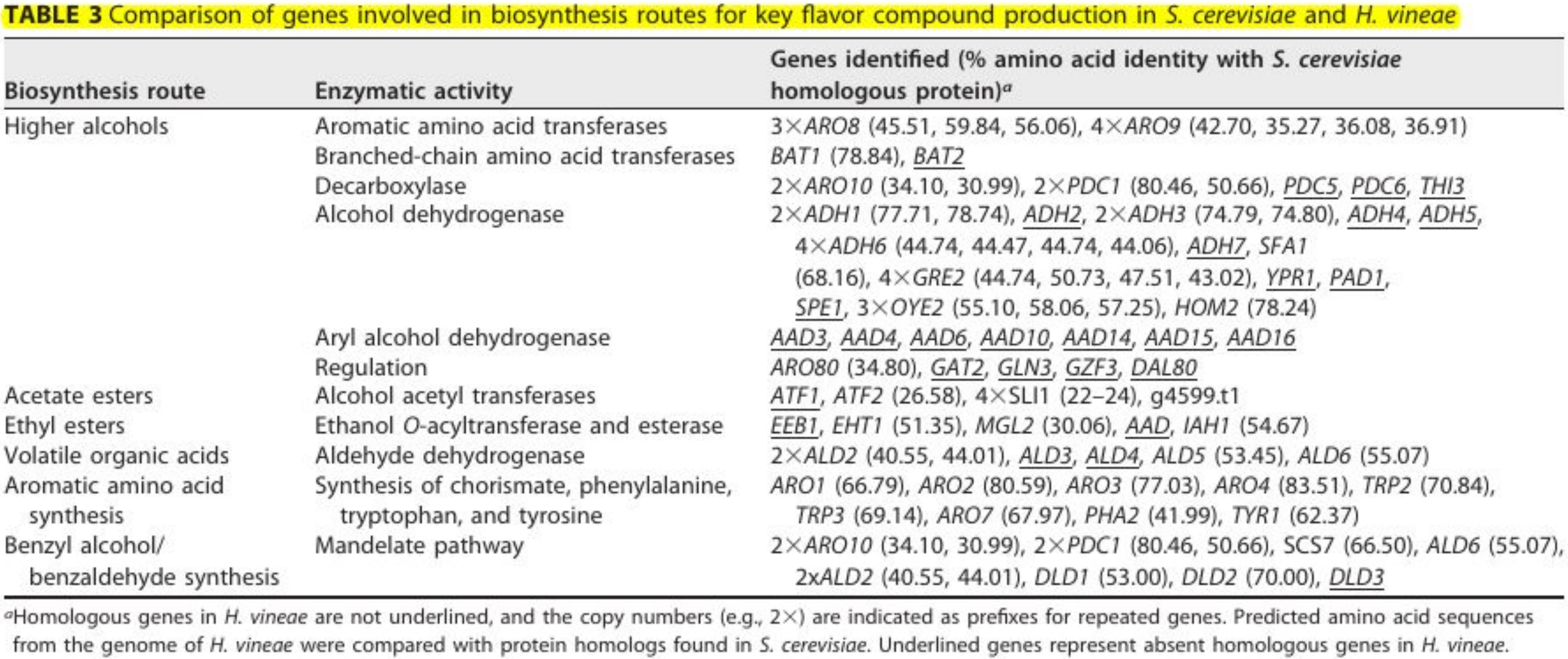
