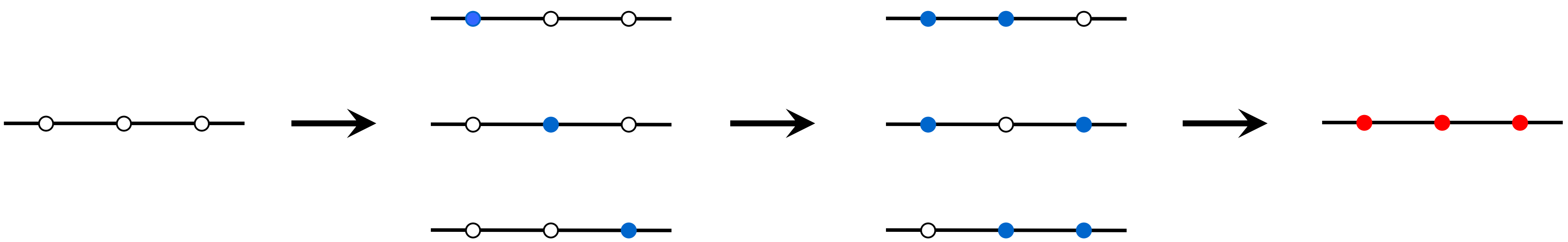
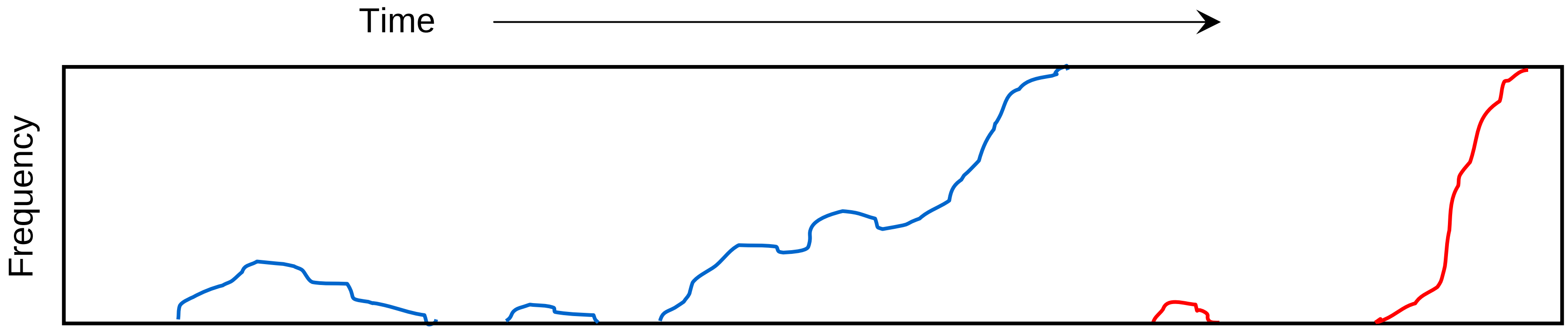
Evolution of a Complex Adaptation Through Neutral / Deleterious Intermediates



