Patterns of genetic diversity and reproductive isolation in natural Saccharomyces *yeast populations.*

KITP, Santa Barbara

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Overview

--Who is *Saccharomyces cerevisiae* and how is it related to its congeners?

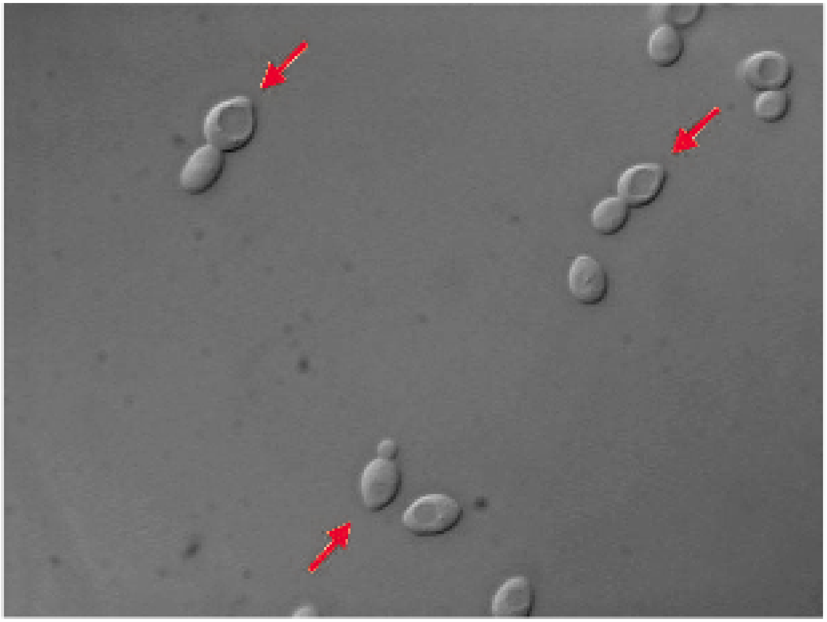
--The evolutionary and ecological status of natural *Saccharomyces* populations.

--Genetic structure of natural *Saccharomyces* populations.

--Patterns of reproductive isolation in *S. paradoxus*.

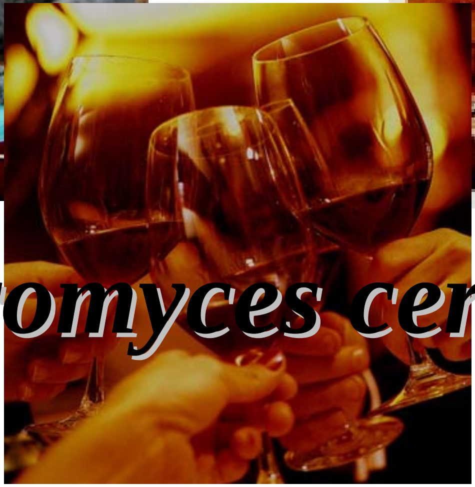
--Conclusion and future prospects.

Unicellular Ascomycete Fungus



Asexual Budding

Four Spores in an Ascus



Saccharomyces cerevisiae

S. cerevisiae

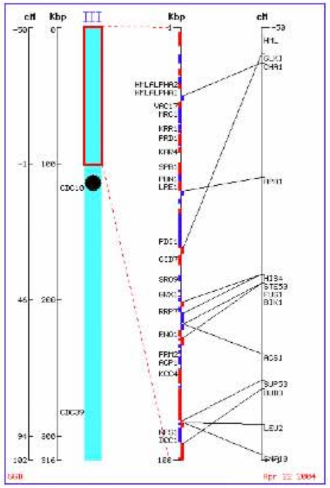
Genetics

Cell and Molecular Biology

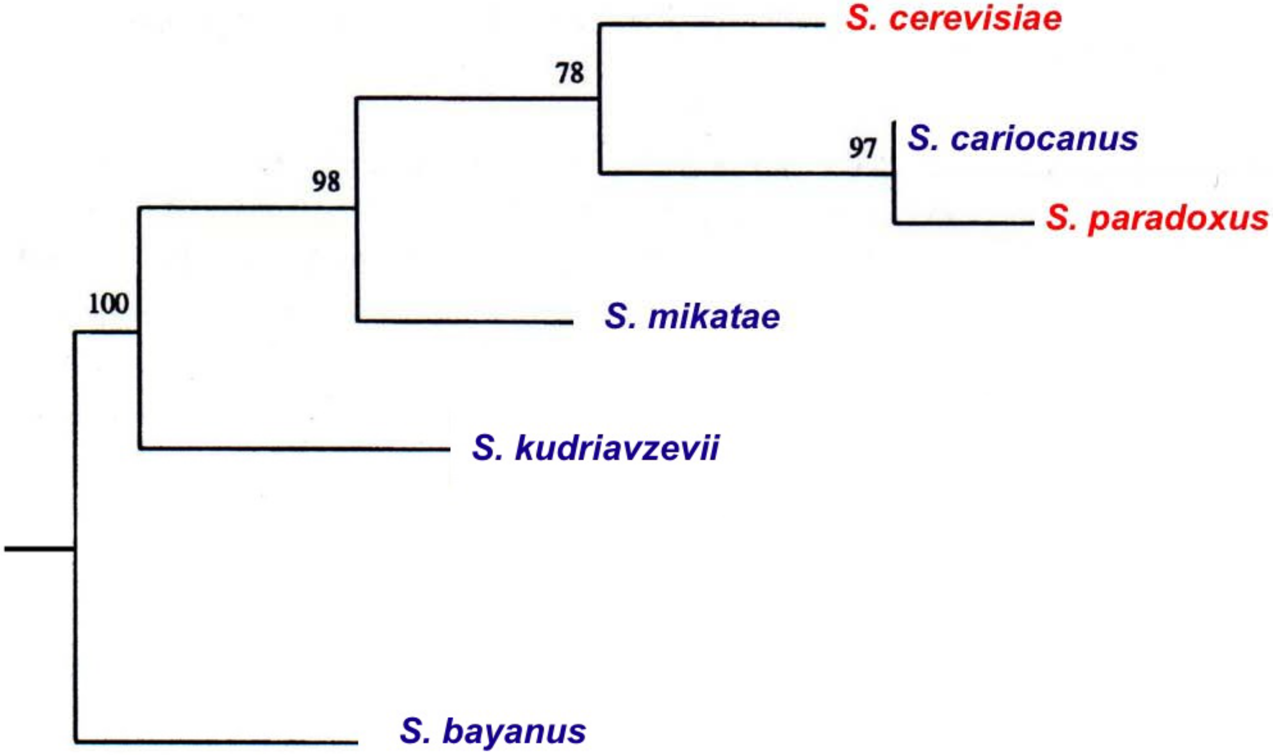
Proteomics

Genomics

Ecology and Evolution



Saccharomyces sensu stricto



After Naumov *et al*. 2000

Yeast in Nature

Woodland Contexts

Yeast Field Collection

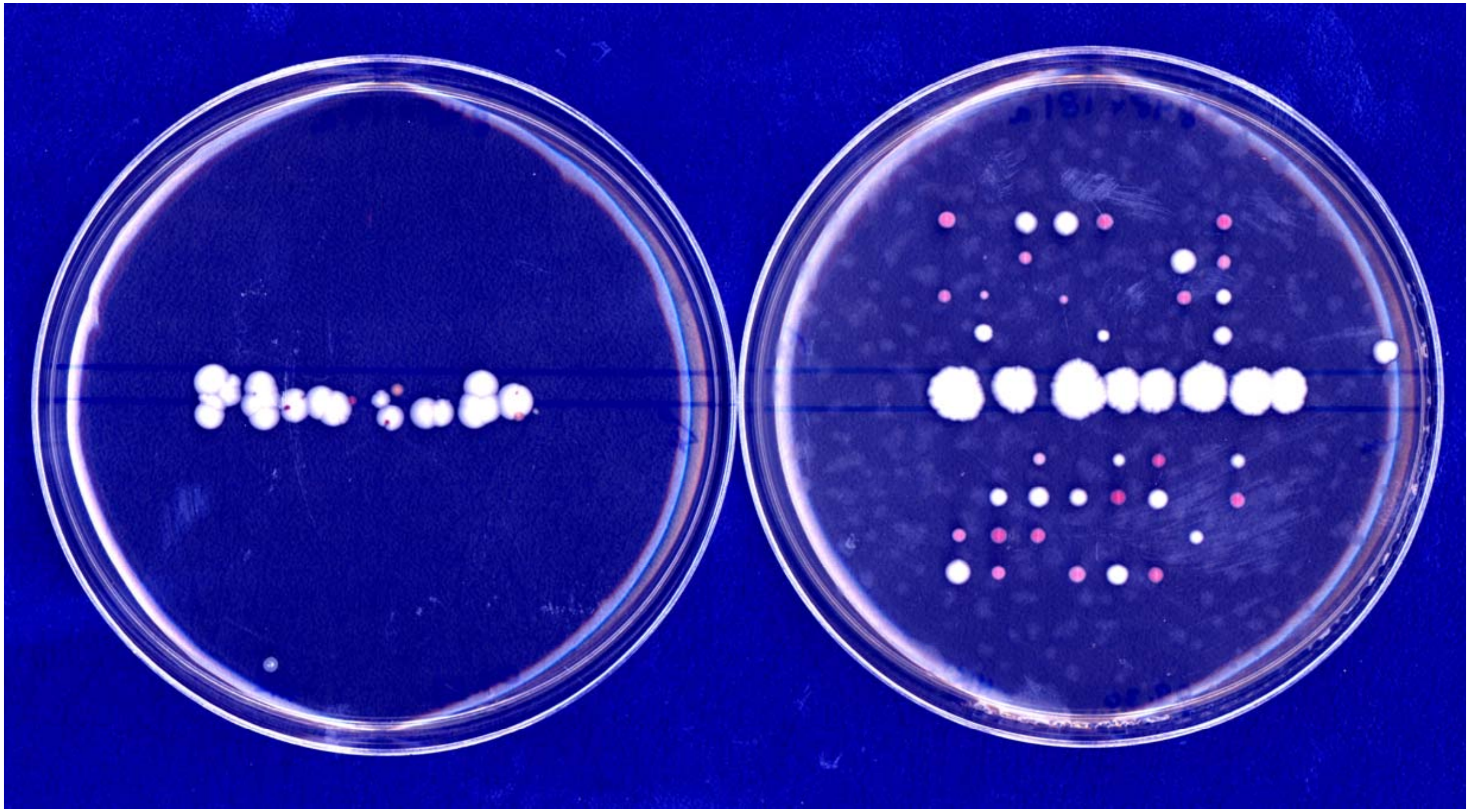
Sampling oak exudate in Ontario, Canada

Photos by M.-A. Lachance

Yeast Isolation

Laboratory Contexts

Testing for reproductive isolation



Heterospecific test cross   Conspecific test cross

Saccharomyces paradoxus and *Saccharomyces cerevisiae* are associated with exudates of North American oaks

Gennadi I. Naumov, Elena S. Naumova, and Paul D. Sniegowski

Table 1. *Saccharomyces* strains from which monosporic cultures were used.