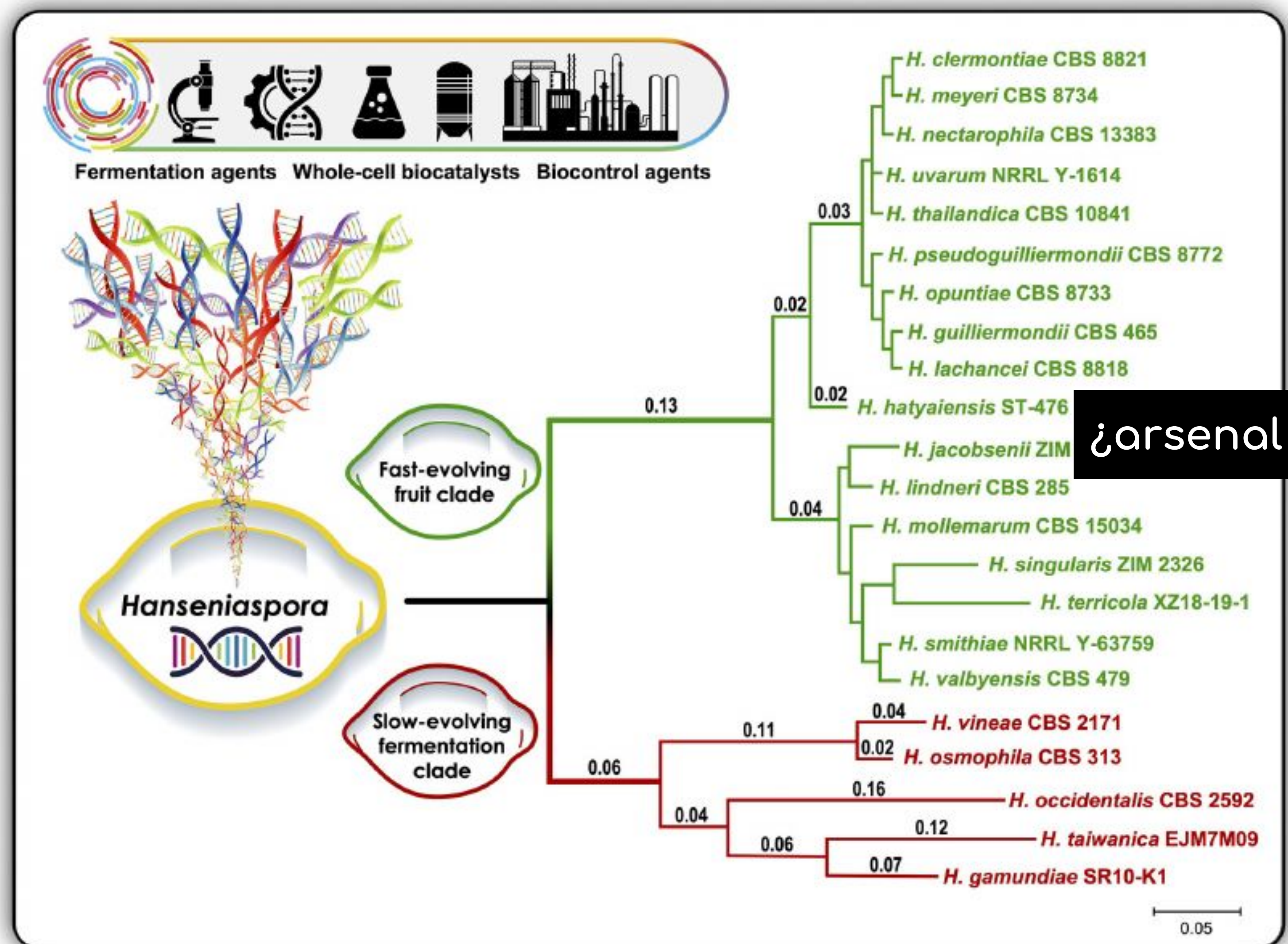


