

Volume 36, Issue 1
January 2019

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Dmitry A Filatov 

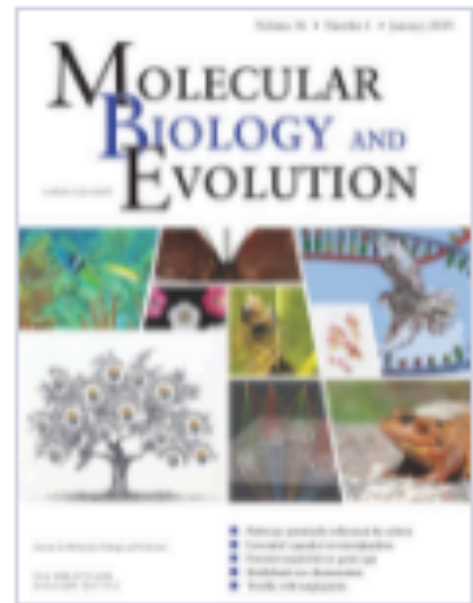
Molecular Biology and Evolution, Volume 36, Issue 1, January 2019, Pages 4–14,
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Published: 23 October 2018



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Comp Bio Seminar
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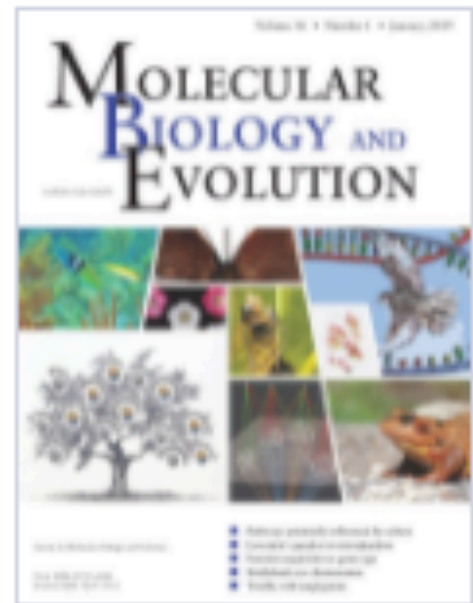
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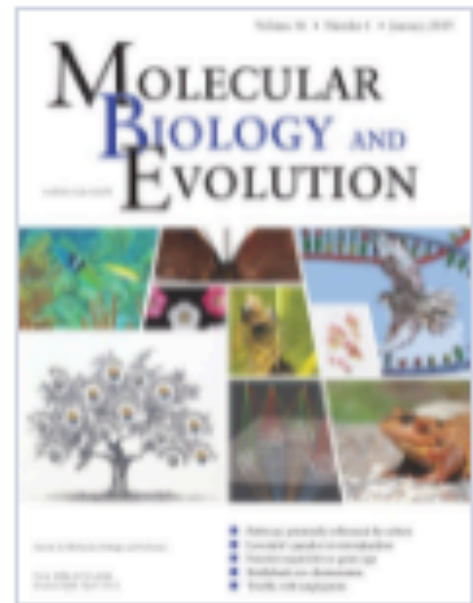
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Author Background

Dmitry A Filatov

“I’m interested in how evolutionary forces, such as natural selection, drive the change at the levels of genes and genomes.”

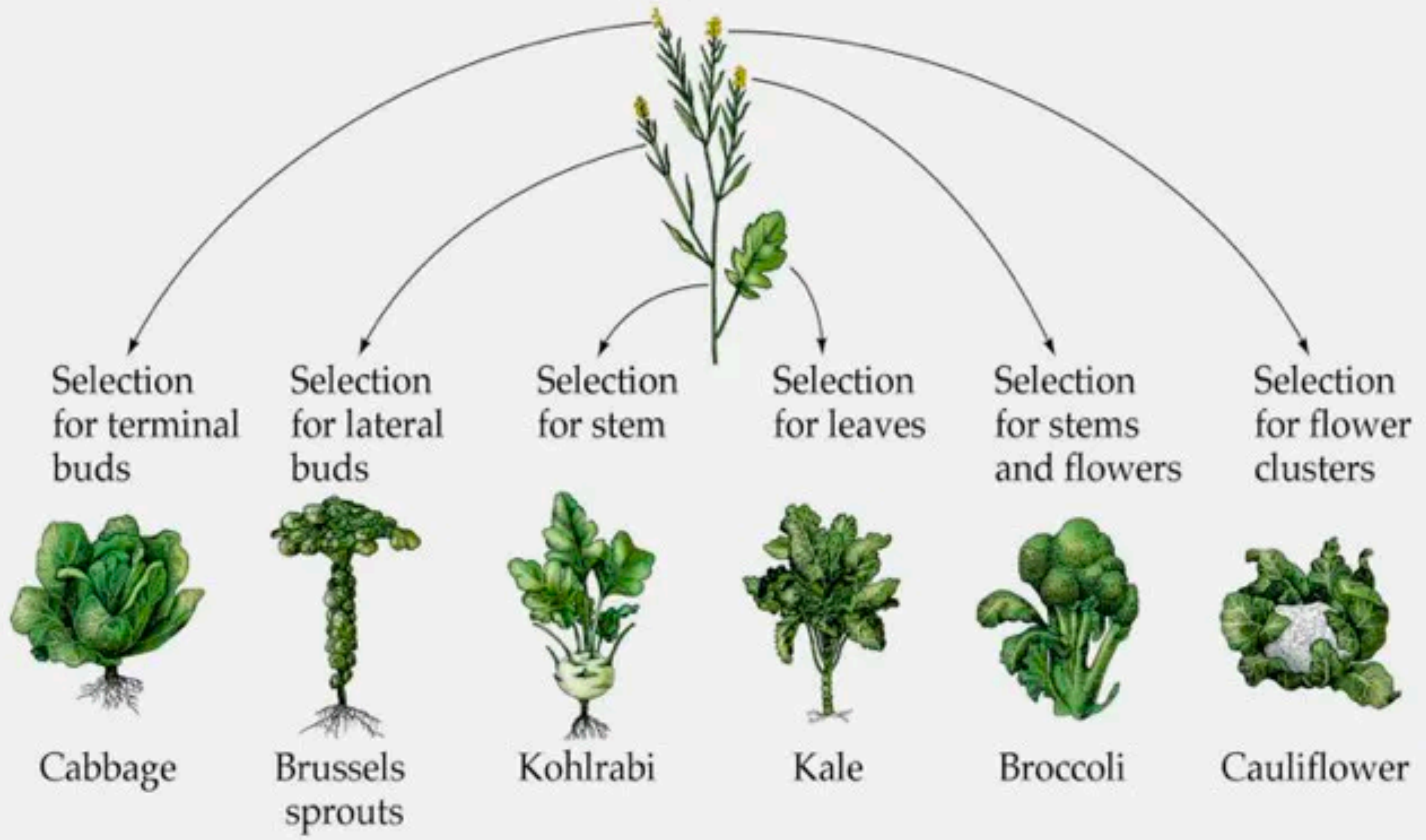
Mostly interested in:

1. Sex chromosome evolution
2. Speciation and adaptation in plants



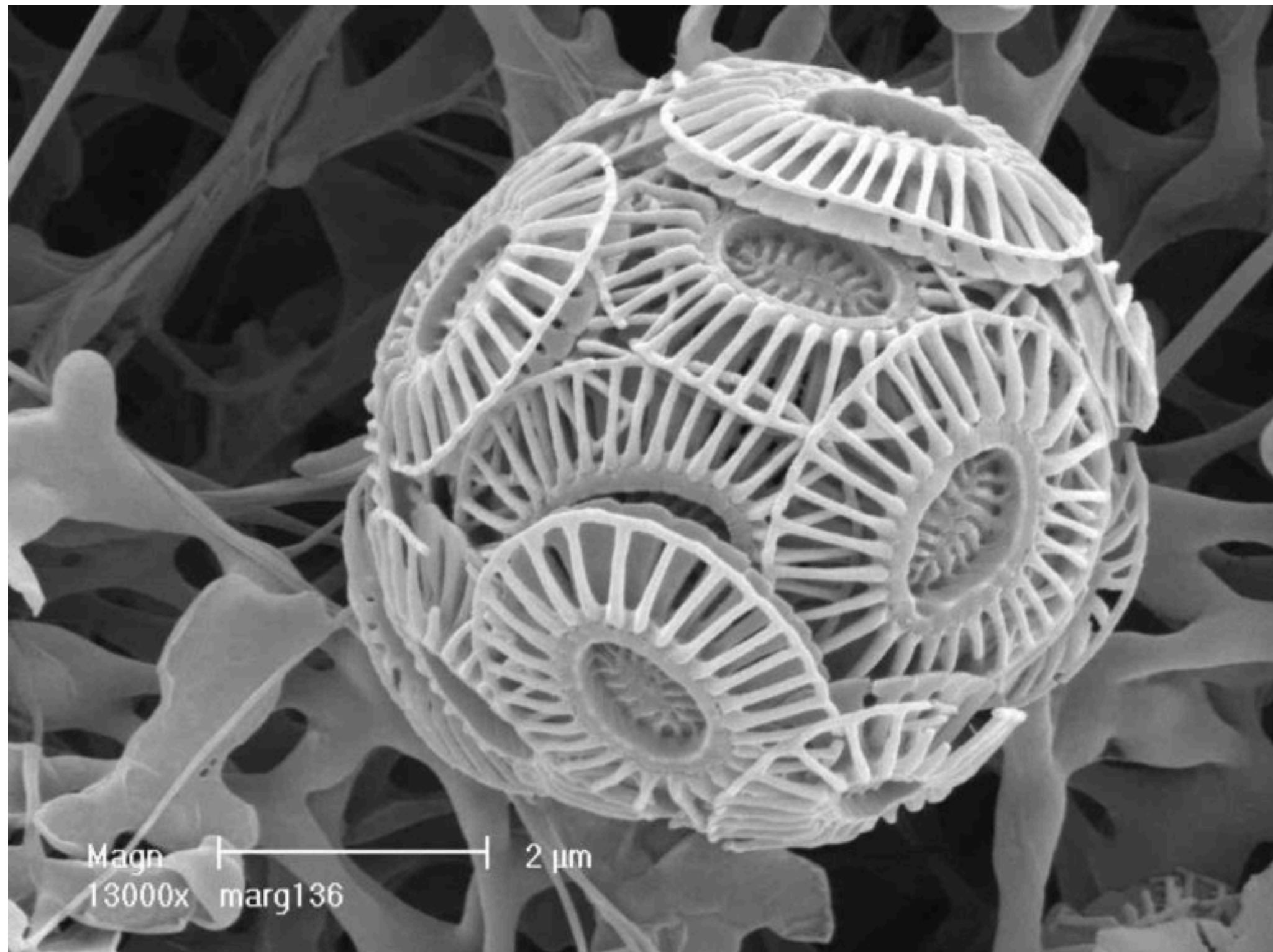
Professor Dmitry Filatov

Brassica oleracea

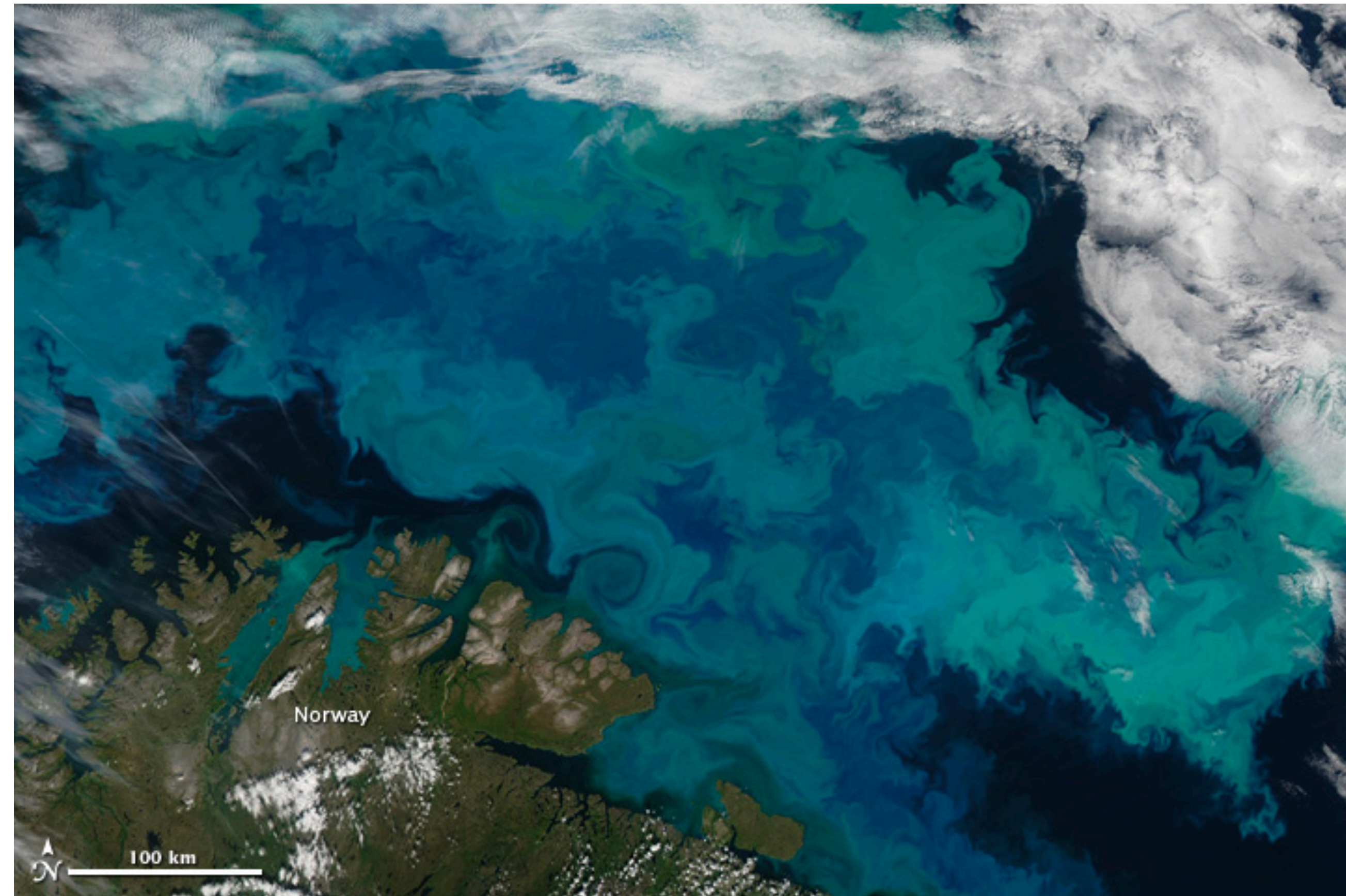


Phytoplankton Background

Single-celled algae

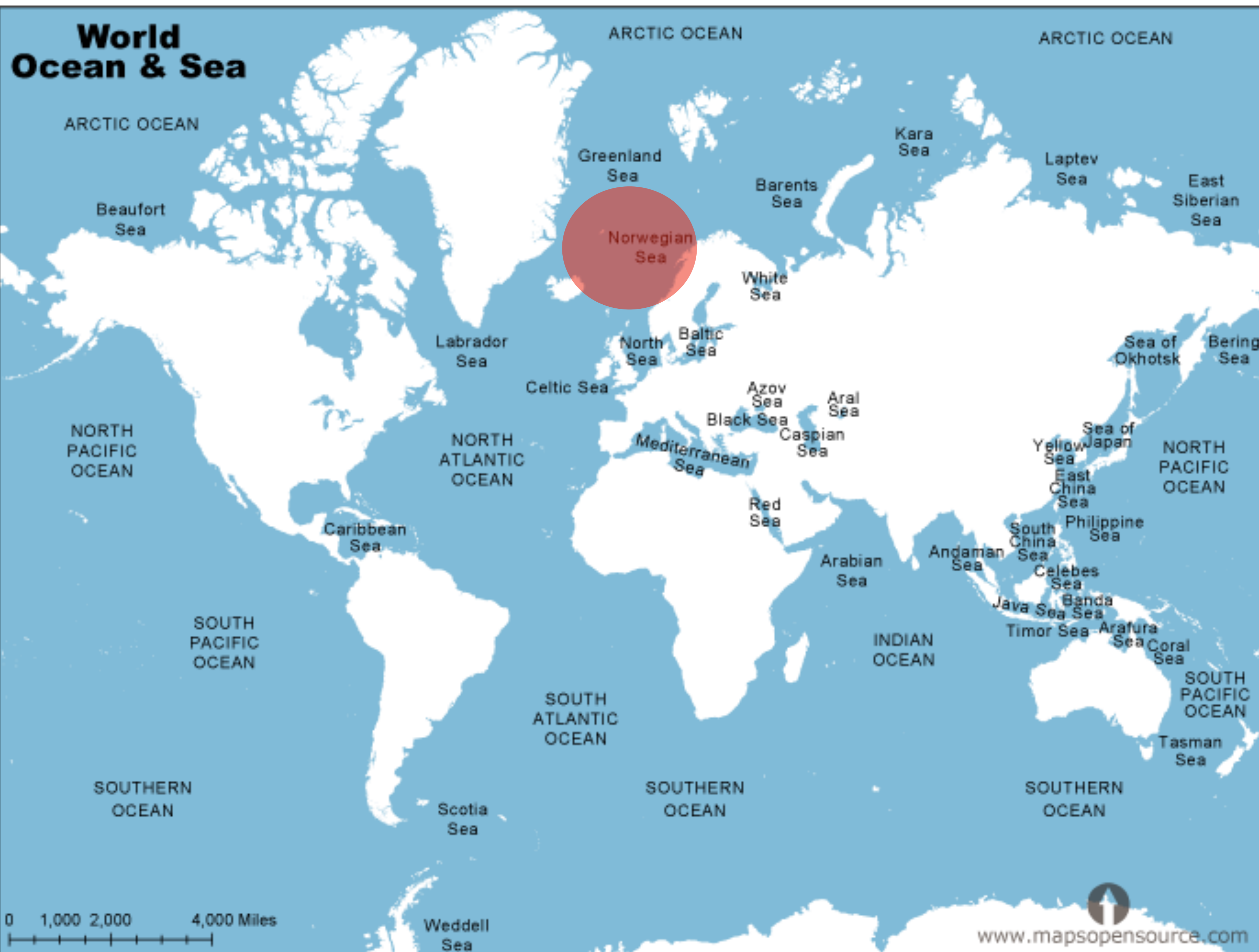


Emiliana huxleyi - a coccolith



Yields 50-85% of our O₂ | Sensitive to acidification | Basis of basically every ocean food web

World Ocean & Sea



25 M individuals per 100 mL

Norwegian Sea area: 1,383,000 km²

Max depth of sunlight: 200 m

$$\frac{25 \cdot 10^6}{100} \cdot 10^6 \cdot 1.3 \cdot 10^9 \cdot 50$$

$$1.6 \cdot 10^{22}$$

Lewontin's paradox (1974)

Of course the greater the population, the greater the genetic diversity.



Early student - overconfident, still believes biology is intuitive

Uh oh...that's actually false. And still nobody really understands why?!



Late stage grad student - lacks all confidence having realized they know nothing, accepts that nothing is intuitive