Species	Strain	Source	Place of isolation	Author
S. cerevisiae	VKM Y-502	Grape berries	Russian Far East	I.A. Mazilkin
	YNN 295	Genetic line	—	D. Vollrath and R.W. Davis
	95-5	*Quercus* sp.	Long Woods, W.K. Kellogg Biological station, Michigan State Univ.	G.I. Naumov
	95-6	*Quercus* sp.	Long Woods, W.K. Kellogg Biological station, Michigan State Univ.	G.I. Naumov
S. paradoxus	CBS 5829	Mor soil	Denmark	V. Jensen
	CBS 432	Unknown	Unknown	Unknown
	95-1	*Quercus* sp.	Saugatuck Dunes State Park, Mich.	G.I. Naumov
	95-3	*Q. alba*	Long Woods, W.K. Kellogg Biological station, Michigan State Univ.	G.I. Naumov
	95-4	*Q. rubra*	Long Woods, W.K. Kellogg Biological station, Michigan State Univ.	G.I. Naumov
	95-7	*Q. rubra*	Michigan State Univ. Campus, East Lansing	G.I. Naumov
	95-8	*Q. rubra*	Michigan State Univ. Campus, East Lansing	G.I. Naumov
	52-153[a]	*Drosophila* sp.	U.S.A.	H.J. Phaff
	61-359[a]	*Ulmus* sp.	U.S.A.	H.J. Phaff
Saccharomyces sp.	97-3[b]	*Q. alba*	Allaire State Park, N.J.	G.I. Naumov

Can. J. Microbiol. 44: 1045–1050 (1998)

Saccharomyces cerevisiae and *Saccharomyces paradoxus* coexist in a natural woodland site in North America and display different levels of reproductive isolation from European conspecifics

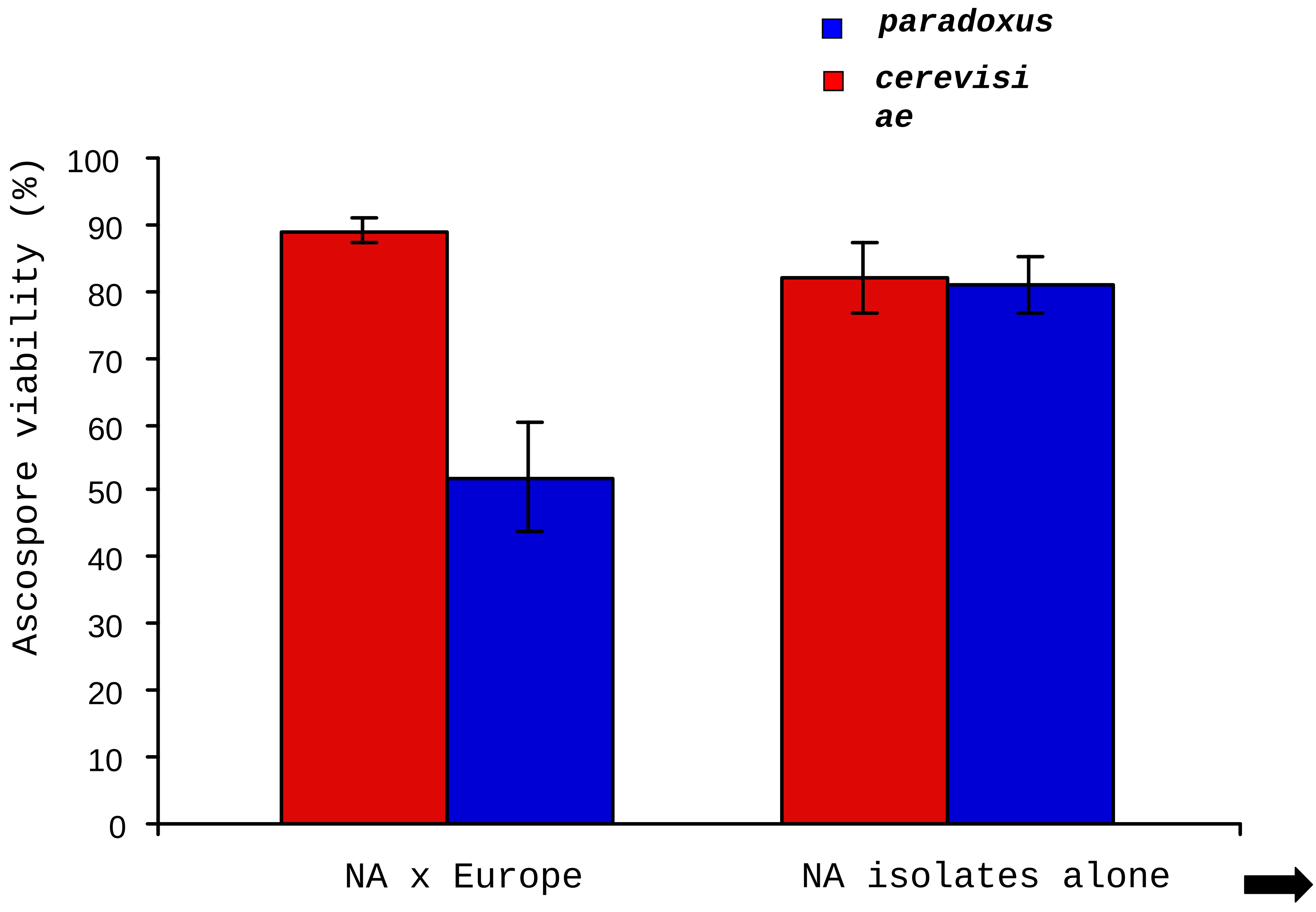
Paul D. Sniegowski *, Peter G. Dombrowski, Ethan Fingerman

Table 1
Identified isolates of *S. paradoxus* and *S. cerevisiae* and their source habitats in a Pennsylvanian woodland

Species	Strain	Source
S. cerevisiae	YPS 128	Soil beneath *Q. alba*
	YPS 129	Flux from *Q. alba*
	YPS 133	Soil beneath *Q. alba*
	YPS 134	Soil beneath *Q. velutina*
	YPS 139	Soil beneath unidentified *Quercus* spp.
	YPS 141	Soil beneath *Q. velutina*
	YPS 142	Bark of *Q. rubra*
	YPS 143	Soil beneath *Q. rubra*
	YPS 154	Bark of *Q. velutina*
	YPS 163	Soil beneath *Q. rubra*
S. paradoxus	YPS 125	Flux of *Q. rubra*
	YPS 138	Soil beneath *Q. velutina*
	YPS 145	Soil beneath *Q. alba*
	YPS 150	Bark of *Q. velutina*
	YPS 151	Soil beneath *Q. velutina*
	YPS 152	Soil beneath *Q. rubra*
	YPS 155	Bark of *Q. rubra*
	YPS 158	Soil beneath *Q. alba*

FEMS Yeast Research 1 (2002) 299–306

Geographic reproductive isolation in *paradoxus* but not *cerevisiae*?



Heidi A. Kuehne

Ph.D. Thesis, University of Pennsylvania

The genetic structure and biogeography of natural *Saccharomyces* populations.

Setting the Table

What <u>is</u> a population? Are there broad subdivisions in nature?

How are these populations structured genetically?

How are these populations structured spatially?

What types of breeding systems are realized in nature?

GENETIC POPULATION STRUCTURE

Mutation

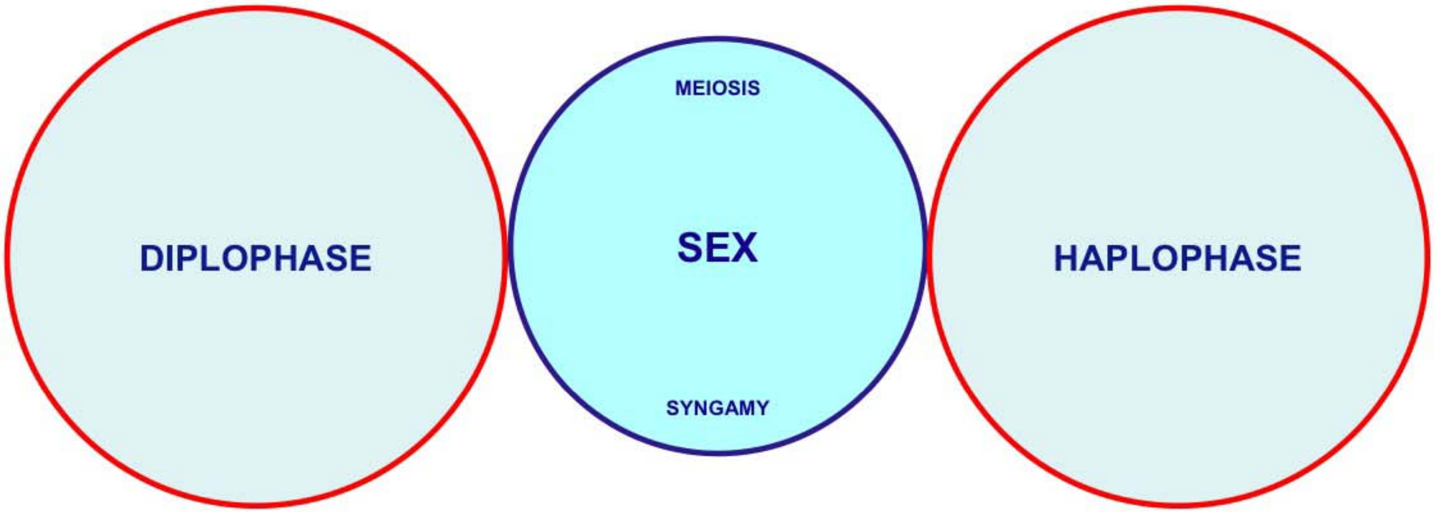
Selection

GPS is the distribution and abundance of genetic variation within and among populations.

