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Article

Comparison of Phylogenetic Tree Topologies for Nitrogen Associated Genes Partially Reconstruct the Evolutionary History of *Saccharomyces cerevisiae*

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Appendix S1. Supplementary material

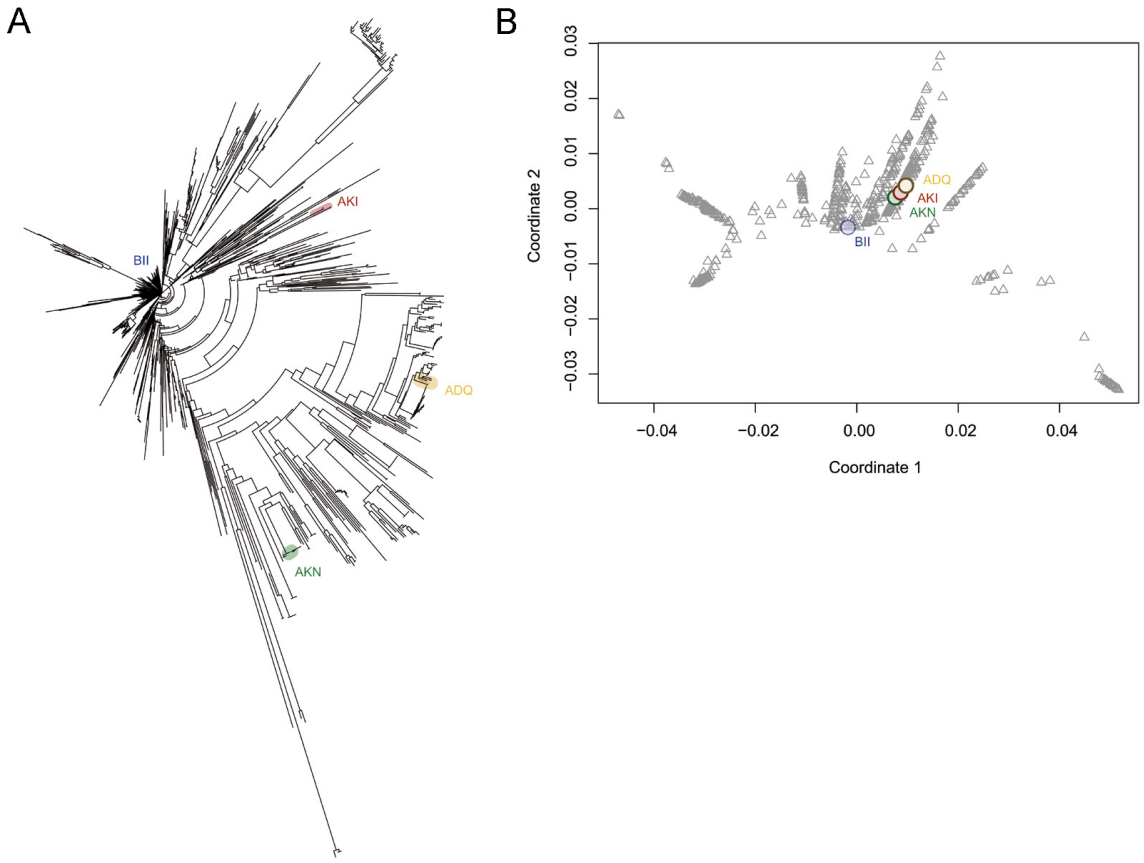


Figure S1. Representative yeast strains in the context of the population structure of the species. (a) TE tree highlighting the position of four strains (BII: DBVPG1106; AKI: DBVPG6044; ADQ: K12 and AKN: YPS128), which are representative of four yeast clean lineages. (b) TE tree represented as bi-dimensional tree spaces, obtained from the phylogenetic distance matrix among strains. The positions of the representative strains are highlighted.

Table S1. Genes evaluated in this work. ASE: Allele specific expression; ASB: Allele-specific transcription factor binding; BSA: Bulked segregant analysis; ISA: Individual segregant analysis.