Lewontin's paradox (1974)

Of course the greater the population, the greater the genetic diversity.



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Late stage grad student - lacks all confidence having realized they know nothing, accepts that nothing is intuitive

Possible explanations:

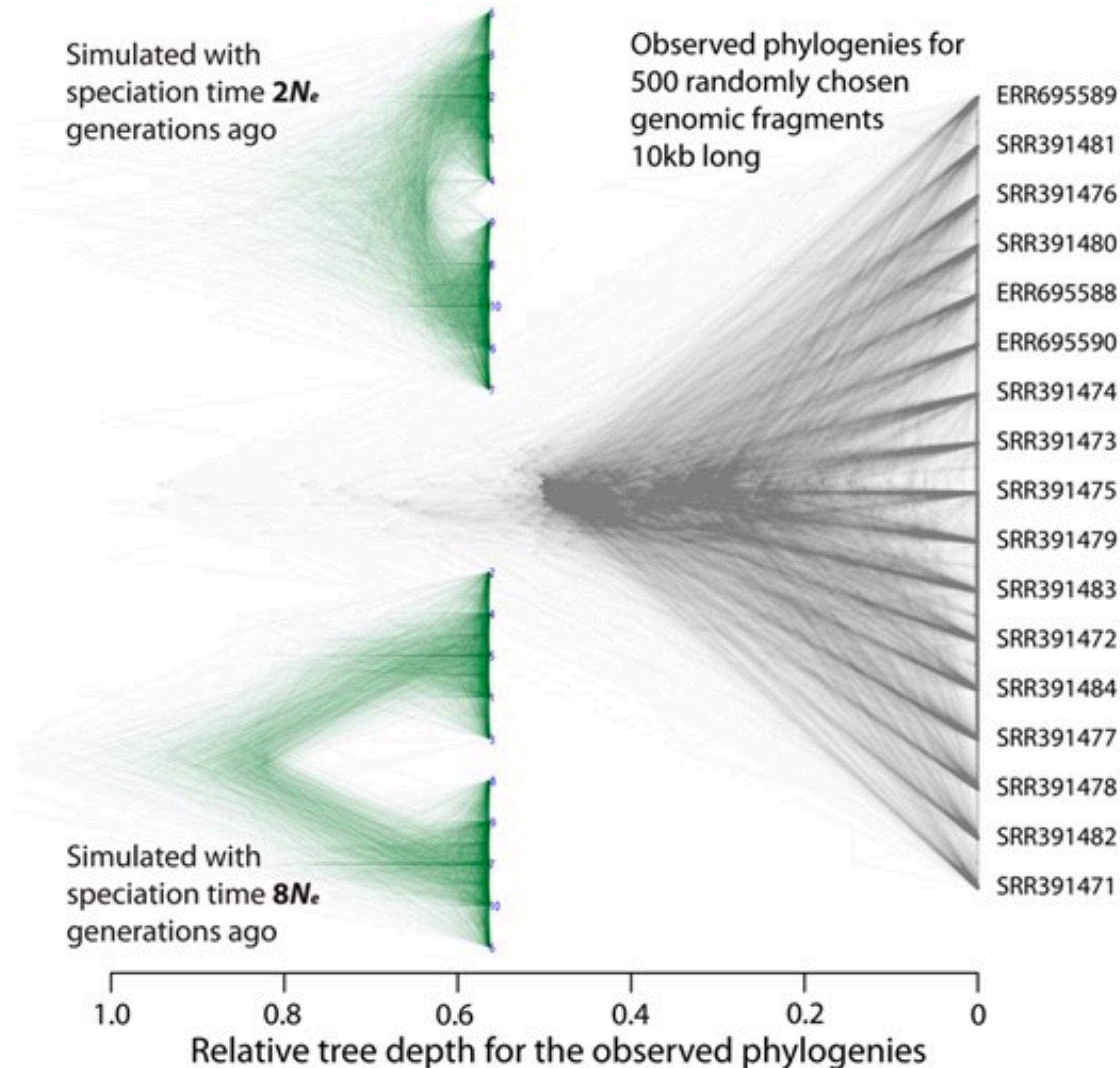
- Frequent adaptive evolution
- Demographic factors (like population size)
- Lower mutation rate in larger populations

How do we figure out what's causing Lewontin's Paradox?

Disproportionately modest genetic diversity in large populations

Look at the worldwide population

Is *E. huxleyi* a single cohesive species?



There's no clustering in the observation data (right), collected all over the world



E. huxleyi is a single, genetically cohesive species

Sample details

Table 1. *Emiliana huxleyi* Strains Analyzed in This Study.