Migration

Drift

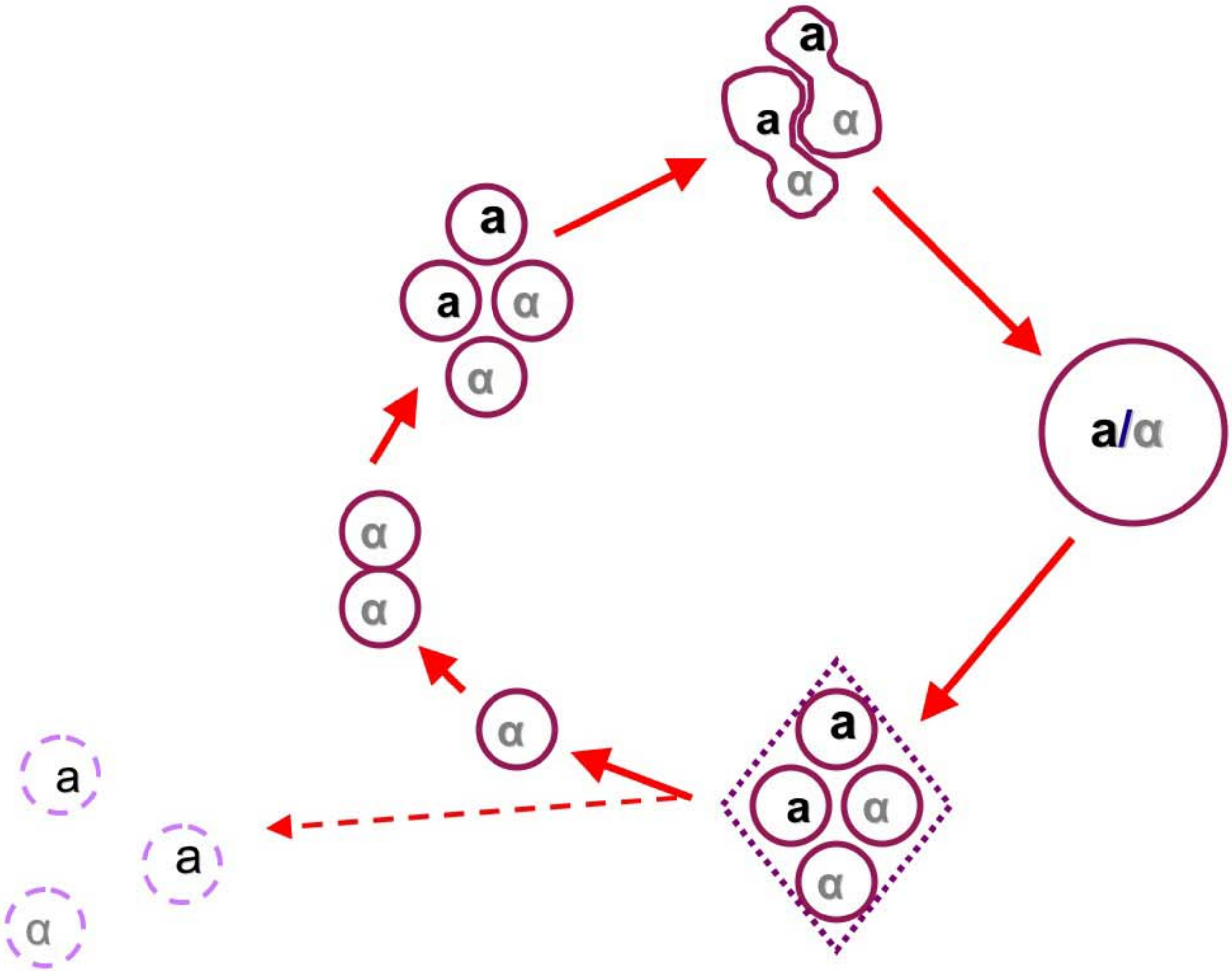
Haplodiplontic Life Cycle



Reproduction and Sex Are Uncoupled

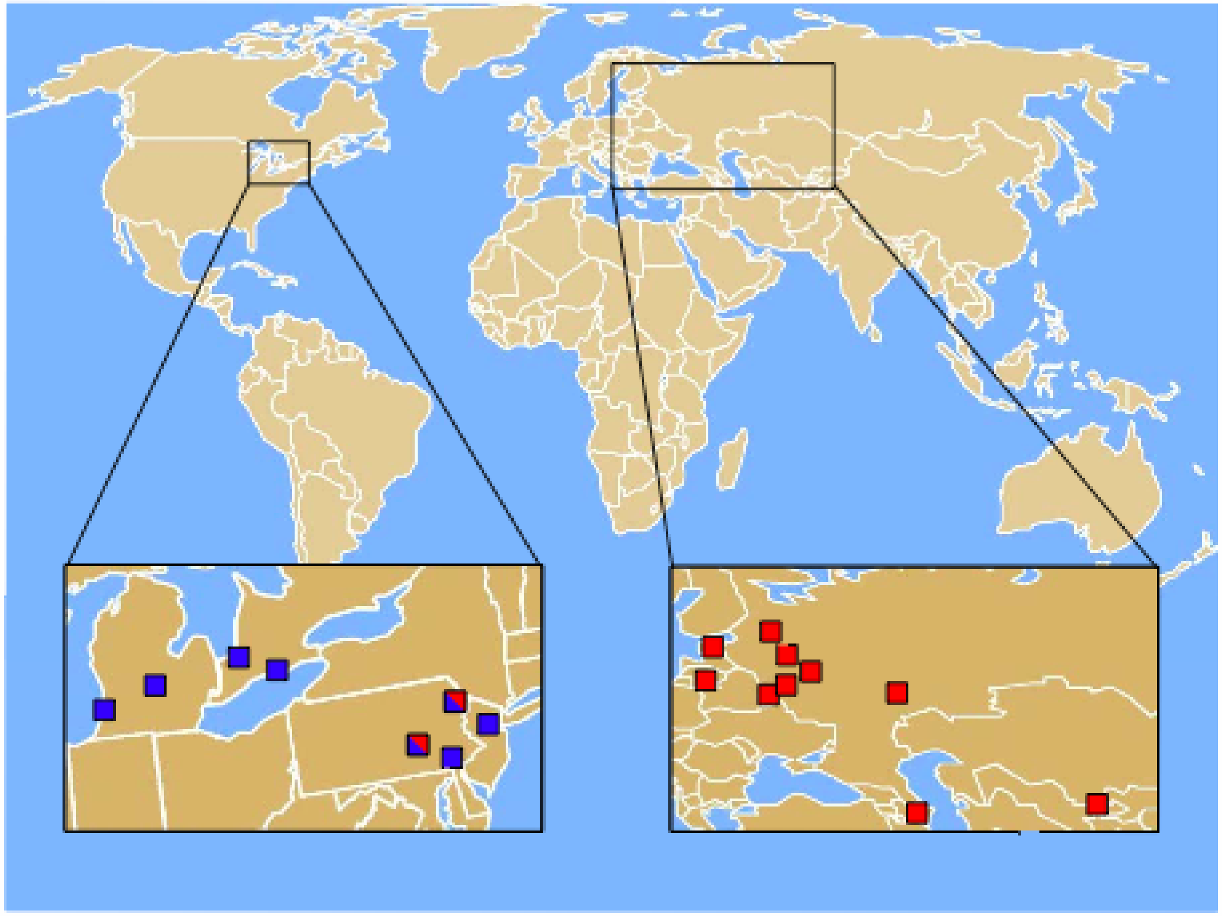
Figure adapted from Bell 1997

Mating-Type Switching



Sex and Recombination Are Uncoupled

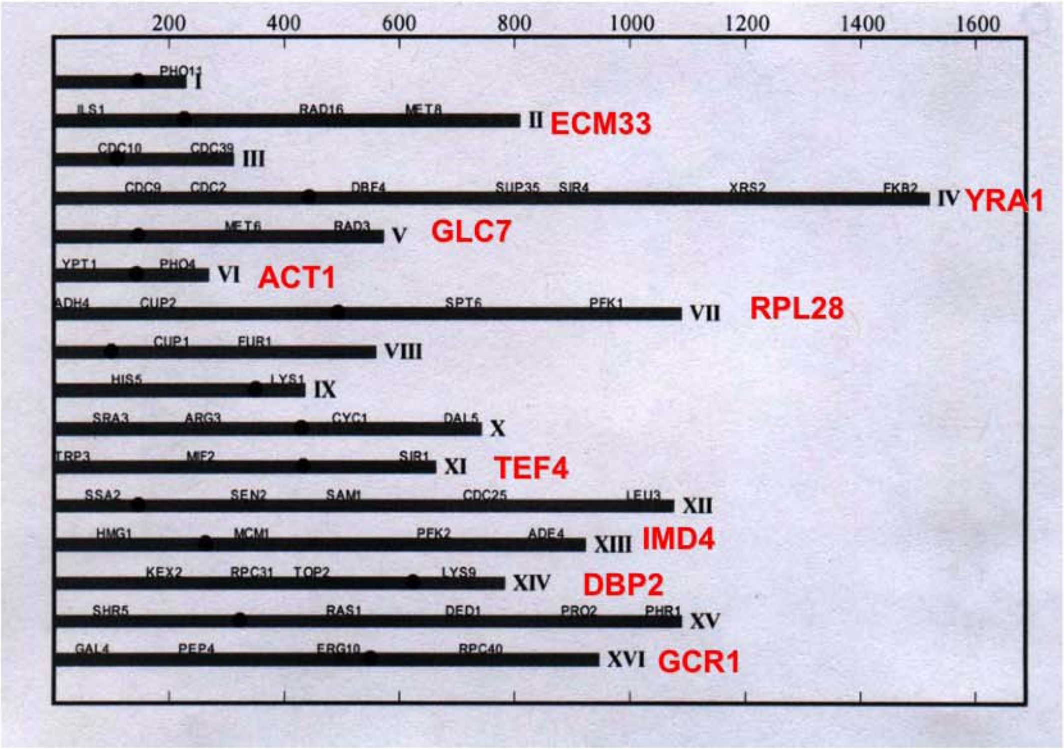
Yeast Collection Sites



51 S. paradoxus
27 S. cerevisiae

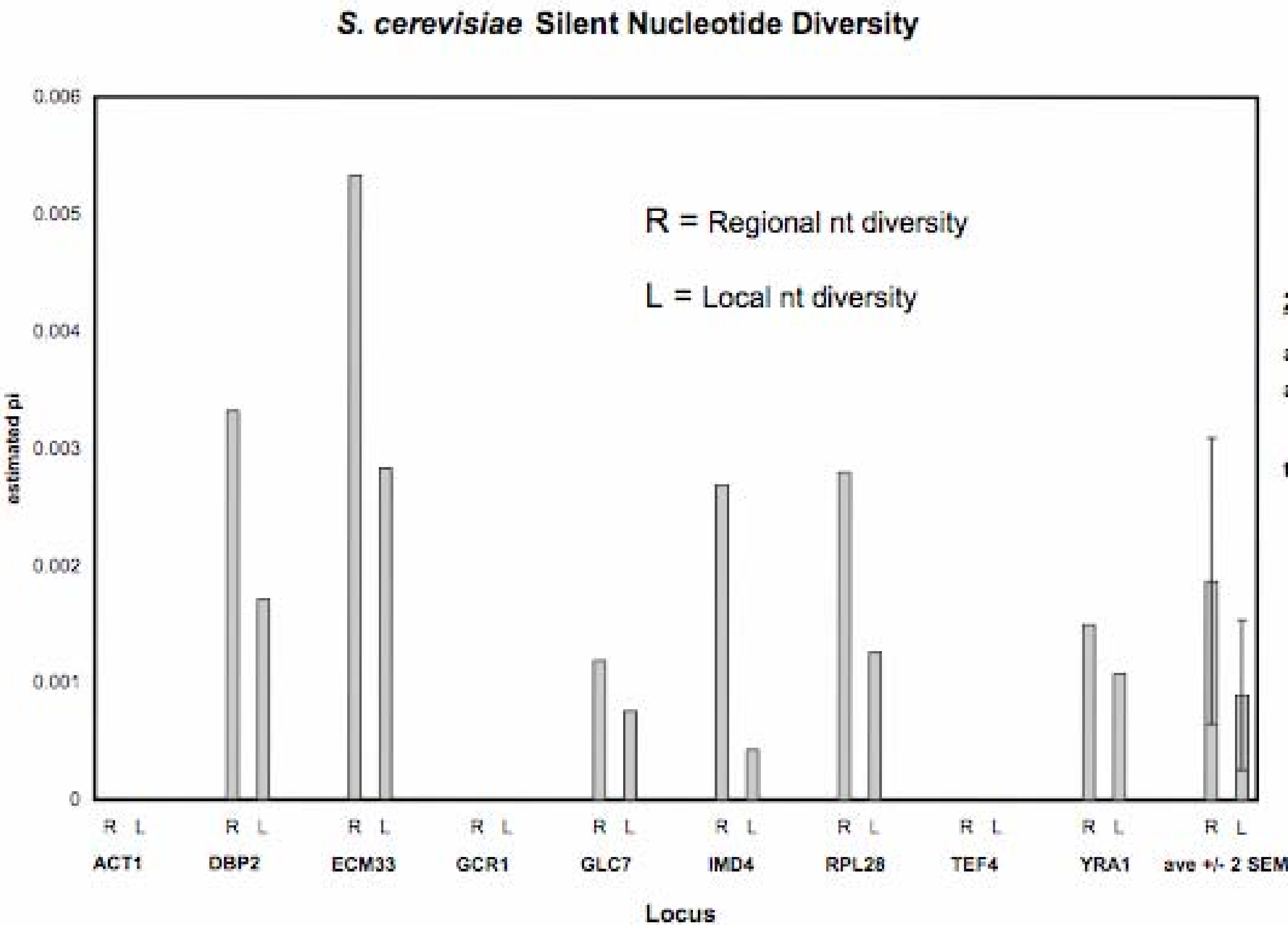