Fitness: 1 $1 - s_1$ $1 - s_1$ $1 + s_2$

A Three-site Model

Michael Lynch, Indiana Univ **Jan 11, 2010** **KITP Evo Cell Program**

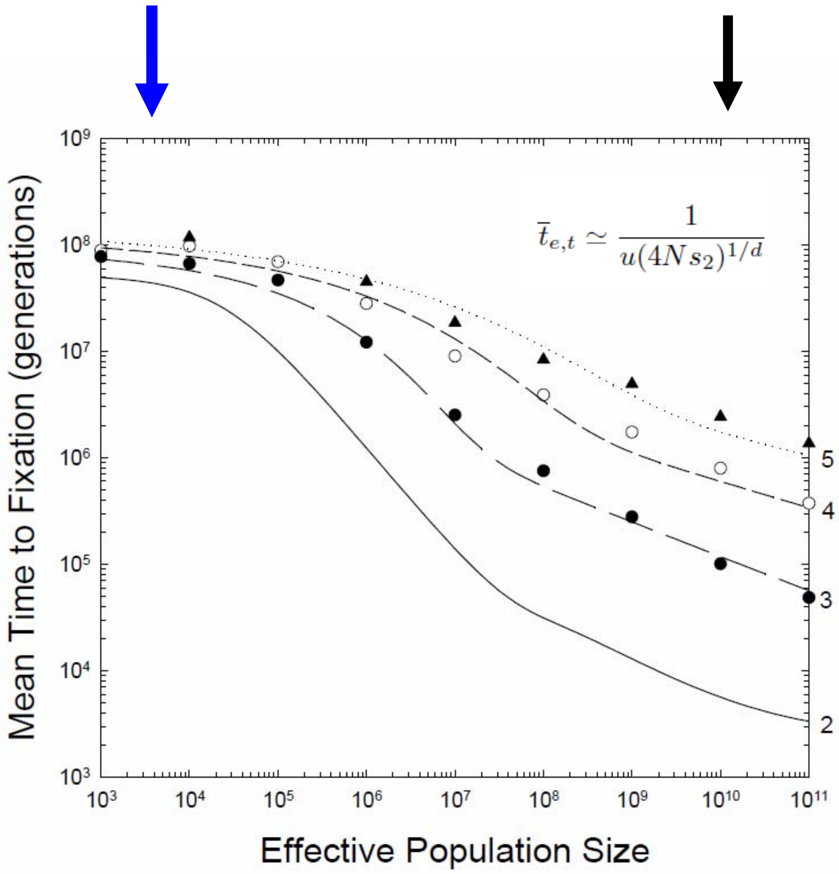


• Small population sizes – adaptation proceeds in a stepwise fashion, which can necessitate a sojourn through a mean-population fitness bottleneck.

• Large population sizes – intermediate deleterious alleles need never be fixed, but are kept at low frequencies by selection-mutation balance, serving as launching pads for final adaptation.

Evolution of a Complex Adaptation Through Neutral Intermediates

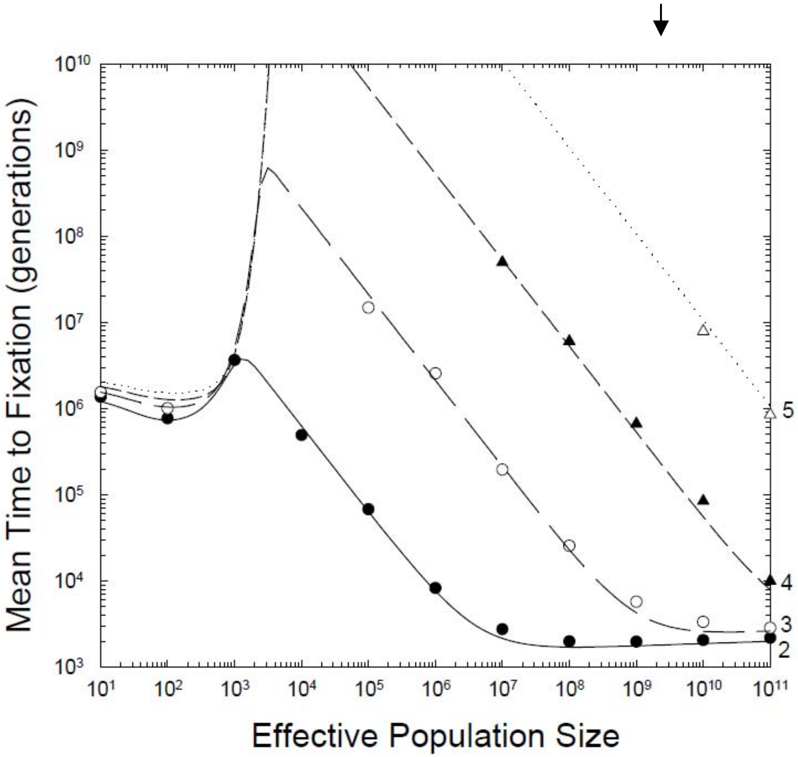
Frequency of d-step alleles at time t = $(ut)^d$
Selection takes hold when the frequency reaches $1/(4Ns_2)$



- Small population size – rate of adaptation is nearly independent of complexity because the larger number of steps is compensated by the larger number of paths.
- Large population size – rate of adaptation is inversely proportional to the mutation rate per site, not the product over all sites.
- As the number of steps increases, the relationship between N and the rate of adaptation becomes progressively flatter.
- With an evolvable mutation rate, the time to adaptation at small N will be reduced (not shown).