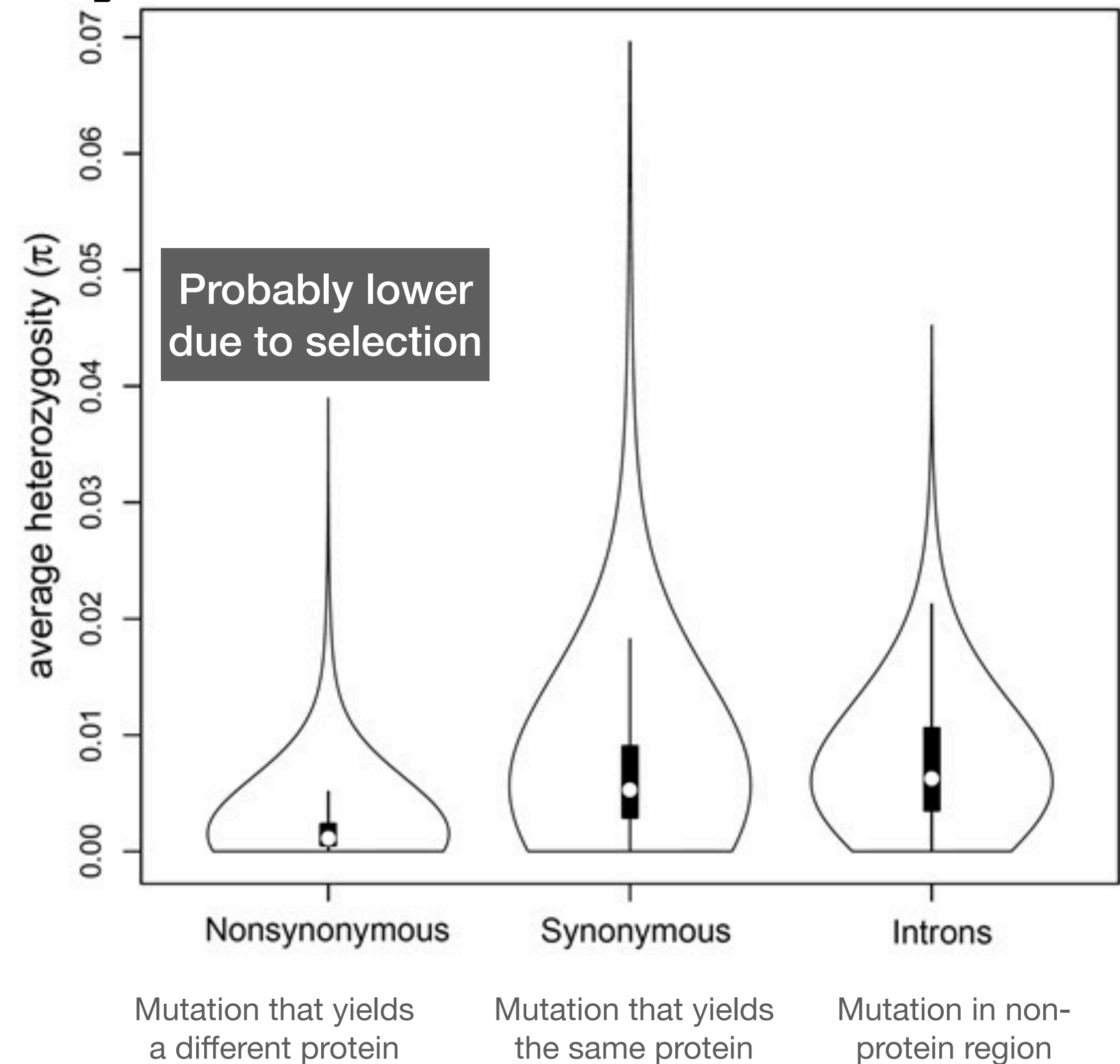
Name	Location	Reference	SRA Acc#	SRA Sample
AWI1516	South Pacific	Read et al. (2013)	SRR391471	SAMN00767675
92D	English Channel	Read et al. (2013)	SRR391472	SAMN00767676
92E	English Channel	Read et al. (2013)	SRR391473	SAMN00767677
92A	English Channel	Read et al. (2013)	SRR391474	SAMN00767678
NZEH	New Zealand	Read et al. (2013)	SRR391475	SAMN00767679
L	Oslo fjord	Read et al. (2013)	SRR391476	SAMN00767680
12-1	Sargasso Sea	Read et al. (2013)	SRR391477	SAMN00767681
EH2	Australia	Read et al. (2013)	SRR391478	SAMN00767682
M219	New Zealand	Read et al. (2013)	SRR391479	SAMN00767683
B11	Bergen Sea	Read et al. (2013)	SRR391480	SAMN00767684
B39	Bergen Sea	Read et al. (2013)	SRR391481	SAMN00767685
M217	Bergen Sea	Read et al. (2013)	SRR391482	SAMN00767686
Van556	Vancouver, BC	Read et al. (2013)	SRR391483	SAMN00767687
92F	English Channel	Read et al. (2013)	SRR391484	SAMN00767688
CHC428	South Pacific	von Dassow et al. (2015)	ERR695590	SAMEA3164474
CHC350	South Pacific	von Dassow et al. (2015)	ERR695589	SAMEA3164475
CHC307	South Pacific	von Dassow et al. (2015)	ERR695588	SAMEA3164476

How Genetically Diverse is *E. huxleyi*?

Looking at 17 whole genomes - not very

- Previous work (Andolfatto 2005) showed large insertion/deletion polymorphism, probably due to high rates of chromosomal rearrangements
- SNP (single nucleotide polymorphism) rate is low

...but why???

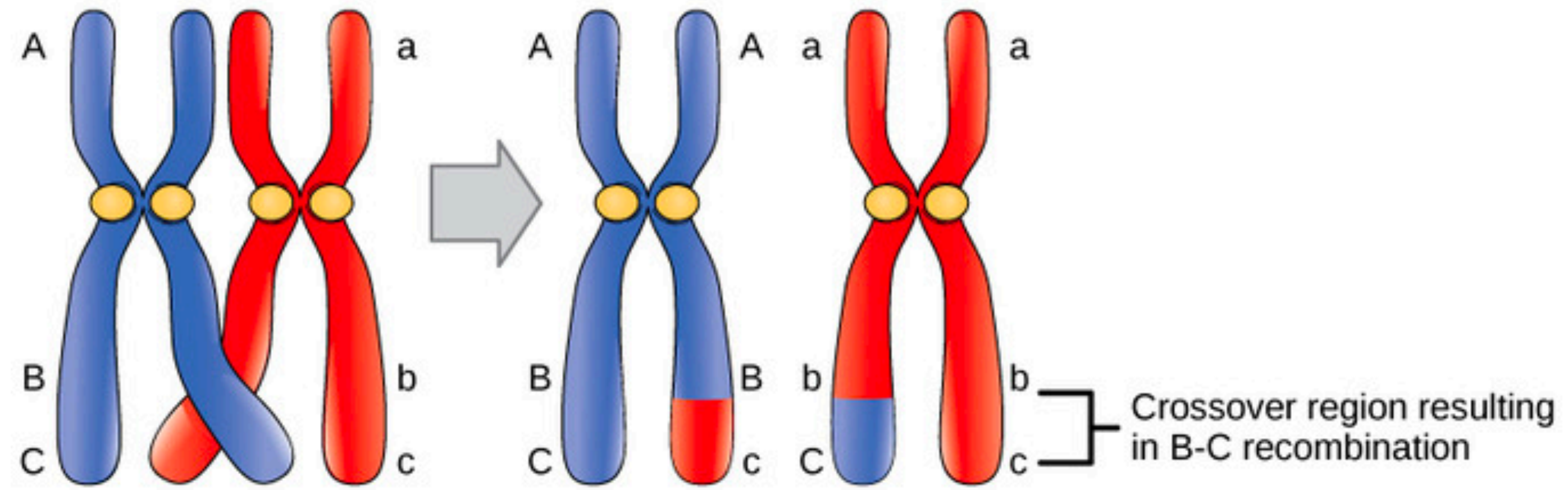
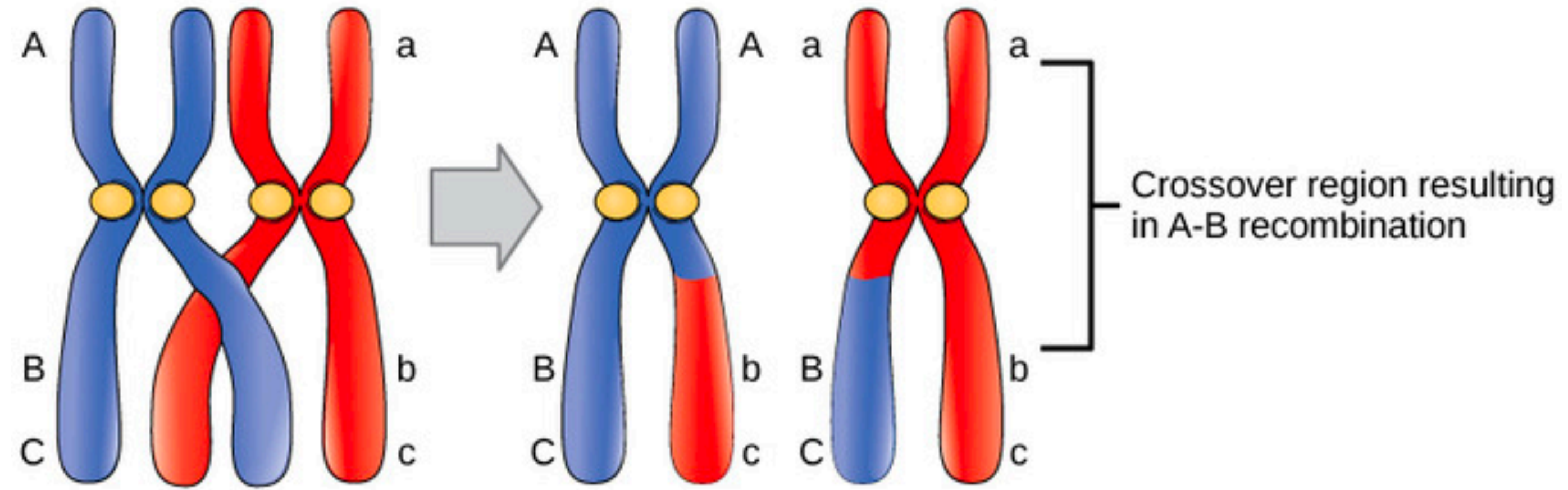


Is *E. huxleyi* Predominantly Clonal?