11 S. paradoxus

Multilocus Sequence Typing



Nine Spliceosomal Introns
350,000 nt

Diversity Patterns



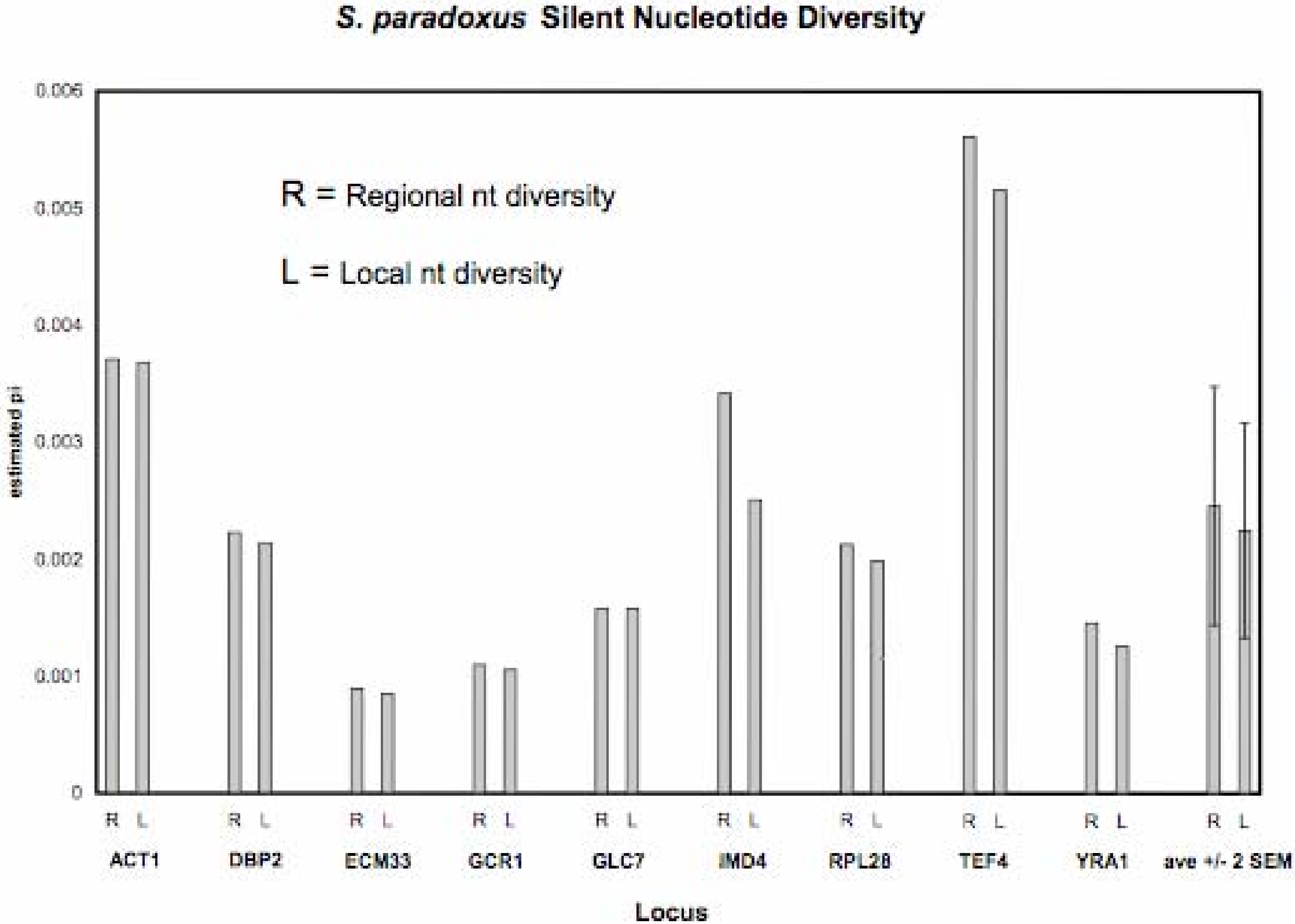
<u>2-sample paired t-test</u>

ave R = .001870 (.00122)

ave L = .000897 (.00064)

t = 2.89, 8 df, p = .020

Diversity Patterns

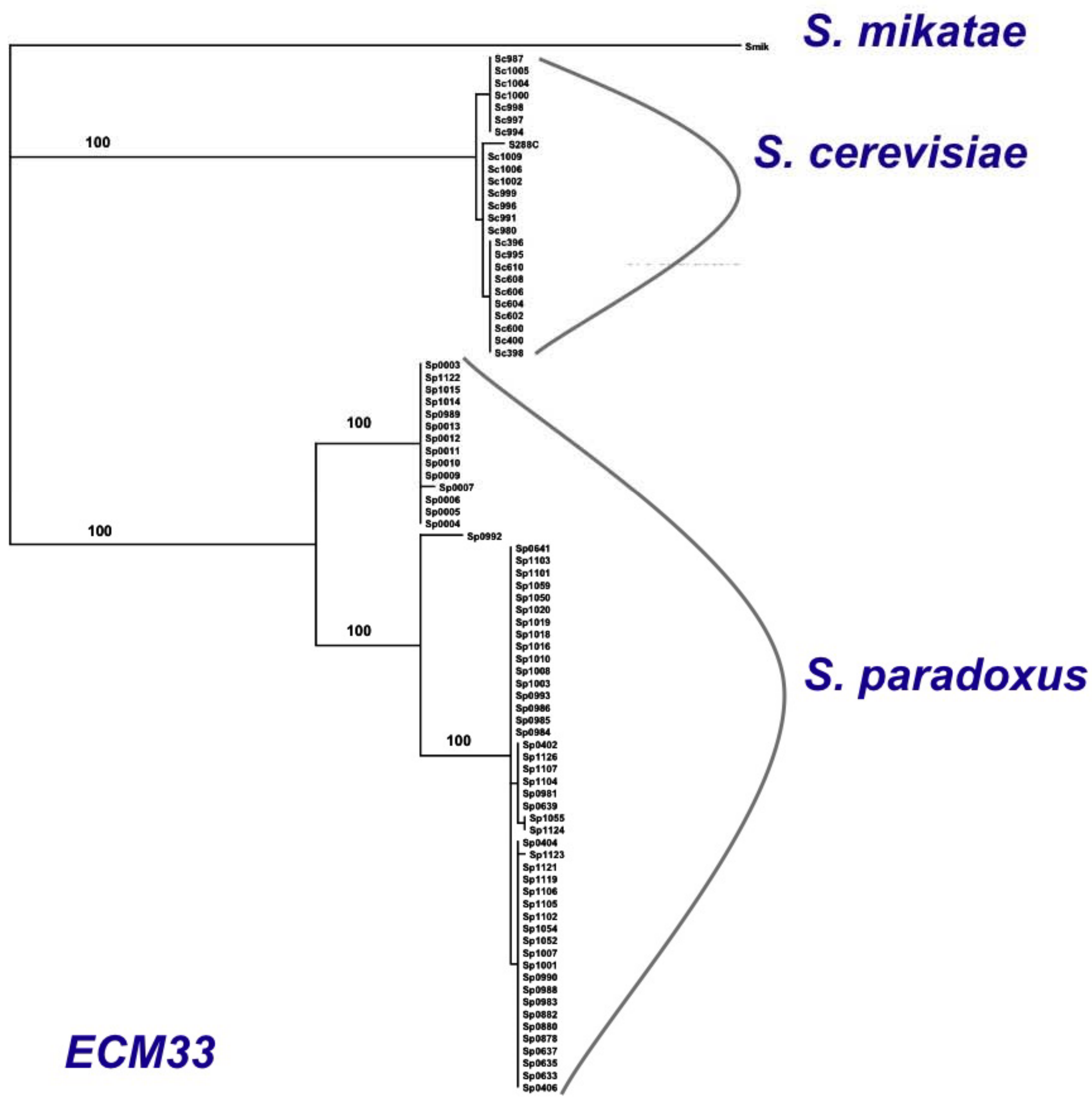


2-sample paired t-test

ave R = .002459 (.00102)
ave L = .002248 (.00092)