Evolution of a Complex Adaptation Through Deleterious Intermediates

Rate of establishment = $4Nd!(u/s_1)^d(s_2/s_1)$



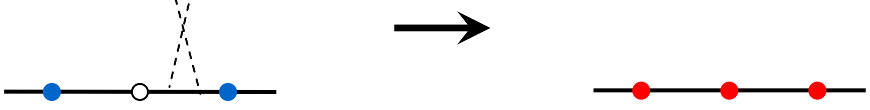
Small populations:

intermediate steps are effectively neutral.

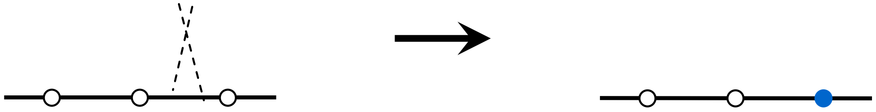
Large populations:

deleterious first-step alleles have half lives of 1 / s_1 generations, and must acquire d-1 additional mutations for adaptation prior to elimination, so the rate scales with $(u/s_1)^d$.

Recombination can facilitate the arrival of the adaptive allele,



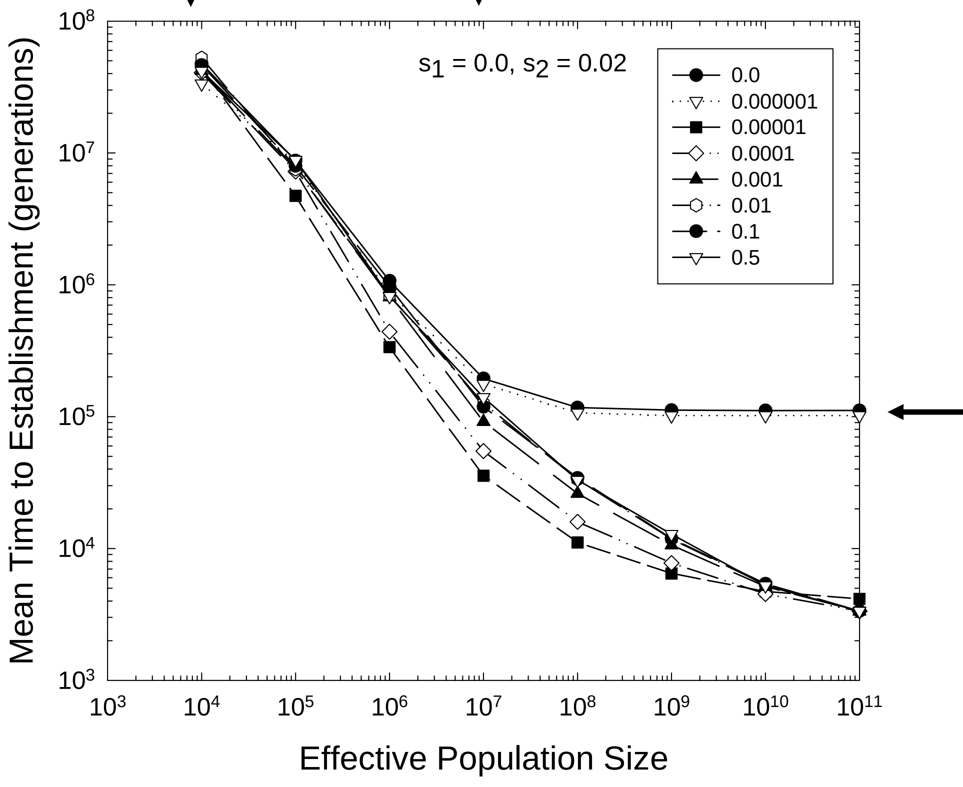
and / or inhibit the fixation of the adaptive allele,



Influence of the Recombination Rate When Intermediate-state Alleles Are Neutral

Small N – recombination has no effect.