No

Linkage Disequilibrium: the nonrandom association of alleles at different loci

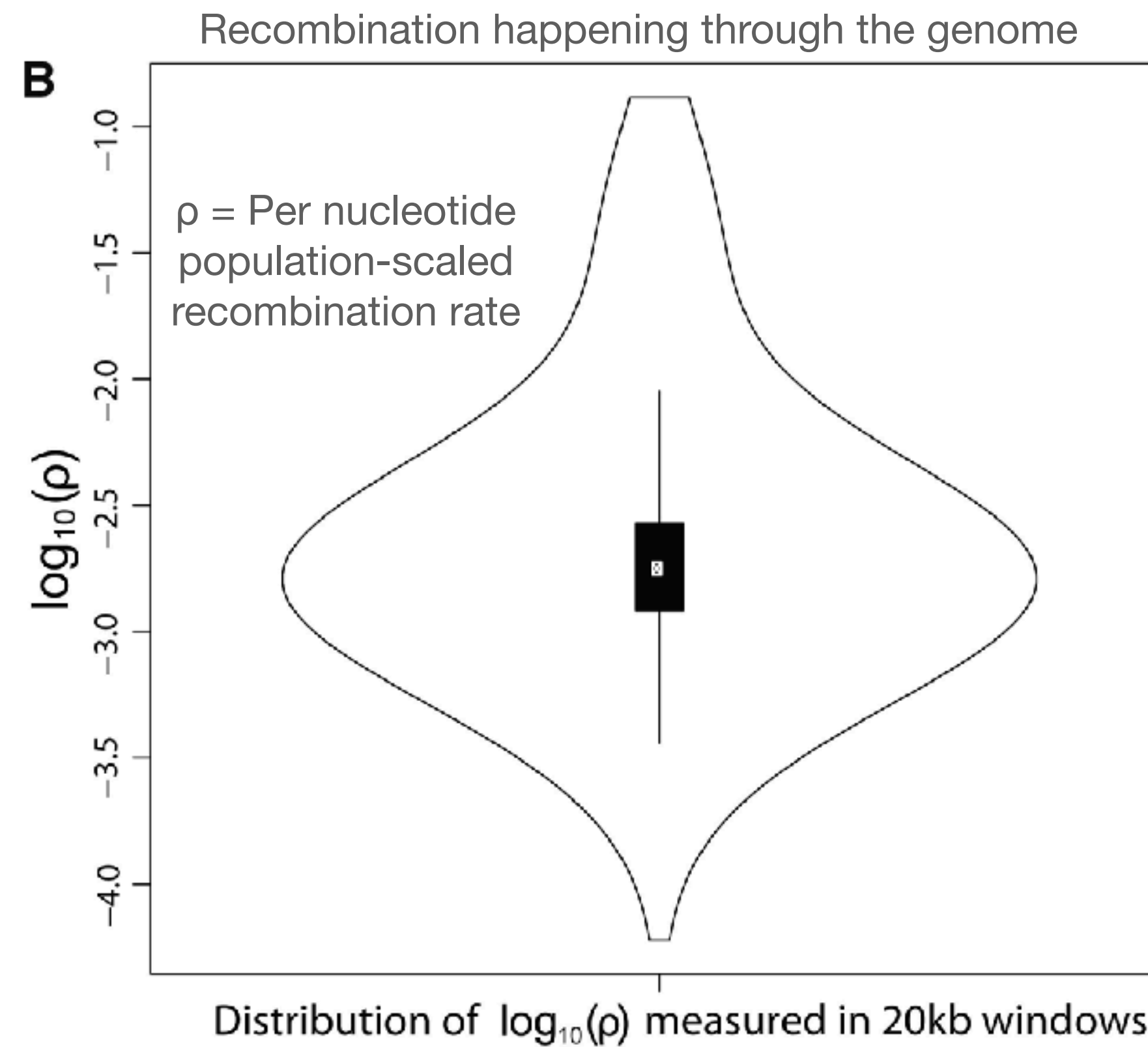
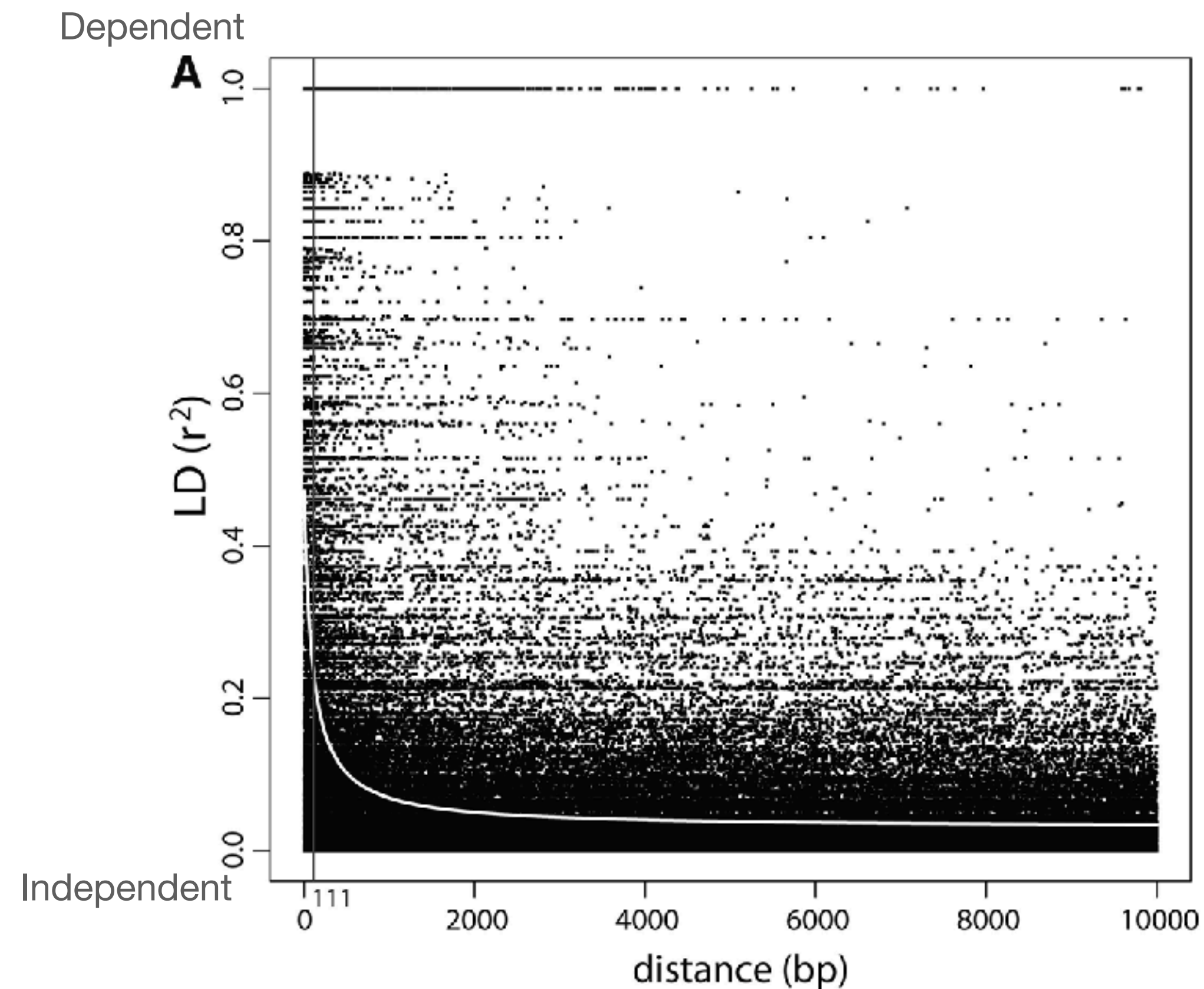
Quick Recap of Linkage



Is *E. huxleyi* Predominantly Clonal?

No

Linkage Disequilibrium: the nonrandom association of alleles at different loci



However...

- Algae blooms may be clonal (Krueger-Hadfield et al. 2014)
- Even occasional sexual reproduction may break down nonrandom associations between alleles (yielding low LD)
- We can't study this in a lab because “this species is not amenable to crosses”

Can Demography Account for Low Genetic Diversity?