t = 2.14, 8 df, p = .065

Maximum Parsimony Gene Trees

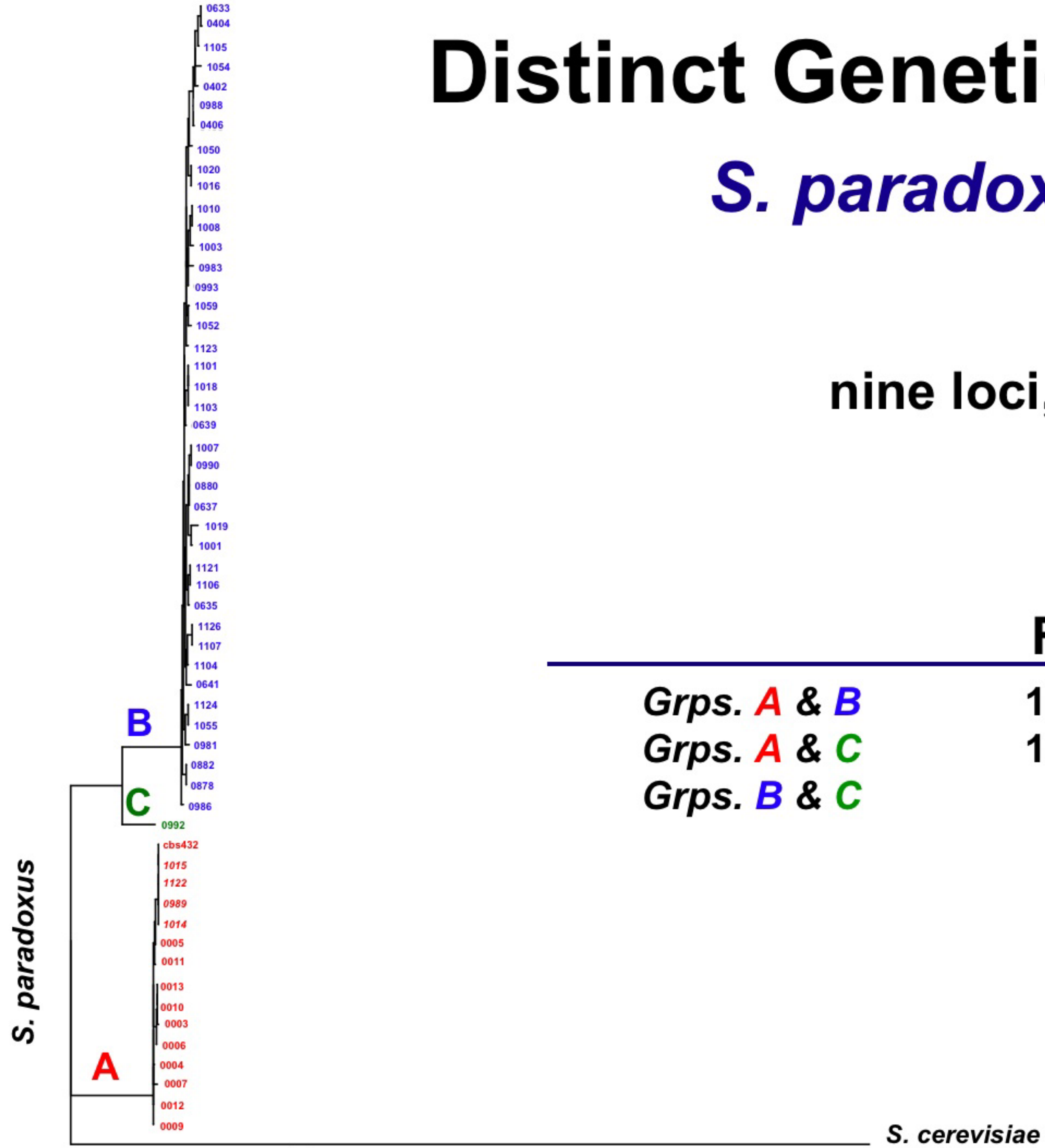


ECM33

578 nt

Distinct Genetic Groups

S. paradoxus

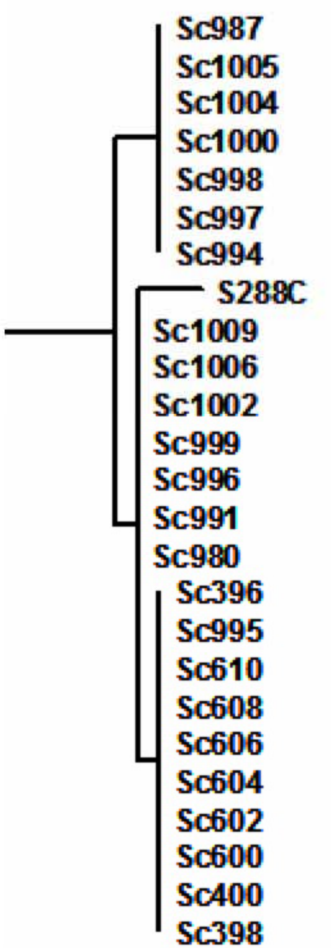


nine loci, 4867 bp

	F	S
Grps. A & B	179	0
Grps. A & C	165	0
Grps. B & C	89	0

Distinct Genetic Groups in Sympatry

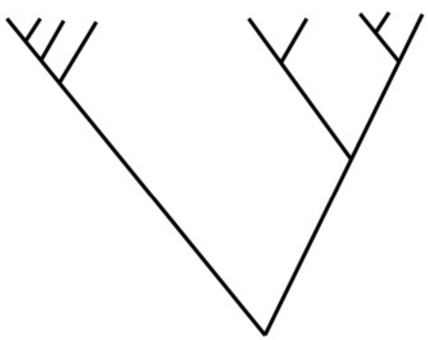
S. cerevisiae



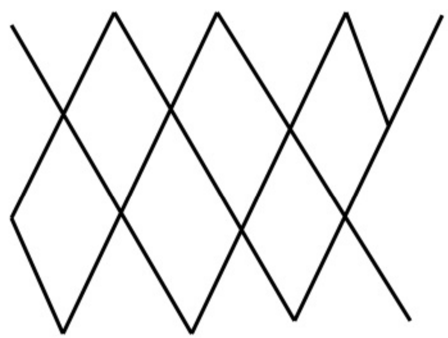
nine loci, 4839 bp

	F	S
Grps. I & II	6	0
Grps. I & III	15	0
Grps. II & III	11	0

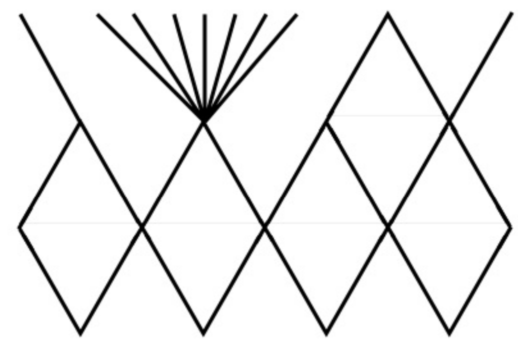
Possible Population Structures



Clonal



Recombining



Epidemic

After Maynard Smith *et al.* 1993

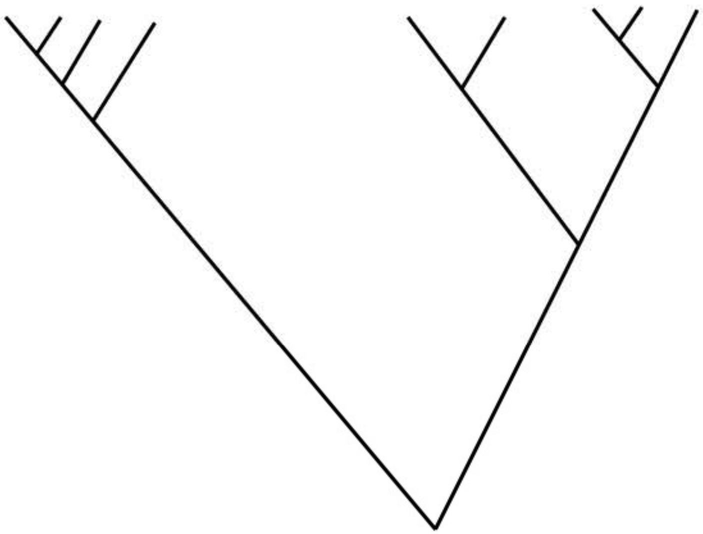
Testing population structure using multilocus sequence data

Index of Association (I_A): Tests for linkage disequilibrium, the nonrandom association of alleles in haplotypes, by analyzing the distribution of genetic distances.

Incongruency Length Difference (ILD): Tests whether different gene trees are congruent (clonality) or incongruent.

Consistency Index (CI): Compares trees for homoplasy (obs. character state arising more than once in tree by nonhomologous means). Recombination is a source of homoplasy.