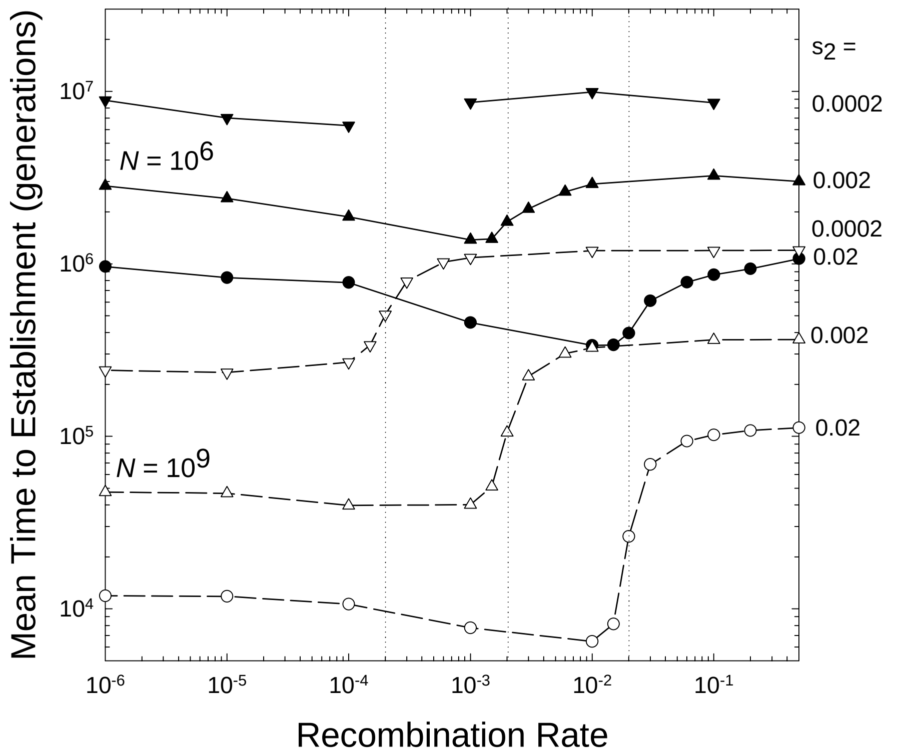
Moderate N – weak recombination leads to a small improvement in the rate of adaptation.



Large N – recombination can strongly impede fixation of the adaptive allele.

• There is a threshold recombination rate, approximately equal to the selective advantage of of the adaptive allele, beyond which the rate of adaption is inhibited.

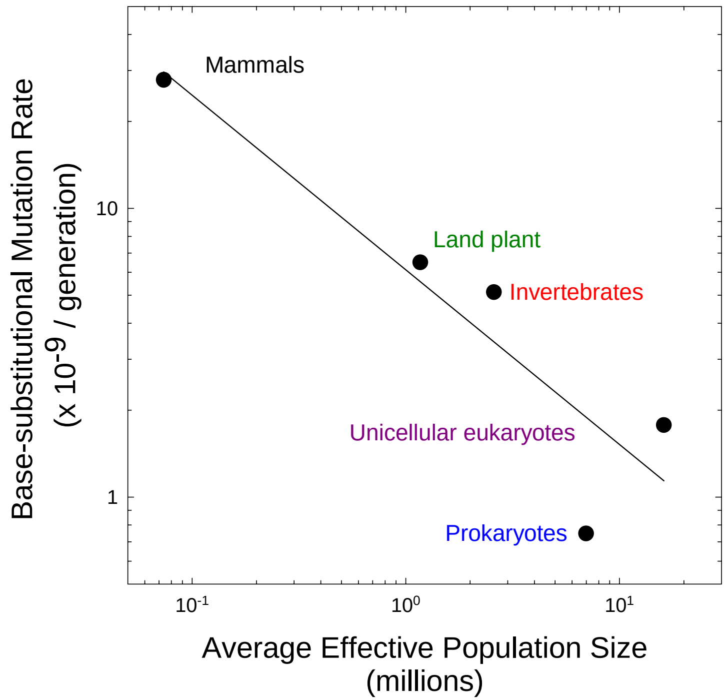
• This effect is diminished in populations of small size and with weak selection.



