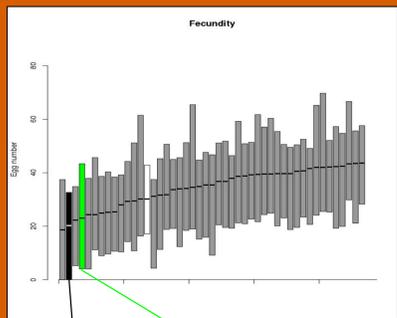


# Evading genetic drift: an experimental test of the probability of fixation of new genetic variants

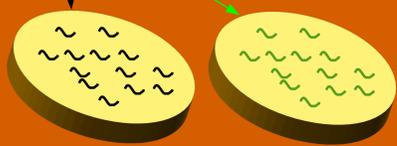
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## Invasion experiments setup



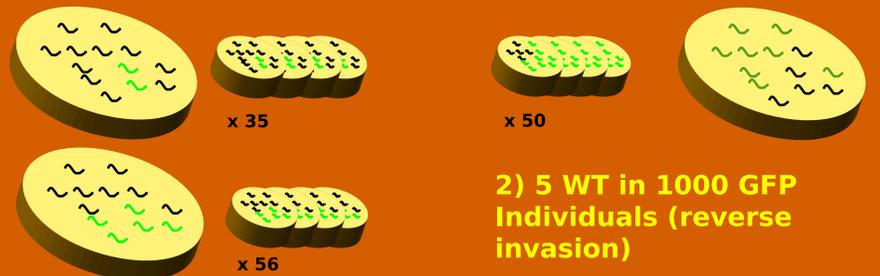
**Inbred lines derived from an adapted population of *C. elegans***

- GFP marked strain
- Wild type (WT) strain with low fecundity



**Replicated invasions with discrete, non-overlapping generations and constant N:**

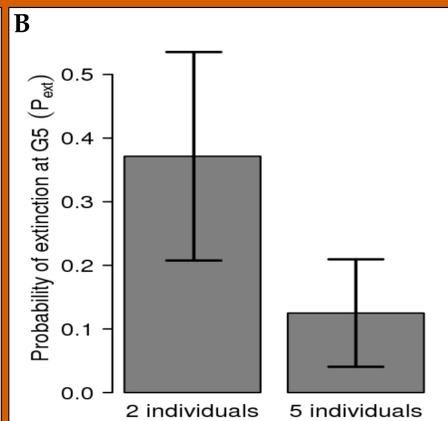
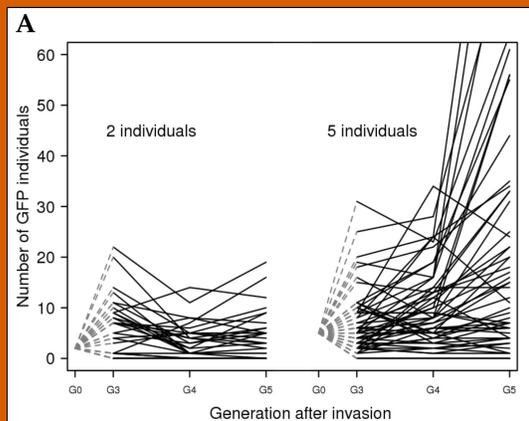
1) 2 or 5 GFP in 1000 WT individuals



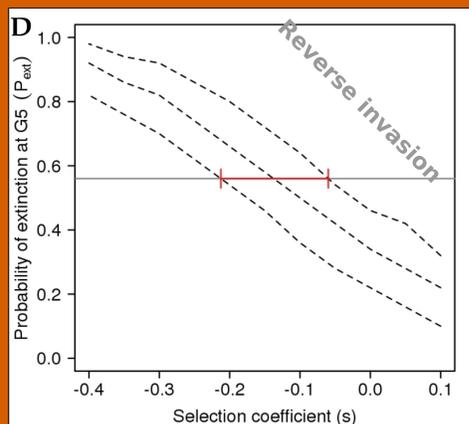
2) 5 WT in 1000 GFP Individuals (reverse invasion)

Count number of GFP individuals until generation 5 and/or extinction rates

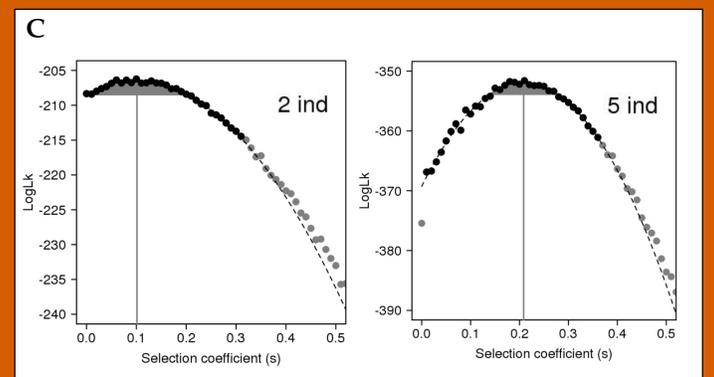
## Beneficial variants are lost because of drift



Loss of GFP individuals during 5 generations of invasion lead to higher rates of extinction in experiments starting with 2 individuals (37%) in comparison with experiments with 5 individuals (12.5%), as expected with drift (A and B).

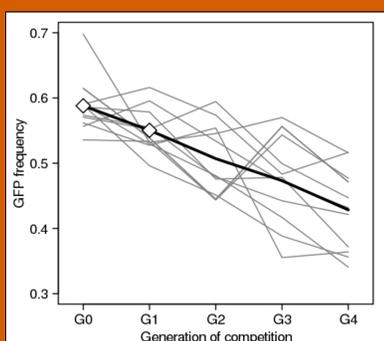


Fitting observed GFP counts with results obtained from individual-based stochastic simulations gives comparable positive (beneficial) selection coefficients,  $s=w-1$ , of the GFP variant ( $s=0.16$ , CI=0.14-0.2). Gray area below ML curve indicate  $\max Lk-2\log Lk$  level.

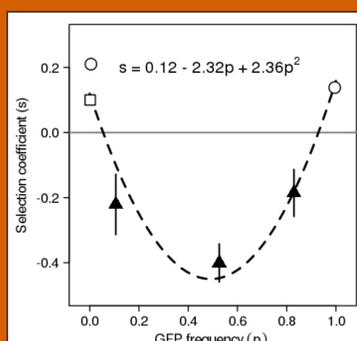


Less fit invaders (WT) increase the rate of extinction from 0.37 (B) to 0.56 (C). Dashed lines indicate the median and 95% CI of extinctions expected for different selection coefficients of the WT line. Comparable absolute values of the selection coefficients are obtained in both experiments (C and D)

## Low frequency dynamics fail to predict expected polymorphism



GFP line is less fit than the WT line in competitions at intermediate frequencies



Frequency-dependent fitness effects predict the maintenance of a polymorphic state at the equilibrium frequency of 0.05. The left panel shows mean estimates of selection coefficients obtained during invasions (open symbols) and competitions at intermediate frequencies (filled triangles). Formula describes the frequency dependence function obtained with a polynomial fit. In the right panel, simulations show that frequency-dependence maintains both genotypes in the same population for longer than with frequency-independence.