TABLE 3 Comparison of genes involved in biosynthesis routes for key flavor compound production in *S. cerevisiae* and *H. vineae*

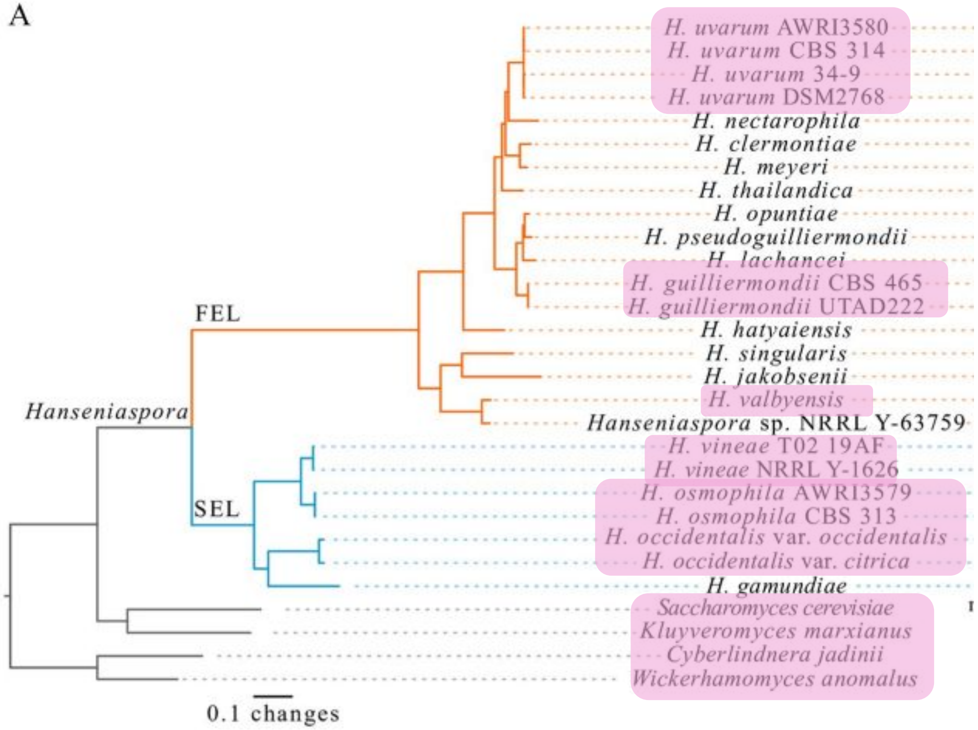
Biosynthesis route	Enzymatic activity	Genes identified (% amino acid identity with *S. cerevisiae* homologous protein)[a]
Higher alcohols	Aromatic amino acid transferases	3×*ARO8* (45.51, 59.84, 56.06), 4×*ARO9* (42.70, 35.27, 36.08, 36.91)
	Branched-chain amino acid transferases	*BAT1* (78.84), *BAT2*
	Decarboxylase	2×*ARO10* (34.10, 30.99), 2×*PDC1* (80.46, 50.66), *PDC5*, *PDC6*, *THI3*
	Alcohol dehydrogenase	2×*ADH1* (77.71, 78.74), *ADH2*, 2×*ADH3* (74.79, 74.80), *ADH4*, *ADH5*, 4×*ADH6* (44.74, 44.47, 44.74, 44.06), *ADH7*, *SFA1* (68.16), 4×*GRE2* (44.74, 50.73, 47.51, 43.02), *YPR1*, *PAD1*, *SPE1*, 3×*OYE2* (55.10, 58.06, 57.25), *HOM2* (78.24)
	Aryl alcohol dehydrogenase	*AAD3*, *AAD4*, *AAD6*, *AAD10*, *AAD14*, *AAD15*, *AAD16*
	Regulation	*ARO80* (34.80), *GAT2*, *GLN3*, *GZF3*, *DAL80*
Acetate esters	Alcohol acetyl transferases	*ATF1*, *ATF2* (26.58), 4×SLI1 (22–24), g4599.t1
Ethyl esters	Ethanol *O*-acyltransferase and esterase	*EEB1*, *EHT1* (51.35), *MGL2* (30.06), *AAD*, *IAH1* (54.67)
Volatile organic acids	Aldehyde dehydrogenase	2×*ALD2* (40.55, 44.01), *ALD3*, *ALD4*, *ALD5* (53.45), *ALD6* (55.07)
Aromatic amino acid synthesis	Synthesis of chorismate, phenylalanine, tryptophan, and tyrosine	*ARO1* (66.79), *ARO2* (80.59), *ARO3* (77.03), *ARO4* (83.51), *TRP2* (70.84), *TRP3* (69.14), *ARO7* (67.97), *PHA2* (41.99), *TYR1* (62.37)
Benzyl alcohol/ benzaldehyde synthesis	Mandelate pathway	2×*ARO10* (34.10, 30.99), 2×*PDC1* (80.46, 50.66), SCS7 (66.50), *ALD6* (55.07), 2x*ALD2* (40.55, 44.01), *DLD1* (53.00), *DLD2* (70.00), *DLD3*

[a] Homologous genes in *H. vineae* are not underlined, and the copy numbers (e.g., 2×) are indicated as prefixes for repeated genes. Predicted amino acid sequences from the genome of *H. vineae* were compared with protein homologs found in *S. cerevisiae*. Underlined genes represent absent homologous genes in *H. vineae*.

Paper Giorello et al.



¿arsenal difiere?