ARG81	Zinc finger transcription factor involved in arginine-responsive genes	Fermentative capacity	BSA	[1]
BIO3	7,8-diamino-pelargonic acid aminotransferase (DAPA)	Fermentative capacity	BSA	[1]
GCN1	Positive regulator of the Gcn2p kinase activity	Fermentative capacity	BSA	[1]
MDS3	Putative component of the TOR regulatory pathway	Fermentative capacity	BSA	[1]
AGP1	Low-affinity amino acid permease with broad substrate range	Nitrogen consumption	ISA	[2]
ASI1	Subunit of the inner nuclear membrane Asi ubiquitin ligase complex	Nitrogen consumption	ISA	[2]
GLT1	NAD(+)-dependent glutamate synthase (GOGAT)	Nitrogen consumption	ISA	[2]
RIM15	Protein kinase involved in cell proliferation in response to nutrients	Fermentative capacity	ISA	[3]
ASN1	Asparagine synthetase	Nitrogen consumption	ASE, ASB	[4]
ARO1	Pentafunctional arom protein	Nitrogen consumption	ISA	[5]
ALP1	Arginine transporter	Nitrogen consumption	ISA	[5]
ASI2	Subunit of the inner nuclear membrane Asi ubiquitin ligase complex	Nitrogen consumption	ISA	[5]
CPS1	Vacuolar carboxypeptidase S	Nitrogen consumption	ISA	[5]
LYP1	Lysine permease	Nitrogen consumption	ISA	[5]
PDC1	Major of three pyruvate decarboxylase isozymes	Nitrogen consumption	ISA	[5]
EAP1	eIF4E-associated protein, competes with eIF4G for binding to eIF4E	Nitrogen consumption	ISA	[6]
GTR1	Subunit of a TORC1-stimulating GTPase and the EGO/GSE complex	Nitrogen consumption	ISA	[6]
NPR1	Protein kinase, stabilizes several plasma membrane amino acid transporters	Nitrogen consumption	ISA	[6]
SAP185	Protein that forms a complex with the Sit4p protein phosphatase	Nitrogen consumption	ISA	[6]
SCH9	AGC family protein kinase, phosphorylated by Tor1p	Nitrogen consumption	ISA	[6]
SIT4	Ceramide-activated, type 2A-related serine-threonine phosphatase	Nitrogen consumption	ISA	[6]
TOR2	PIK-related protein kinase, subunit of TORC1 and TORC2	Nitrogen consumption	ISA	[6]

Table S2. Tree topologies comparison for the subclades previously described by [7]. N: Number of strains. TE: Total Evidence phylogenetic tree. REF: Reference phylogenetic tree. OUT: Randomly generated tree.