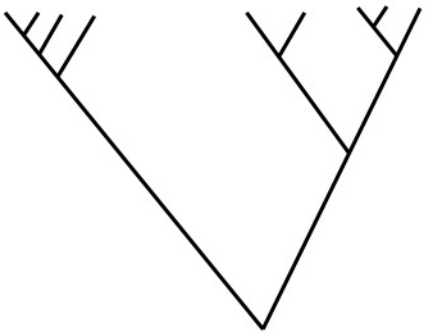
S. cerevisiae



I_A p = .001
ILD p = 1.00
CI = 1.00

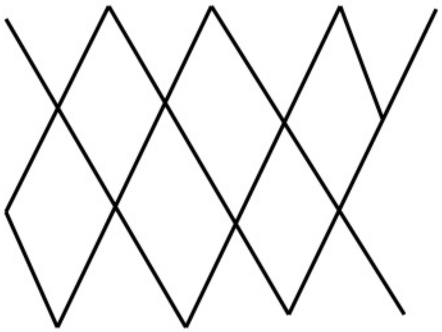
Clonal in Northeast American Woodlands

S. paradoxus



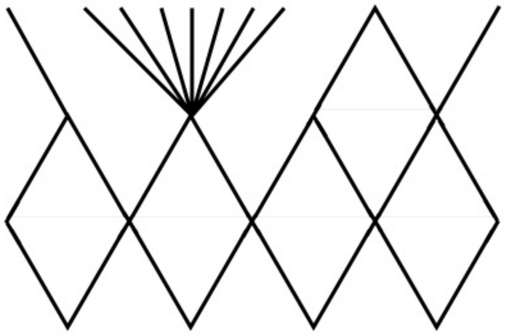
Group A
NE America

NA



Group A
Eurasia

I_A p = .373
ILD p = .552
CI = .86

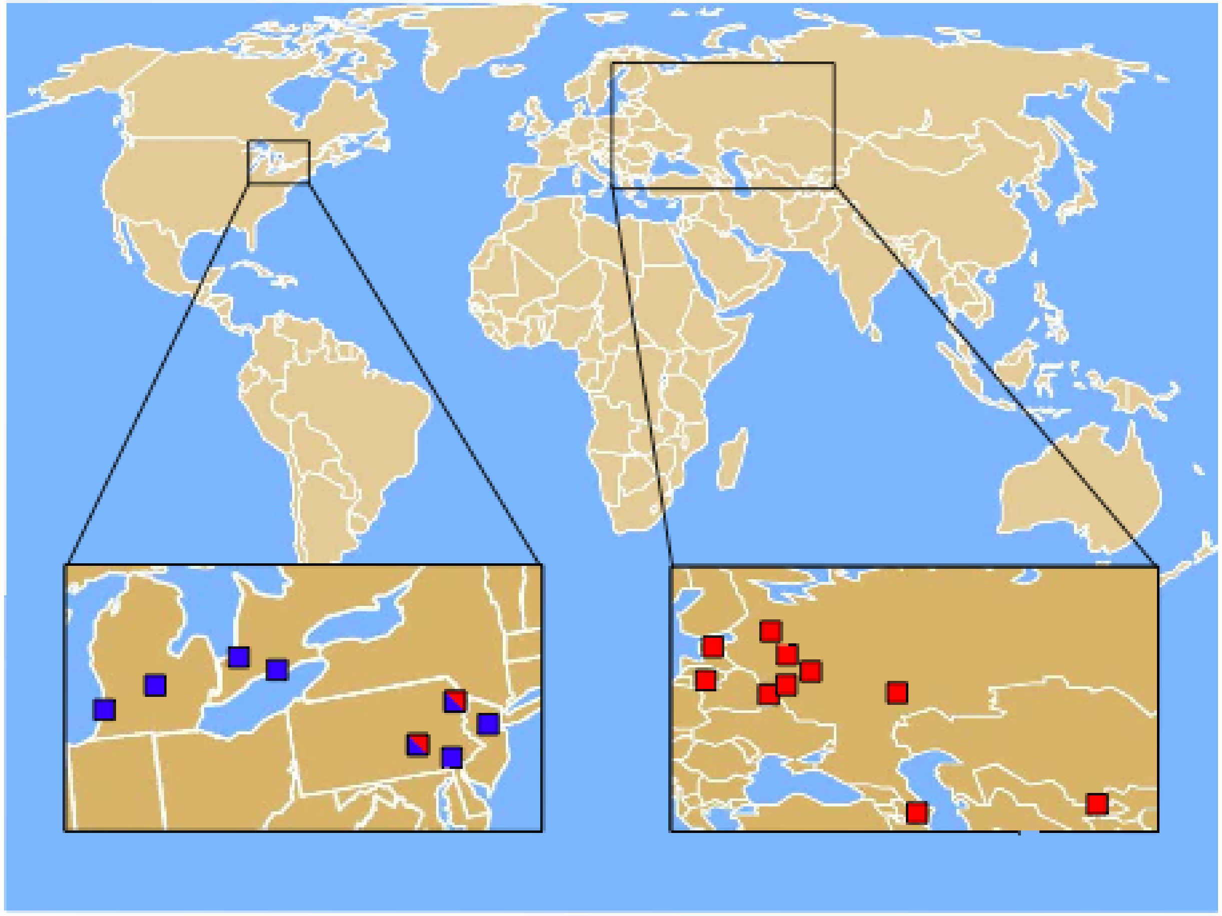


Group B
NE America

I_A p = .1914
ILD p = .001
CI = .41

Multiple Structures in the Northern Hemisphere

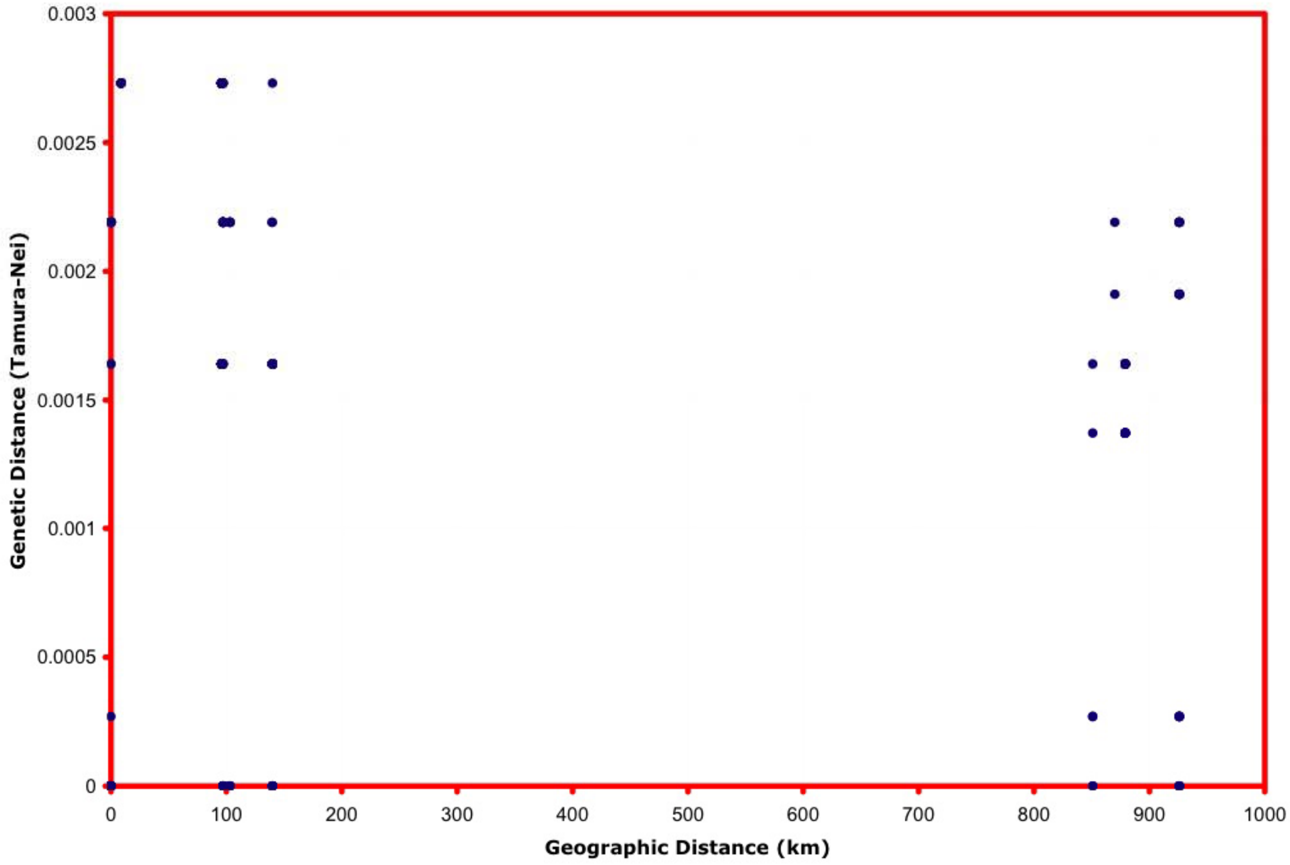
Yeast Collection Sites



51 *S. paradoxus*
27 *S. cerevisiae*

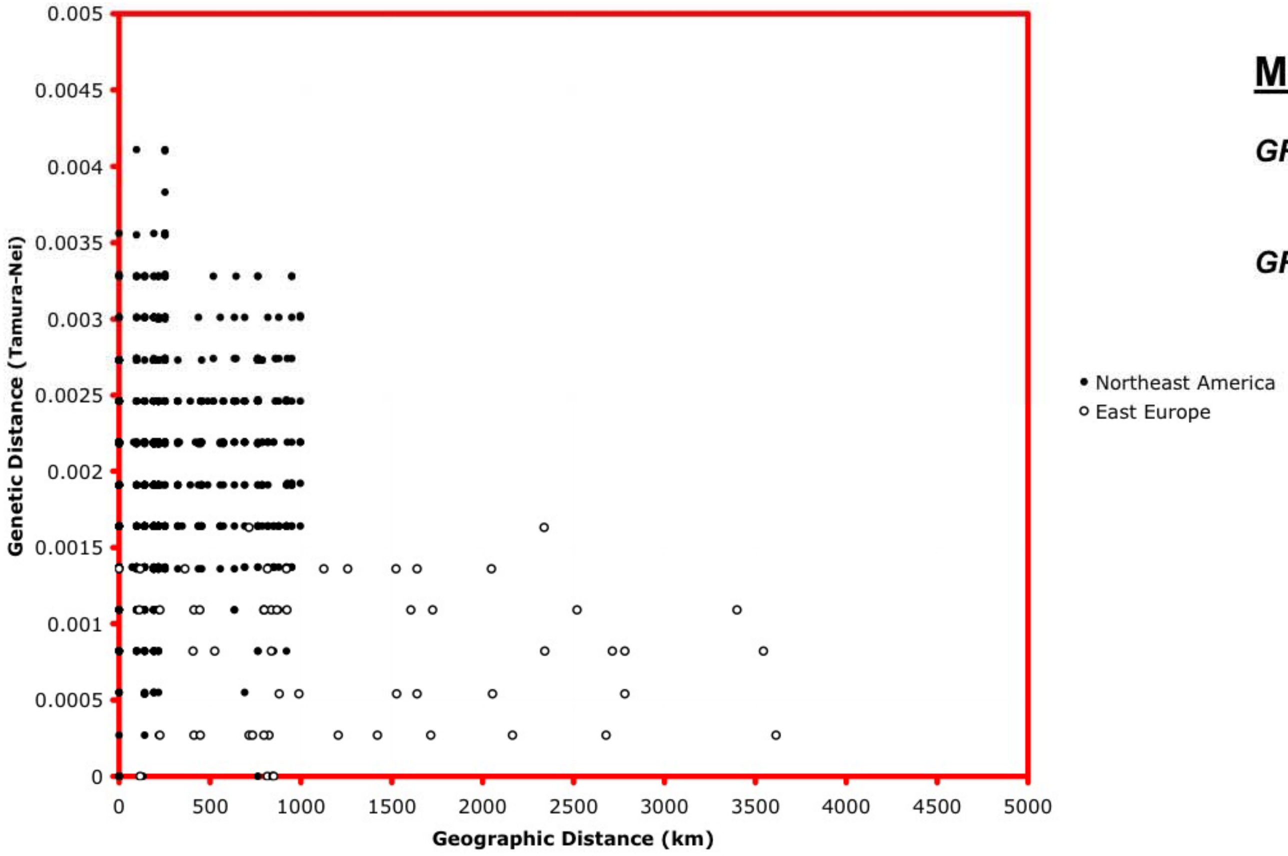
11 *S. paradoxus*

Regional Biogeography



S. cerevisiae

Regional Biogeography



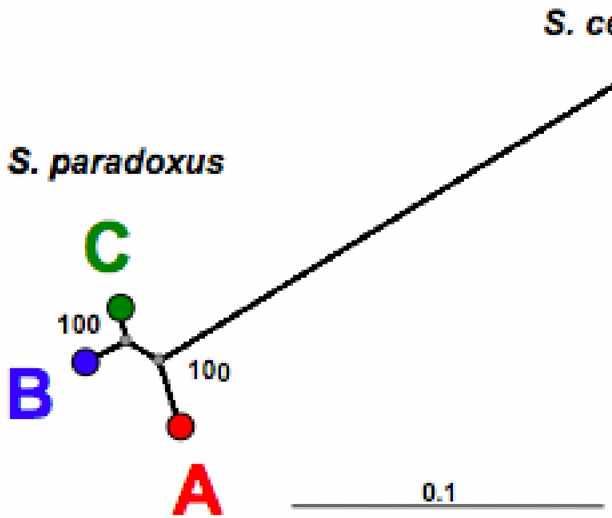
Mantel Tests

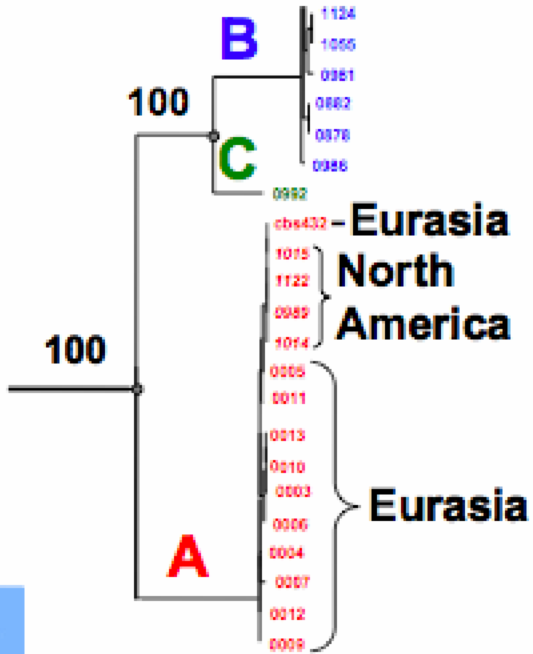
GRP. ***B*** **(all) p = .09**
(uni) p = .22

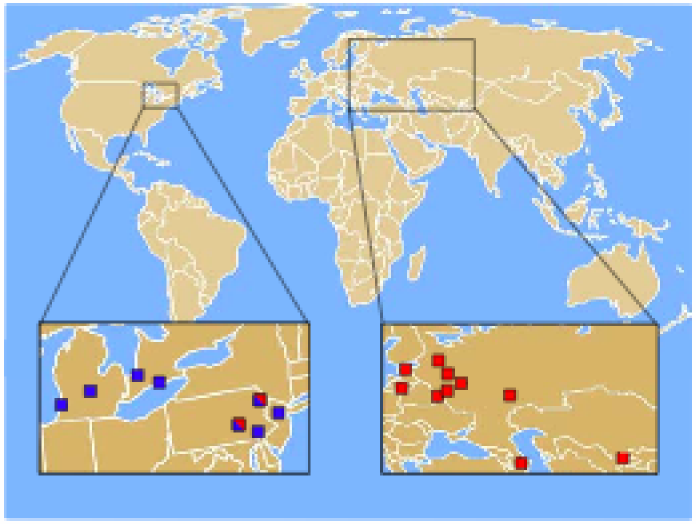
GRP. ***A*** **(EE) p = .45**

S. paradoxus

Global Biogeography: S. *paradoxus*



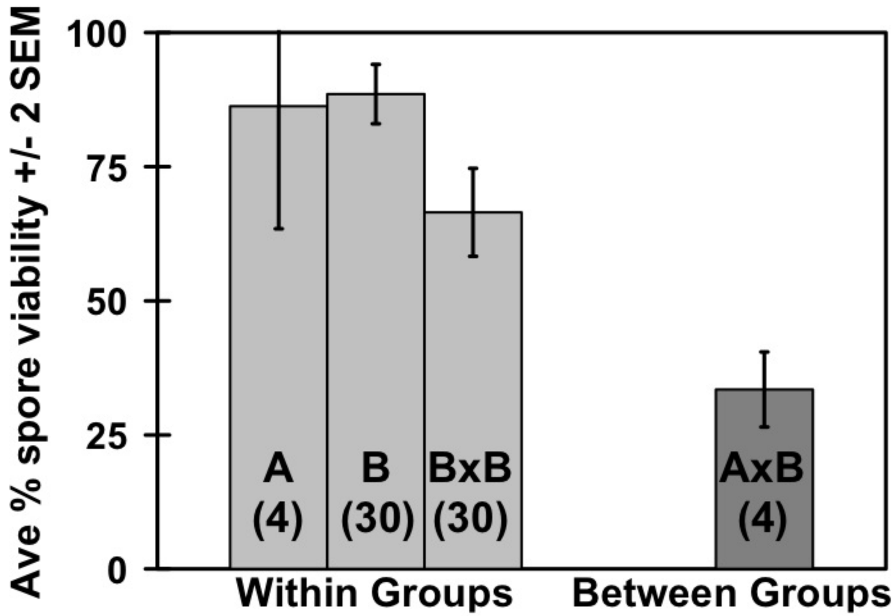




Evolution in allopatry followed by migration

Current Biology 17: 407 – 411.