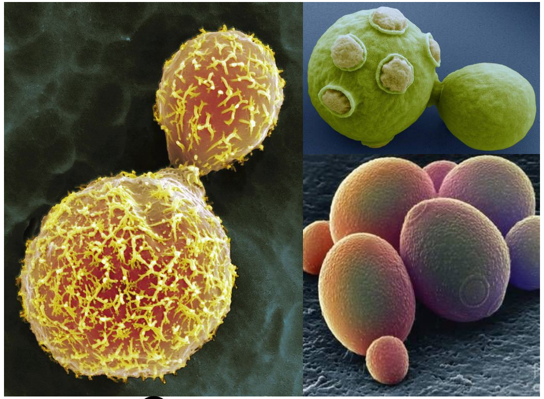
Spp a incluir **hoy**

- ☐ *Hanseniaspora uvarum*
- ☐ *Hanseniaspora guilliermondii*
- ☐ *Hanseniaspora valbyensis*
- ☐ *Hanseniaspora vineae*
- ☐ *Hanseniaspora occidentalis*
- ☐ *Hanseniaspora osmophila*

- ☐ *Cyberlindnera jadinii*
- ☐ *Kazachstania servazzii*
- ☐ *Saccharomyces cerevisiae*
- ☐ *Wickerhamomyces anomalus*

Diagrama de pipeline a seguir…**(o que queremos)**

Genomas



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Búsqueda de Ortólogos
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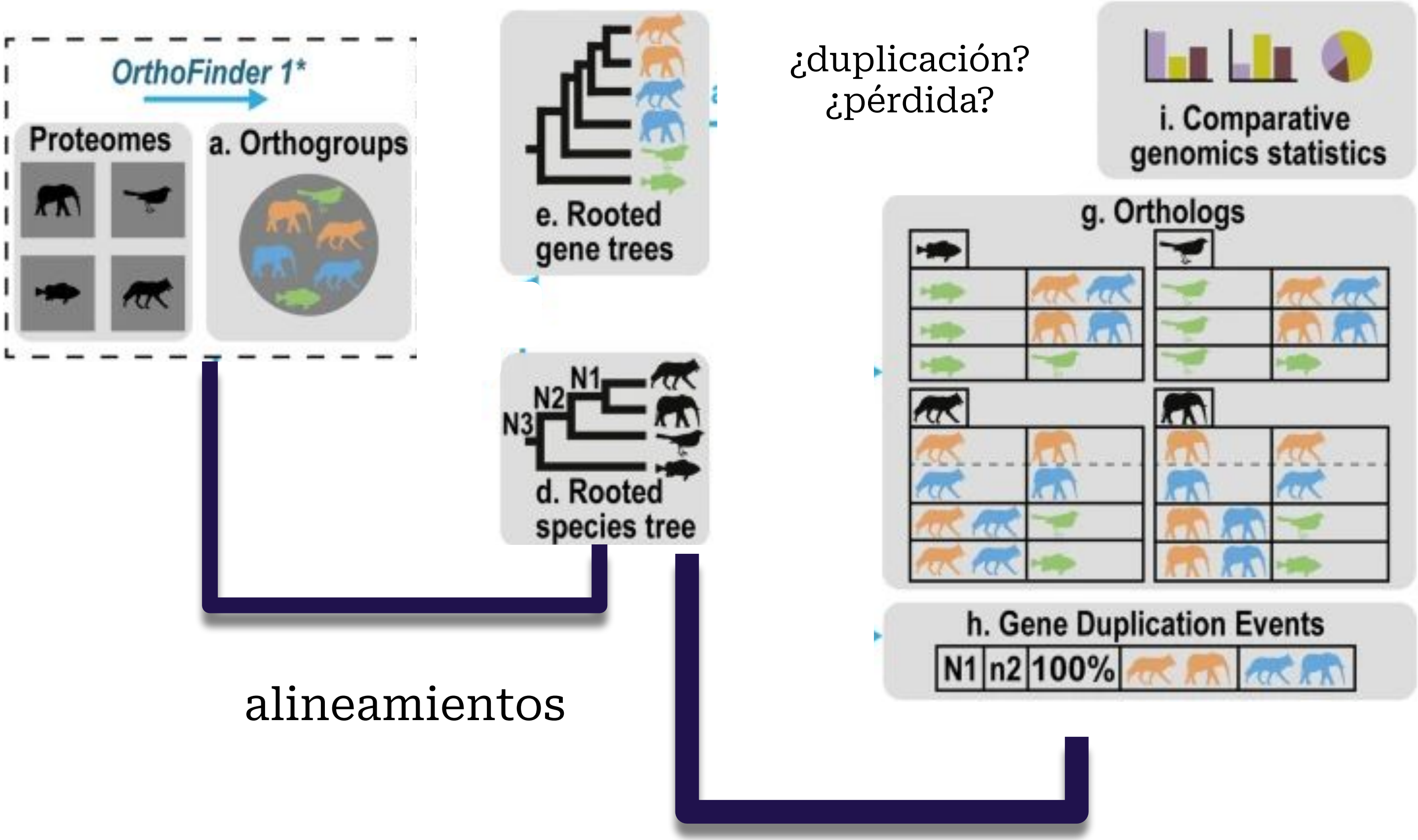
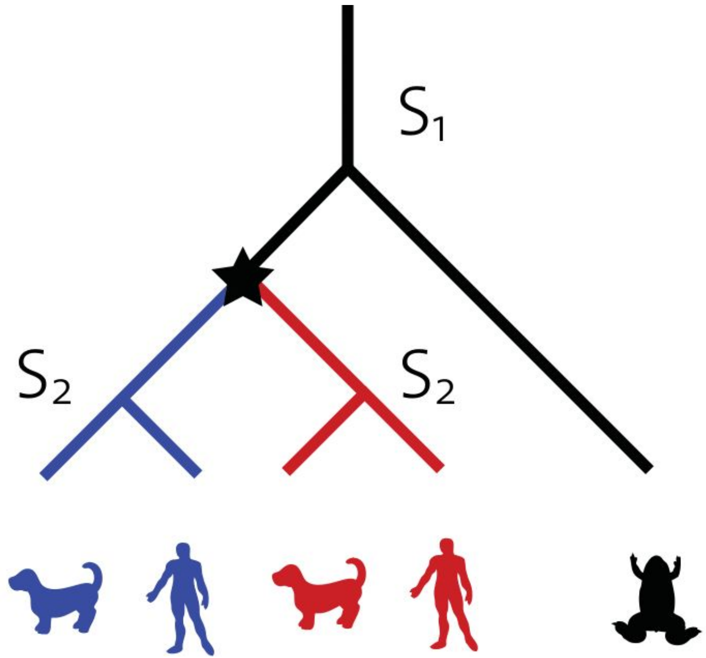