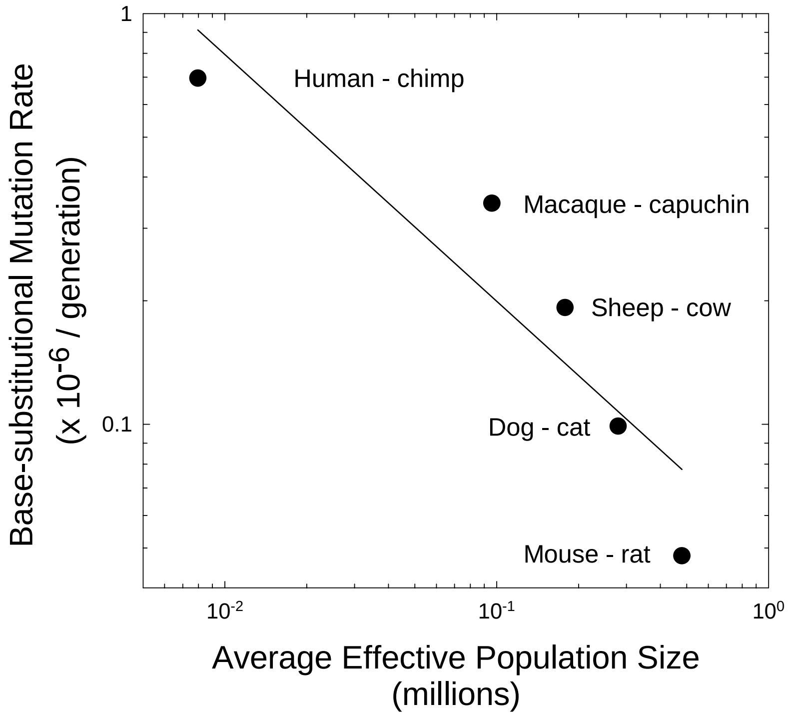
Connecting back to biological reality…..

The Per-generation Mutation Rate Is Inversely Proportional to the Average Effective Population Size of a Lineage

- Both estimated slopes = -0.60, but true values must be closer to -1.0.
- For equivalent effective sizes, mitochondrial rates are ~150x higher.

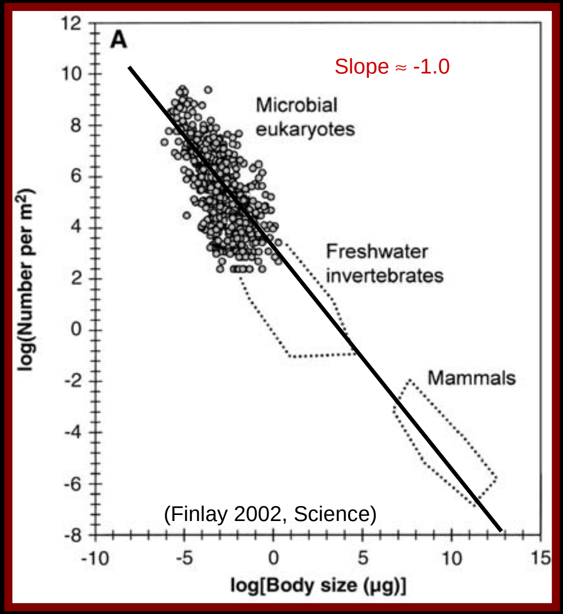


Nuclear genes: Lynch (2010)

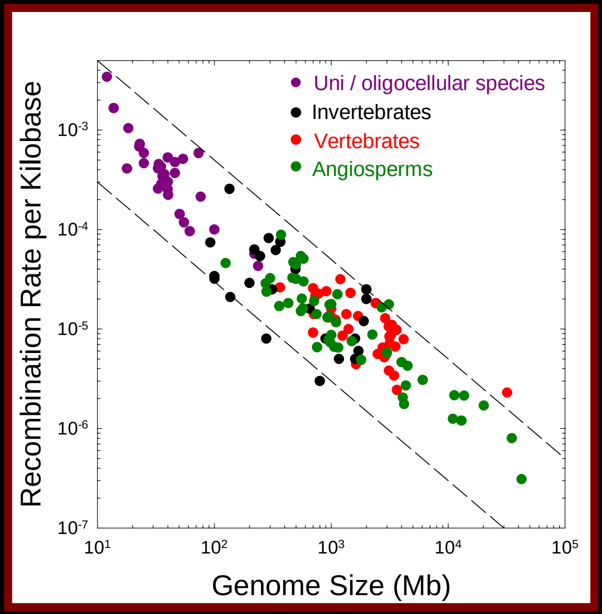


Mitochondrial genes: Piganeau and Eyre-Walker (2009)