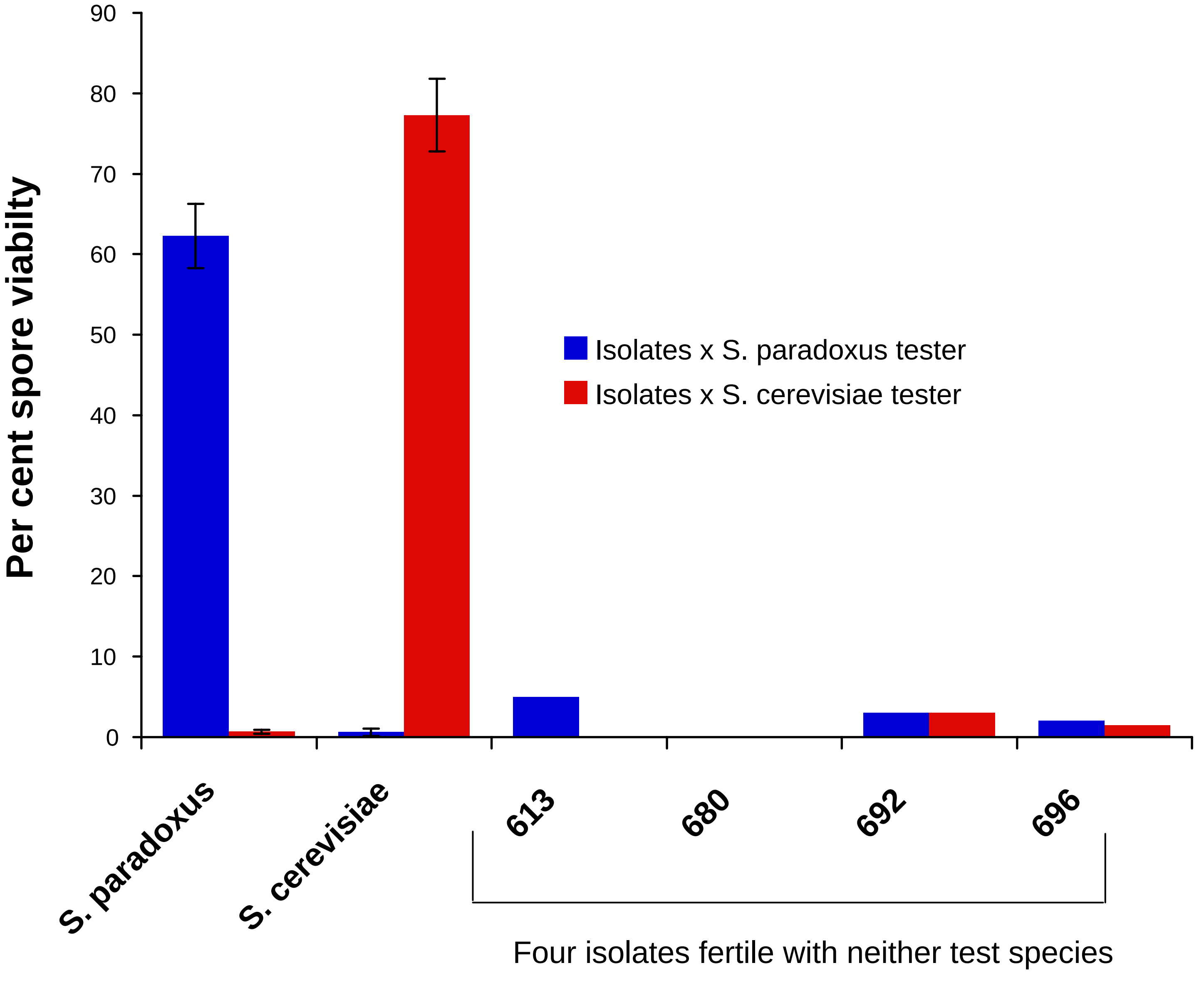
Are These Cryptic Species?



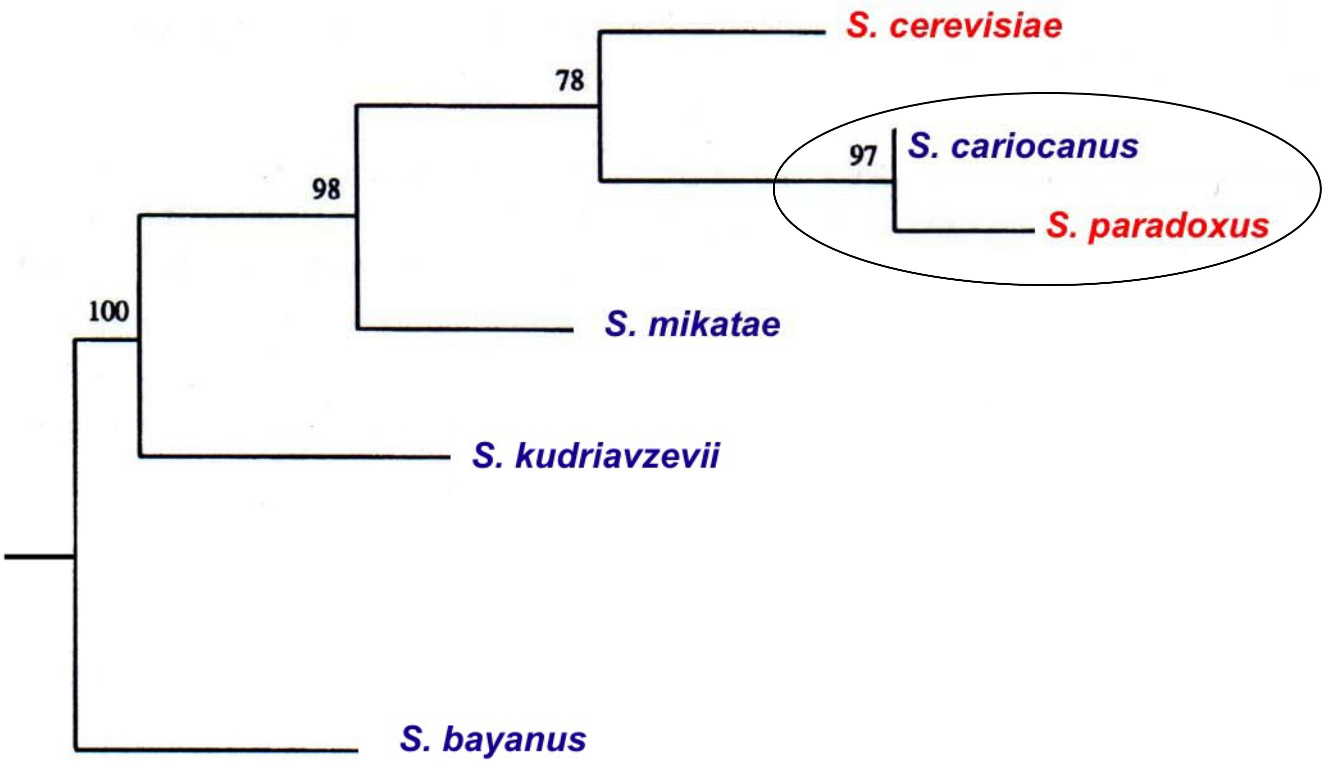
	A (N. America)	B (N. America)	C (N. America)
A (Eurasia)	3	176	160
A (N. America)		181	165
B (N. America)			89

Current Biology ***17****: 407 – 411.*

“Mystery” isolates



Saccharomyces sensu stricto



After Naumov *et al*. 2000

What are the mystery isolates?

Three possibilities (assuming that they are all the same thing).

1. Hybrids. This appears to be ruled out by recent sequence data.

2. *S. cariocanus*. Sequence data can’t rule this out, as *S. cariocanus* is *closer* in sequence to NA *S. paradoxus* (indeed, almost identical) than to EU *S. paradoxus*. (Interesting, huh?)

3. A newly diverging, previously unknown lineage closely related to *S. paradoxus*; a species *in statu nascendi*. (Most exciting to me…)

Conclusions

--Evidence suggests the existence of natural *S. cerevisiae* populations.

--S. cerevisiae and its known wild congener *S. paradoxus* are sympatric in nature and occupy the same habitat, at least in North America.

--Within geographical region (e.g., NA, Eurasia) neither species shows much evidence of geographic population structure.

--The two species exhibit markedly different genetic population structures in nature: *cerevisiae* populations are clonal, *paradoxus* populations are recombining.

--paradoxus exhibits genetic differentiation between continental regions and shows evidence of multiple, genetically isolated sympatric lineages, at least one of which is likely to have initially diverged in allopatry.

--There is emerging evidence (Duncan Greig, Helen Murphy) that prezygotic isolation and reinforcement are involved in speciation in yeast.

Some Future Prospects

--Does *S. cerevisiae* exhibit global population differentiation like *paradoxus*? (Are there globally distributed natural *cerevisiae* populations and are they genetically differentiated?)

--Nagging question: Are *S. cerevisiae* natural populations truly wild, or just feral?

--What is the nature of speciation processes in *Saccharomyces*? How many sympatric, genetically isolated lineages are there related to *S. paradoxus,* and what keeps them apart genetically? How big a role does mating behavior play in reproductive isolation? How important is allopatric divergence? Etc.

--What are the important ecological differences between natural *S. cerevisiae* and *paradoxus* populations?

--What are the important ecological, genomic and physiological differences within and between natural *Saccharomyces* populations?

Acknowledgments and Thanks

For actually doing much of the work described here: Heidi Kuehne (now postdoc U. Edinburgh) and Helen Murphy (now postdoc Wake Forest U.).