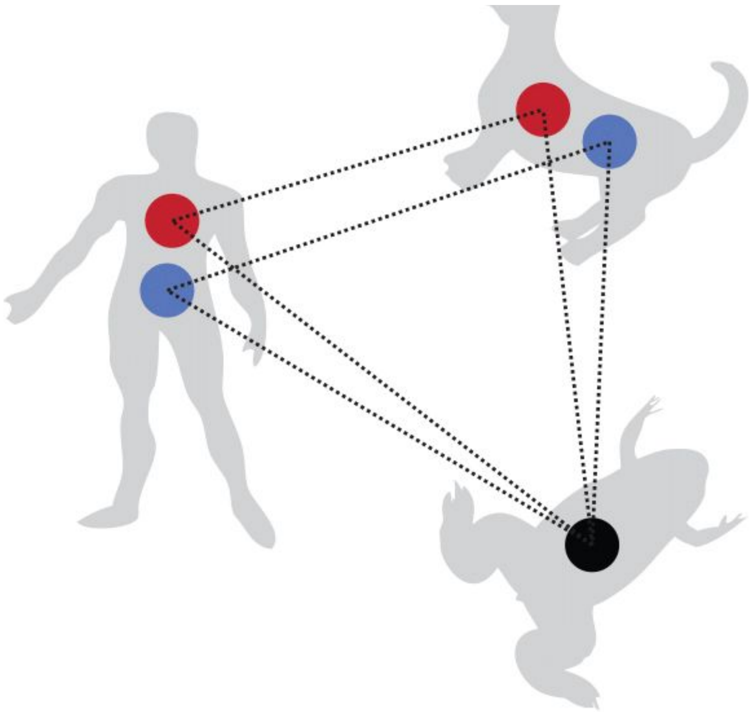
¿duplicación?
¿pérdida?