Not really

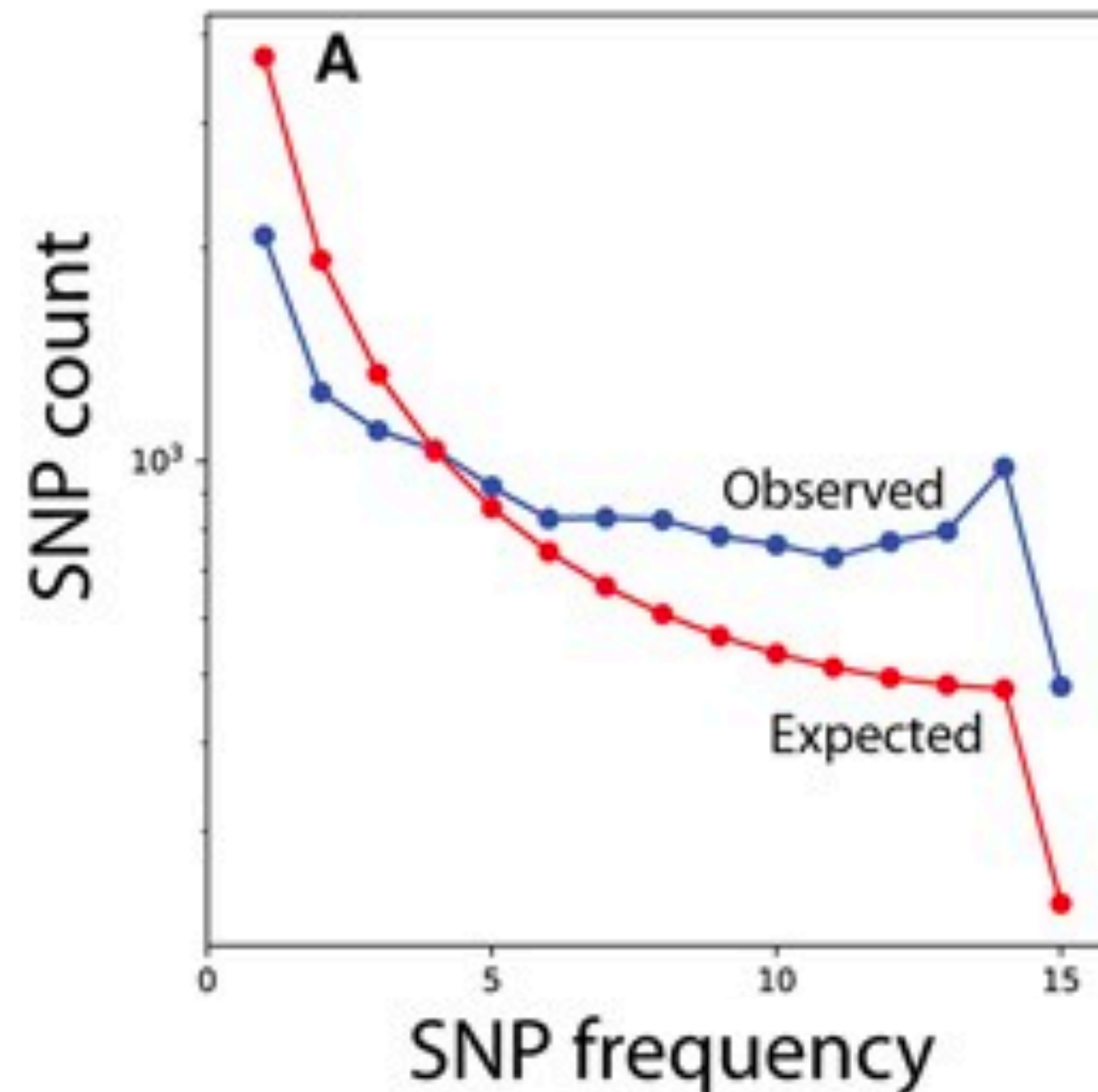
A: What if the population was recently small and exploded?

Too many frequent SNPs, not enough lowly present SNPs

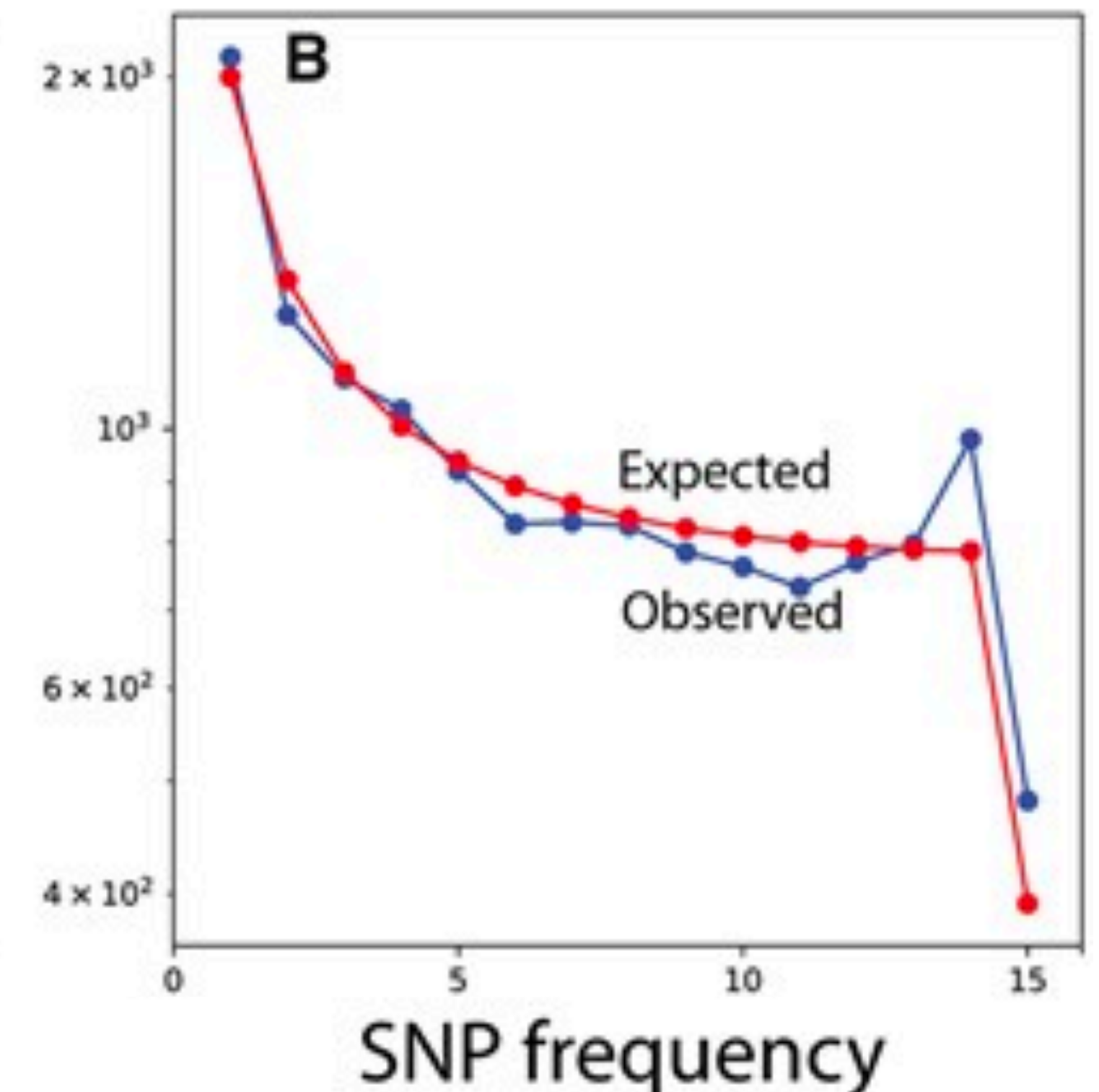
B: What if there were two big population changes?

Model fit doesn't significantly improve.

Standard neutral model



Three epochs model



Can Low Mutation Rate Account for Low Genetic Diversity?

Lol no

Even IF it had a mutation rate an order of magnitude lower than any other organism studied so far, this wouldn't sufficiently explain how conserved this genome is.