Clades/Subclades	N	*AGP1*	*ALP1*	*ARG81*	*ARO1*	*ASI1*	*ASI2*	*ASN1*	*BIO3*	*CPS1*	*EAP1*	*GCN1*	*GLT1*	*GTR1*	*LYP1*	*MDS3*	*NPR1*	*PDC1*	*RIM15*	*SAP185*	*SCH9*	*SIT4*	*TOR2*	TE	REF	OUT
1. Wine/European (subclade 0)	268	1	4	7	6	5	2	1	3	4	5	9	4	1	2	8	3	3	9	4	6	3	7	25	100	0
1. Wine/European (subclade 1)	18	0	13	7	13	13	0	0	0	0	7	13	0	0	0	0	0	0	20	7	7	0	20	20	100	0
1. Wine/European (subclade 2)	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	100	0
1. Wine/European (subclade 3)	24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0
1. Wine/European (subclade 4)	39	5	0	8	8	0	0	0	0	0	0	8	2	0	0	2	0	0	8	0	0	0	0	36	100	0
2. Alpechin	17	2	16	2	9	9	9	0	2	0	9	45	37	2	30	23	2	0	52	9	9	2	30	73	100	0
3. Brazilian bioethanol	35	6	3	3	6	0	0	0	3	9	12	3	3	0	3	0	0	12	3	0	9	0	9	12	100	0
4. Mediterranean oak	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0
5. French dairy	32	0	7	3	3	7	7	0	10	10	10	3	7	0	7	3	0	7	10	7	7	3	14	17	100	0
6. African beer	20	12	47	29	35	12	12	6	24	12	24	24	41	6	59	24	29	24	24	35	53	12	24	59	100	0
7. Mosaic beer	21	6	11	11	0	17	11	6	0	0	11	0	11	22	11	11	11	6	17	6	22	6	11	44	100	6
8. Mixed origin	72	0	1	1	0	0	1	0	0	0	1	1	0	1	4	1	0	3	0	3	0	0	0	1	100	0
9. Mexican agave	7	0	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	0	0	20	0	0	100	0
10. French Guiana human	31	4	0	11	4	4	4	0	4	0	0	0	4	0	0	4	4	0	4	4	0	4	0	14	100	0
11. Ale beer	18	0	13	13	13	40	20	13	33	7	20	33	13	13	13	20	27	13	7	0	7	7	7	40	100	0
12. West African cocoa	13	7	0	27	0	7	0	0	0	0	0	7	7	7	0	7	0	7	7	7	0	7	0	27	100	0
13. African palm wine	28	16	20	20	20	12	8	16	28	20	16	24	36	16	20	16	12	28	24	24	28	4	36	40	100	0
14. CHNIII	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
15. CHNII	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16. CHNI	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
17. Taiwanese	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
18. Far East Asia	9	0	21	0	0	0	5	0	0	0	0	5	0	5	0	0	0	0	21	0	5	0	5	38	100	0
19. Malaysian	6	0	0	0	0	0	0	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0
20. CHN V	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
21. Ecuadorean	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0
22. Far East Russian	4	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	0
23. North American oak	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0
24. Asian islands	11	2	2	2	2	27	2	2	14	2	0	0	14	0	0	27	0	0	14	2	0	0	2	64	100	0
25. Sake	47	2	5	0	11	2	0	0	0	0	7	5	9	7	0	9	2	0	14	2	2	0	11	20	100	0
26. Asian fermentation	39	19	6	8	8	11	8	19	3	3	8	19	11	3	8	19	3	3	11	6	14	6	19	33	100	0
M1. Mosaic region 1	17	21	14	0	21	14	0	14	0	7	36	14	14	7	7	14	14	14	29	14	14	14	14	21	100	0
M2. Mosaic region 2	20	12	18	29	12	18	29	18	12	12	6	18	24	0	18	12	18	18	18	18	18	6	6	24	100	0
M3. Mosaic region 3	113	7	9	14	10	7	4	5	5	5	10	13	11	2	8	10	9	4	15	7	12	3	14	26	100	0
Unclustered	48	20	22	27	24	22	13	16	11	16	16	29	22	9	27	27	13	9	29	20	24	13	18	44	100	0
Total strains	1011																									

Table S3. Tree topologies comparison for the strains representative of the clean lineages previously described by [8]. N: Number of strains. TE: Total Evidence phylogenetic tree. REF: Reference phylogenetic tree. OUT: Randomly generated tree.

Strain/Origin	N	*AGP1*	*ALP1*	*ARG81*	*ARO1*	*ASI1*	*ASI2*	*ASN1*	*BIO3*	*CPS1*	*EAP1*	*GCN1*	*GLT1*	*GTR1*	*LYP1*	*MDS3*	*NPR1*	*PDC1*	*RIM15*	*SAP185*	*SCH9*	*SIT4*	*TOR2*	TE	REF	OUT
Unclustered	1001	5	6	8	6	5	4	3	4	5	6	9	8	2	5	10	4	4	10	6	7	3	8	27	100	0
Chile	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	0
Representatives of clean lineages	4	100	100	100	0	100	0	0	0	100	100	100	100	100	100	100	100	100	0	100	100	0	0	100	100	0

N: Number of strains. TE: Total Evidence phylogenetic tree. REF: Reference phylogenetic tree. OUT: Randomly generated tree.

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