Two Genetic Perils of Evolving Multicellularity

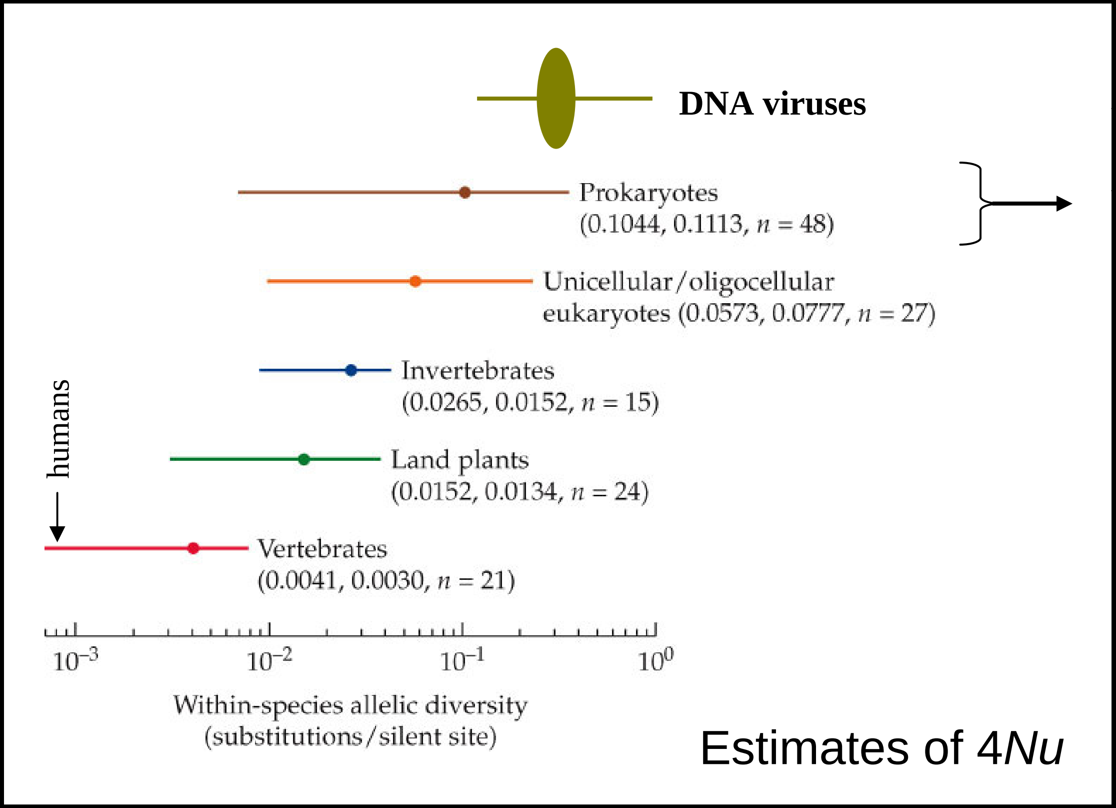


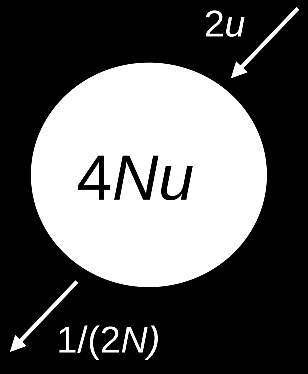
Reduction in absolute population size



Reduced recombination per physical distance

Estimates of the ratio of the power of mutation (2*u*) to the power of random genetic drift (1/2*N*) obtained from standing population-level nucleotide heterozygosity at silent sites.





At equilibrium, average allelic divergence at neutral sites =

ratio of the power of mutation to the power of random genetic drift.