alineamientos

variación en número copias

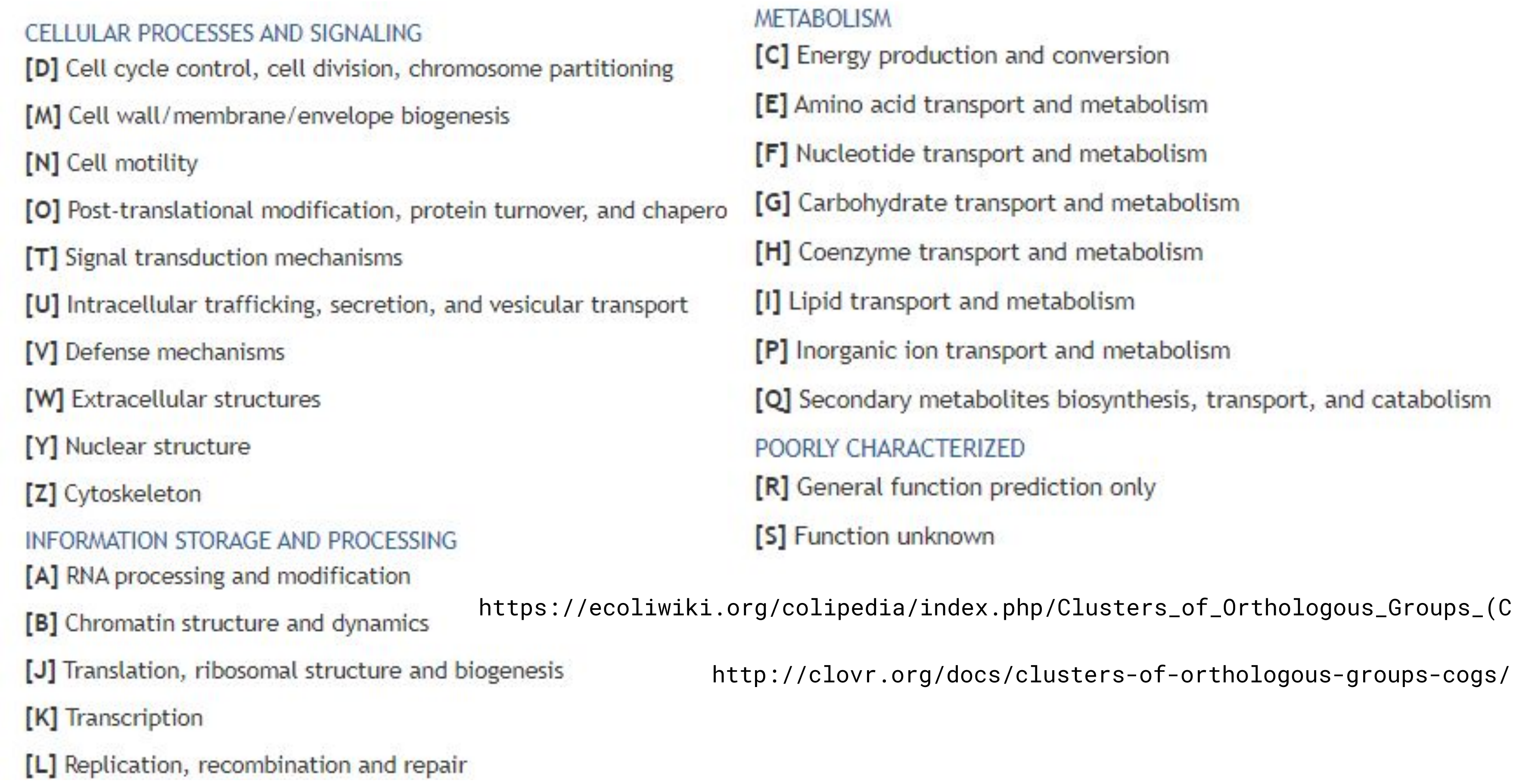
para qué sirve reconocer ortólogos ahora





https://omabrowser.org/oma/type/

categorías COG, funcionales



CELLULAR PROCESSES AND SIGNALING

[D] Cell cycle control, cell division, chromosome partitioning
[M] Cell wall/membrane/envelope biogenesis
[N] Cell motility
[O] Post-translational modification, protein turnover, and chapero
[T] Signal transduction mechanisms
[U] Intracellular trafficking, secretion, and vesicular transport
[V] Defense mechanisms
[W] Extracellular structures
[Y] Nuclear structure
[Z] Cytoskeleton

INFORMATION STORAGE AND PROCESSING

[A] RNA processing and modification
[B] Chromatin structure and dynamics
[J] Translation, ribosomal structure and biogenesis
[K] Transcription
[L] Replication, recombination and repair

METABOLISM

[C] Energy production and conversion
[E] Amino acid transport and metabolism
[F] Nucleotide transport and metabolism
[G] Carbohydrate transport and metabolism
[H] Coenzyme transport and metabolism
[I] Lipid transport and metabolism
[P] Inorganic ion transport and metabolism
[Q] Secondary metabolites biosynthesis, transport, and catabolism

POORLY CHARACTERIZED

[R] General function prediction only
[S] Function unknown

https://ecoliwiki.org/colipedia/index.php/Clusters_of_Orthologous_Groups_(COGs)

http://clovr.org/docs/clusters-of-orthologous-groups-cogs/

The End