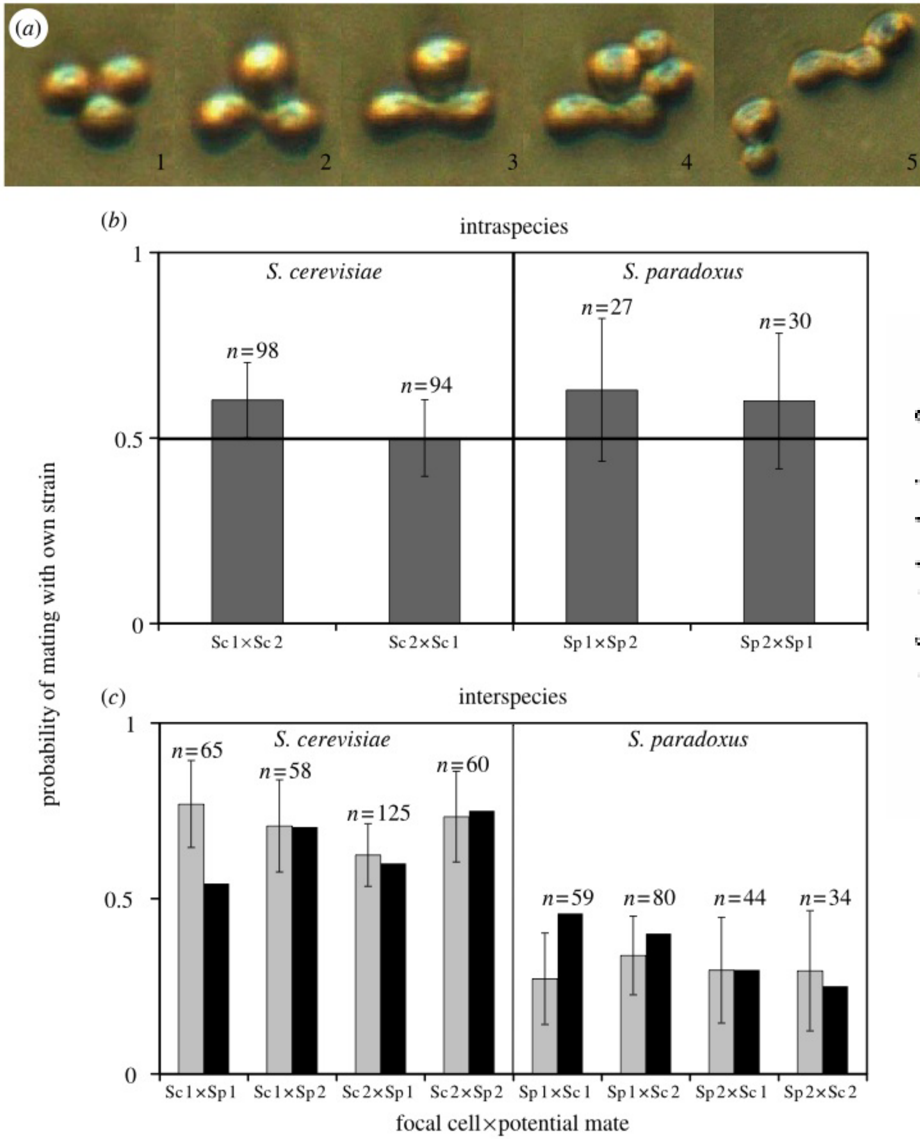
For collaboration and for generously teaching me about yeast: Gennadi Naumov and Elena Naumova.

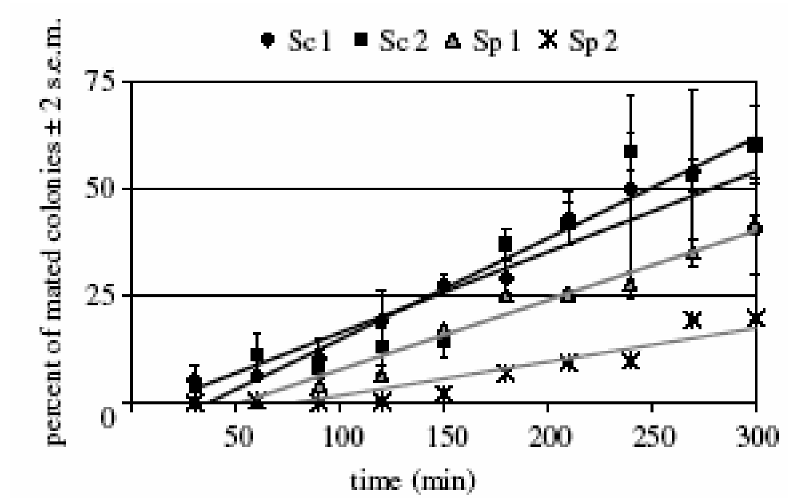
For sage advice and encouragement: André Lachance, Western Ontario U.

For help with the work: Peter Dombrowski, Chantal Francis, Ethan Fingerman, Joe Sweeney; numerous undergraduates.

For funding: Center for Microbial Ecology, Michigan State University; University of Pennsylvania Research Foundation; National Science Foundation

Premating isolation between *cerevisiae* and *paradoxus*?





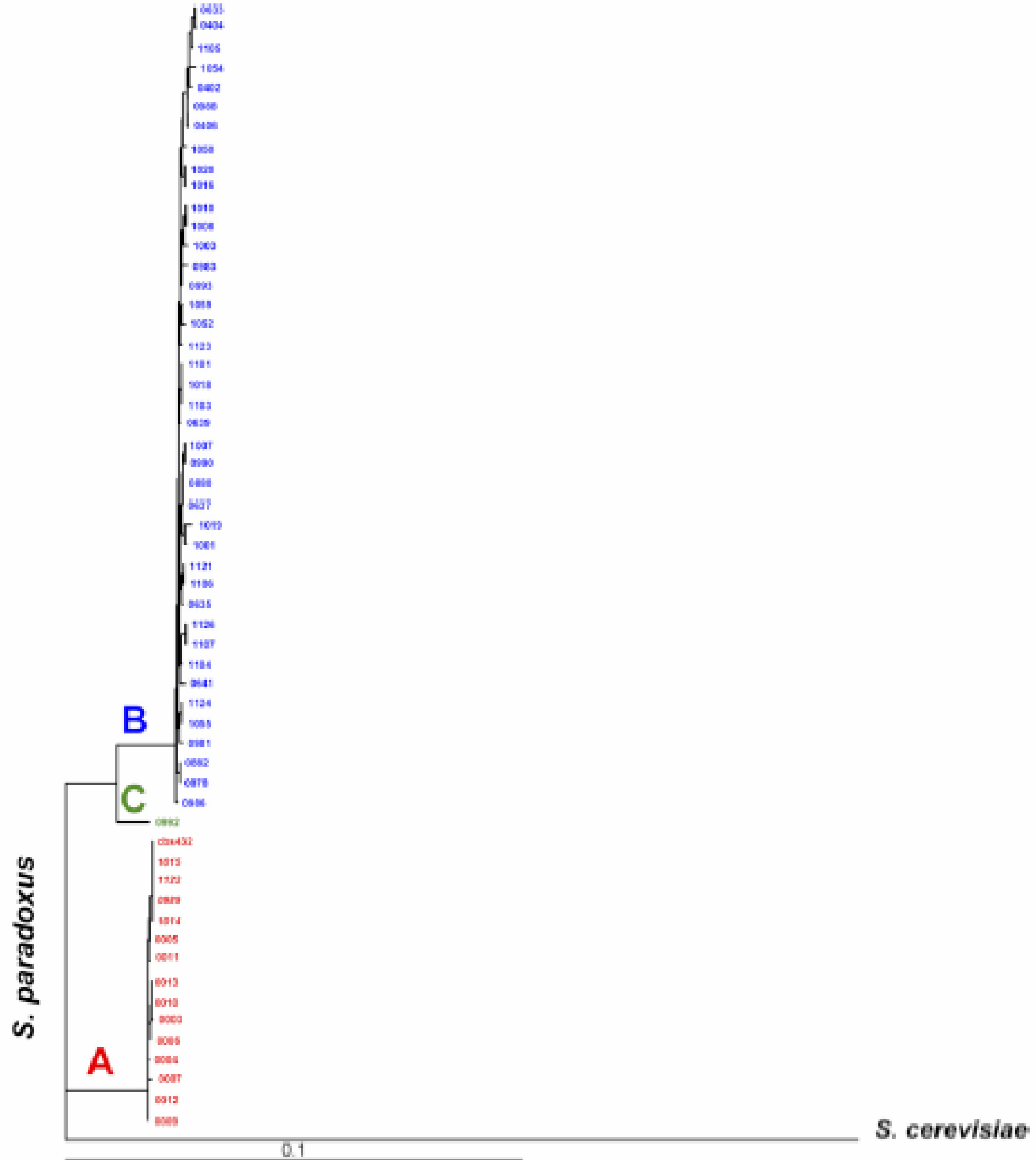


Figure S2. Complete Maximum-Likelihood Tree of the Three *S. paradoxus* Genetic Groups Rooted on *S. cerevisiae*

The tree was constructed with nine concatenated intron sequences from 57 *S. paradoxus* isolates; orthologous *S. cerevisiae* sequences were obtained from the *Saccharomyces* Genome Database. The major nodes separating groups A, B, and C received 100% bootstrap support (1000 replicates); the scale bar represents the number of per-site substitutions.

Different thermal growth profiles in *paradoxus* and *cerevisiae*

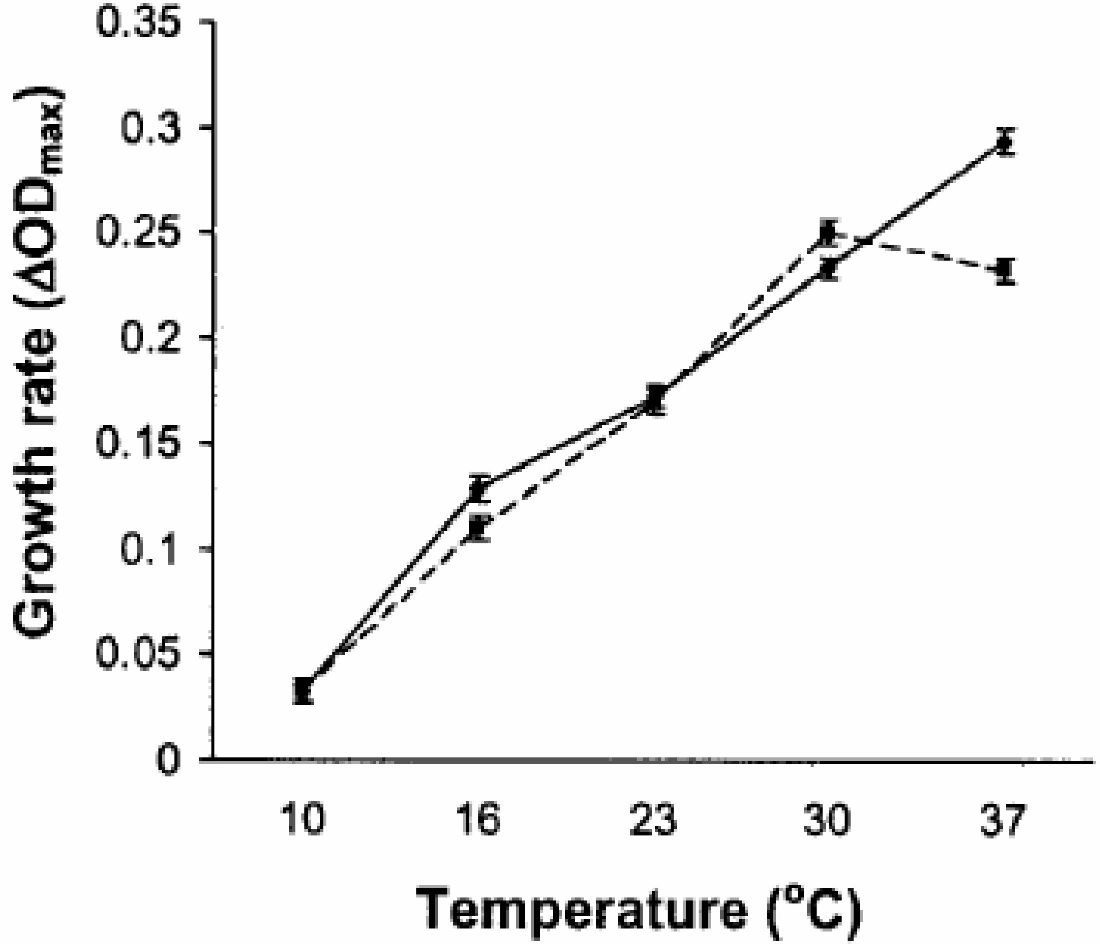


Fig. 1. Average growth rates (± S.E.M.) of sympatric natural *S. cerevisiae* (solid line) and *S. paradoxus* (dashed line) isolates at five temperatures. Growth rate values, shown as ΔOD_{max}, are the maximal hourly change in A_{600} observed during culture growth.

FEMS Yeast Research 4 (2002), 52-525