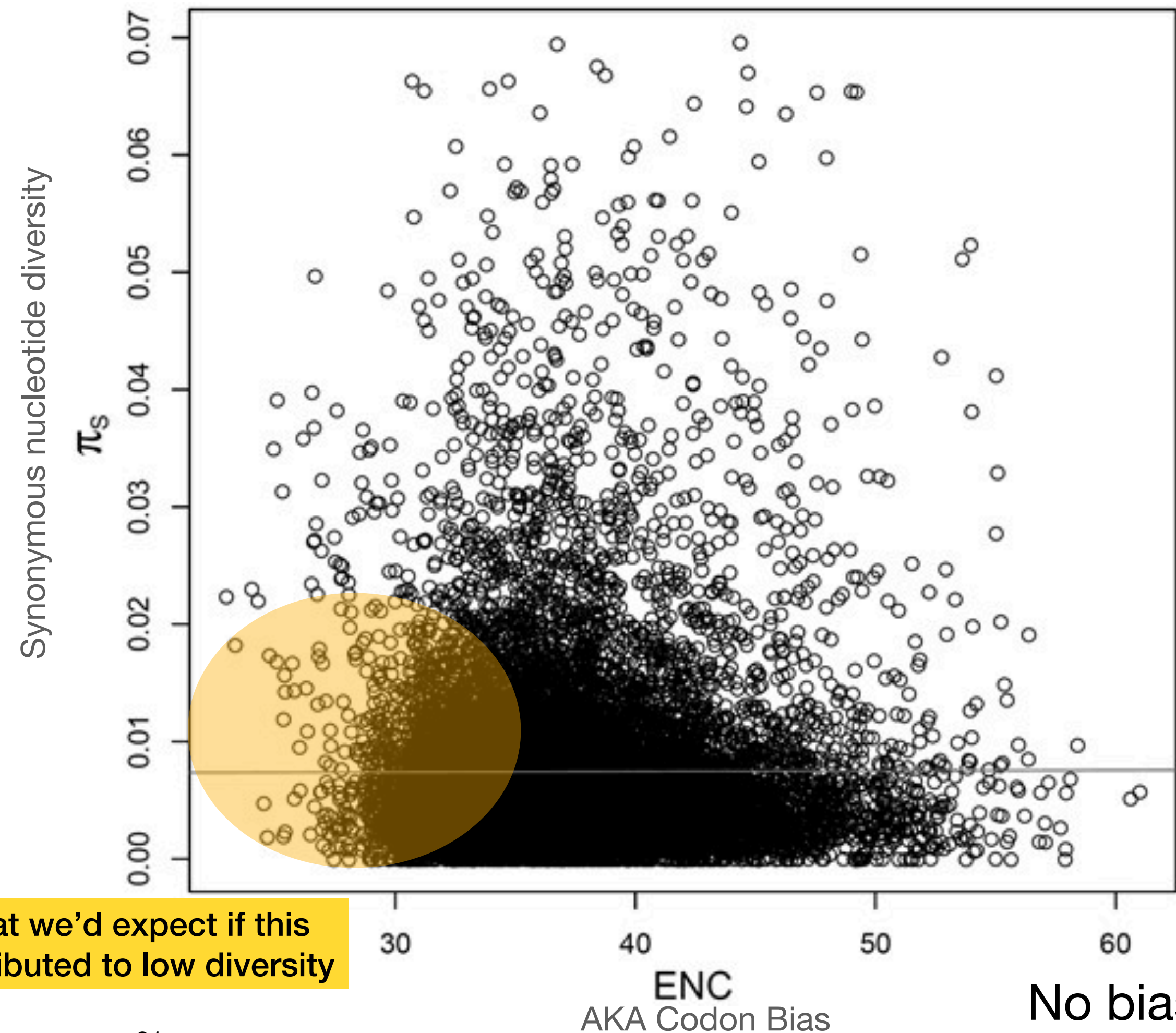
Published a paper solely about this in July 2020:

<https://academic.oup.com/gbe/article/12/7/1051/5869440>

Can Selection on Codon Usage Explain Low Genetic Diversity?

Maybe a little? But not really.

		Second letter				Third letter
		U	C	A	G	
U	UUU } Phe	UCU } Ser	UAU } Tyr	UGU } Cys	U C A G	
	UUC } Leu	UCC } Ser	UAC } Tyr	UGC } Cys		
	UUA } Leu	UCA } Ser	UAA Stop	UGA Stop		
	UUG } Leu	UCG } Ser	UAG Stop	UGG Trp		
C	CUU } Leu	CCU } Pro	CAU } His	CGU } Arg	U C A G	
	CUC } Leu	CCC } Pro	CAC } His	CGC } Arg		
	CUA } Leu	CCA } Pro	CAA } Gln	CGA } Arg		
	CUG } Leu	CCG } Pro	CAG } Gln	CGG } Arg		
A	AUU } Ile	ACU } Thr	AAU } Asn	AGU } Ser	U C A G	
	AUC } Ile	ACC } Thr	AAC } Asn	AGC } Ser		
	AUA } Met	ACA } Thr	AAA } Lys	AGA } Arg		
	AUG } Met	ACG } Thr	AAG } Lys	AGG } Arg		
G	GUU } Val	GCU } Ala	GAU } Asp	GGU } Gly	U C A G	
	GUC } Val	GCC } Ala	GAC } Asp	GGC } Gly		
	GUA } Val	GCA } Ala	GAA } Glu	GGA } Gly		
	GUG } Val	GCG } Ala	GAG } Glu	GGG } Gly		

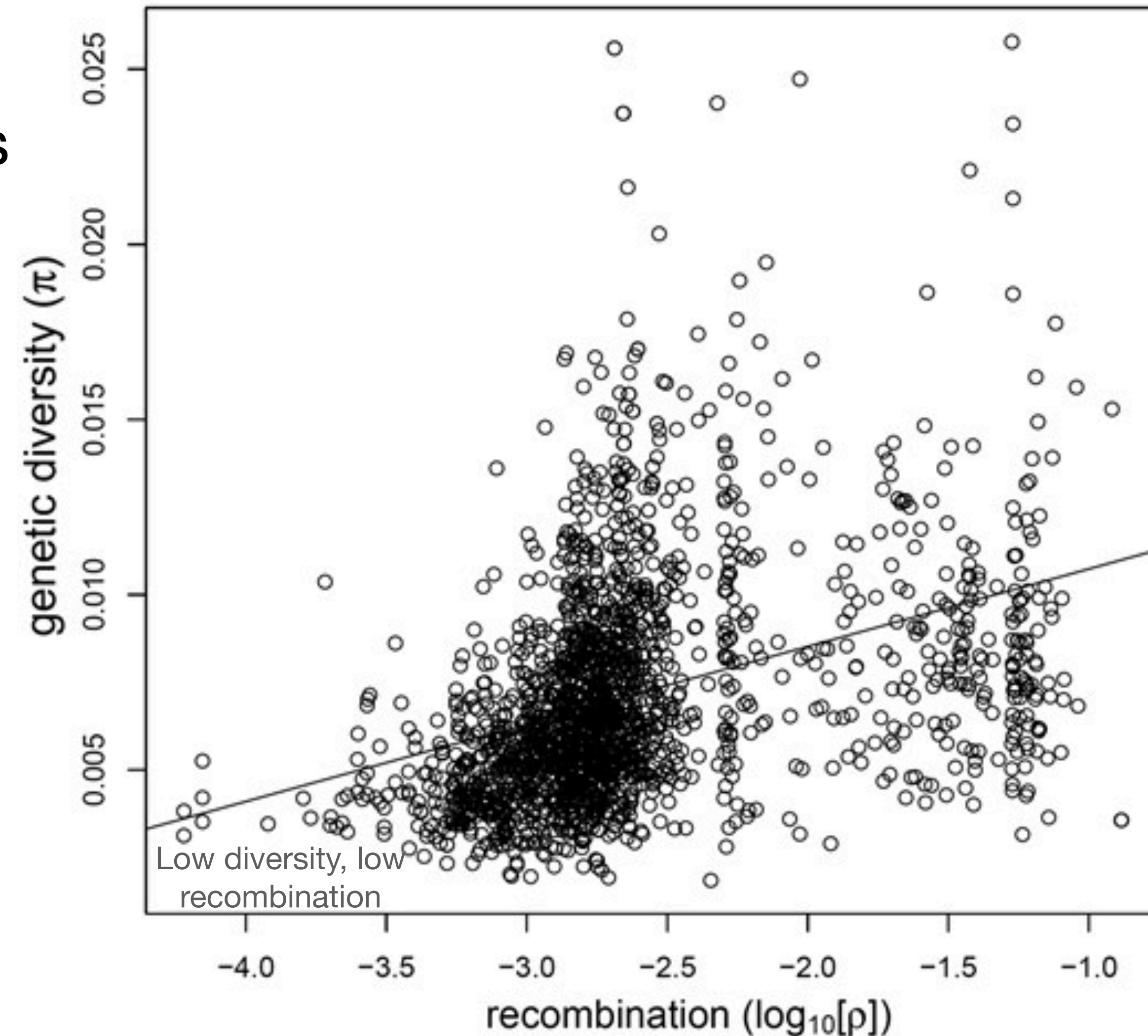


What we'd expect if this contributed to low diversity

Can Linked Selection Explain Limited Diversity?

Maybe a bit?

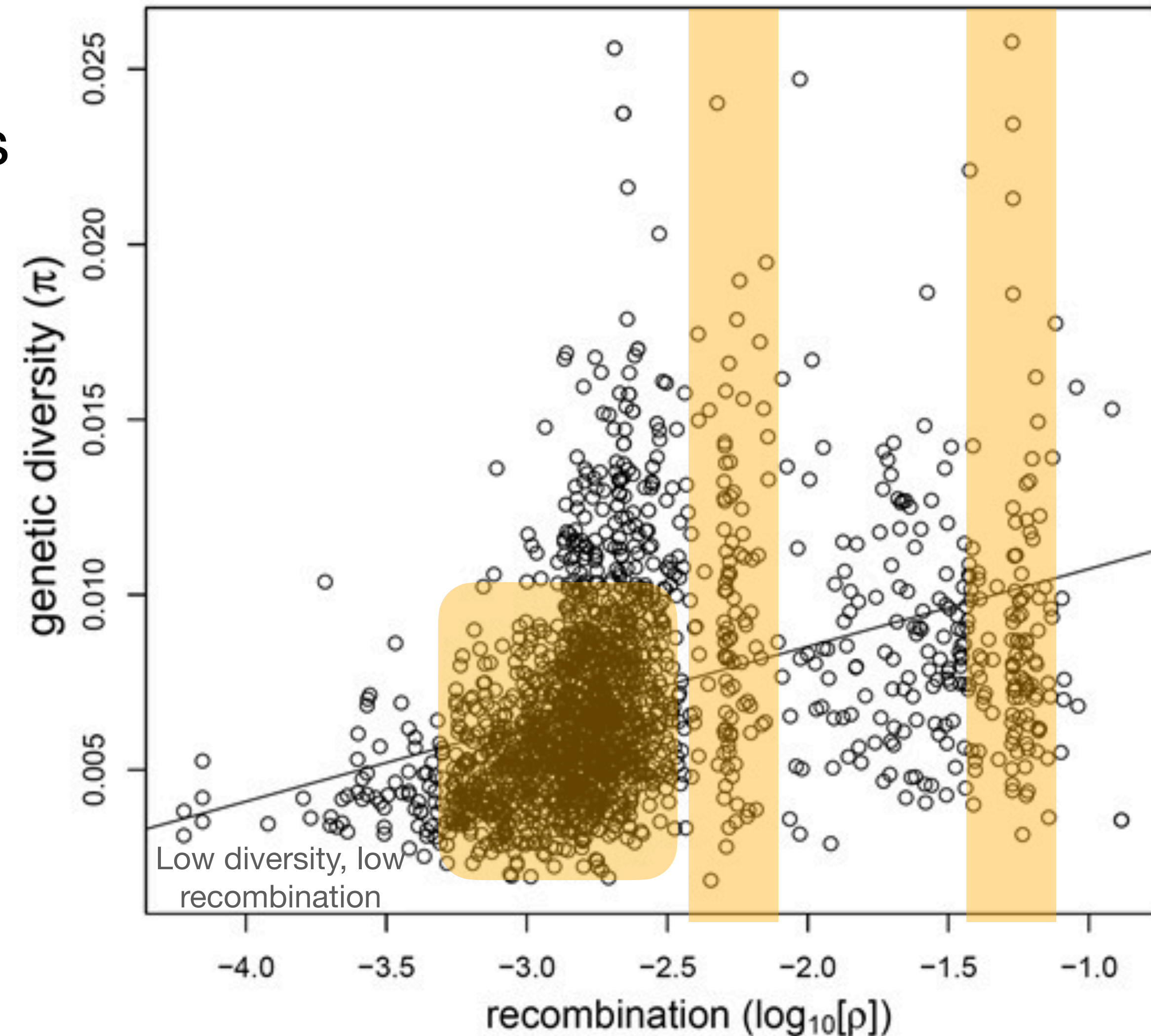
- “A spread of an adaptive allele eliminates genetic diversity at linked sites”
AKA hitchhiking



Can Linked Selection Explain Limited Diversity?

Maybe a bit?

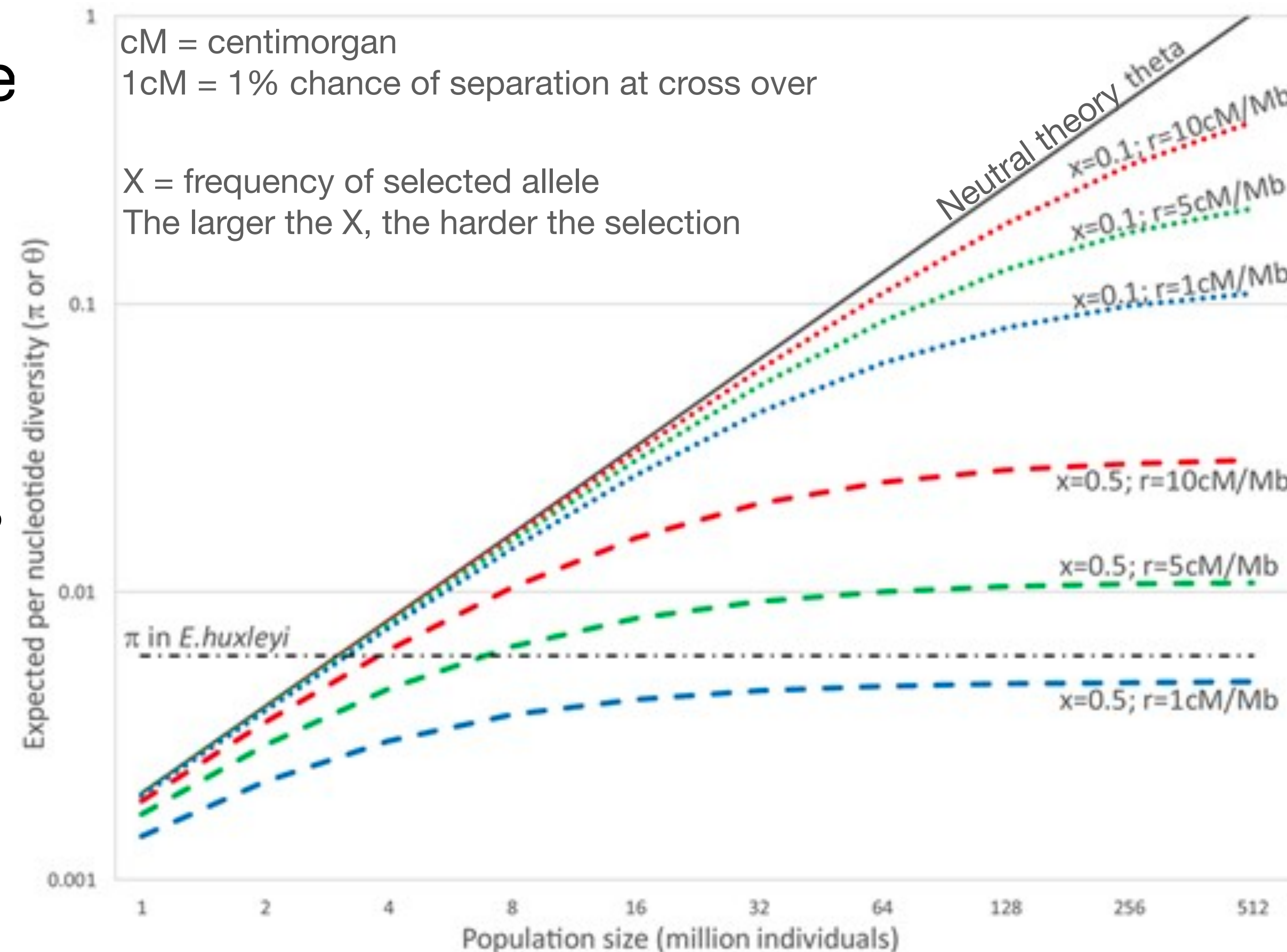
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Can Linked Selection Explain Limited Diversity?

Maybe a bit?

- “A spread of an adaptive allele eliminate genetic diversity at linked sites”
AKA hitchhiking
- Current models are based on much smaller populations and macroscopic eukaryotes...this model is semi-useless



Summary

E. huxleyi

- Not solely clonal
- Not genetically diverse
- No demography (population shapes) that would explain lack of diversity
- No wildly low mutation rate
- Maybe some codon selection
- Maybe some linked adaptation

So where does that leave us?

- *E. huxleyi* DOES sexually reproduce...but also might be clonal sometimes
 - We really need to figure out the basics of this species in the wild
- The presence of SNPs is surprisingly low...but we need to do more complete sequencing to be sure
- We need to know a lot more about *E. huxleyi* and other marine life to begin making models
 - How are they adapting?
 - How are their populations expanding?

Thoughts?

- Are there any new technologies that might help interrogate this paradox?
 - Ex. Nanopore sequencing
- Are there any theories Filatov may have overlooked?
- Are there other populations you'd like to see this analysis applied to?
 - Ex. Other keystone species for climate change analysis
- How does speciation happen then? (Filatov 2021)