Diversity and genetic structure in selfing populations in the absence of selection

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Selfing populations are characterized by a peculiar structure in which some multilocus genotypes reach a high frequency in the population while others are rare (Fig 1). Allard (1975) argued that this structure is a consequence of the combination of selfing and selection favoring locally adapted genotypes. However, genetic drift is expected to strongly affect selfing populations and it is unclear whether genetic drift alone could be responsible for the stochastic increase of one or a few genotypes in the population. Moreover, we lack analytical predictions for multilocus diversity under predominant selfing.

Can we explain the structure of predominantly selfing populations using neutral processes only? Are genotypes maintained over time? How is genetic diversity distributed in the populations?
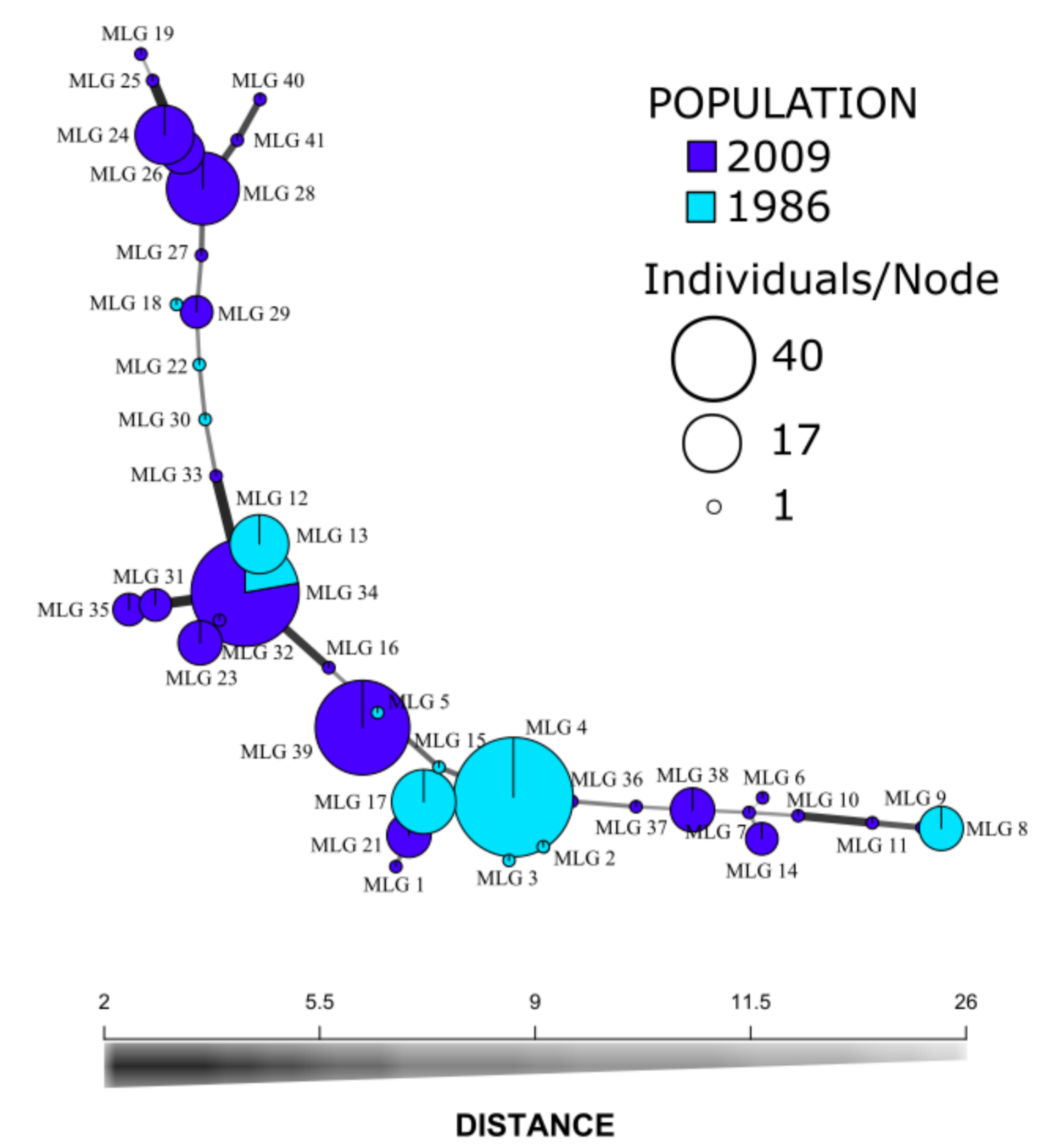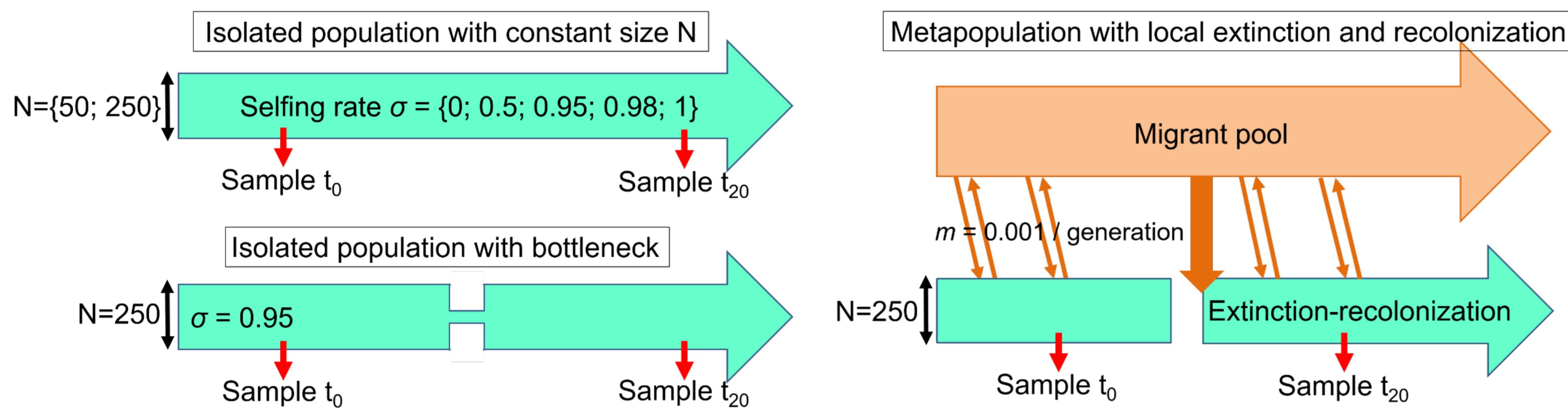

Figure 1: Multilocus genotypes (MLG) network in a selfing population of *Medicago truncatula* sampled in two generations

Simulation framework

- Multilocus genotype (**MLG**) frequencies over time
- Single and multilocus diversity (**H_e** and Simpson's index, λ)
- Genetic distance between MLGs within generation (**D**, D_{max})
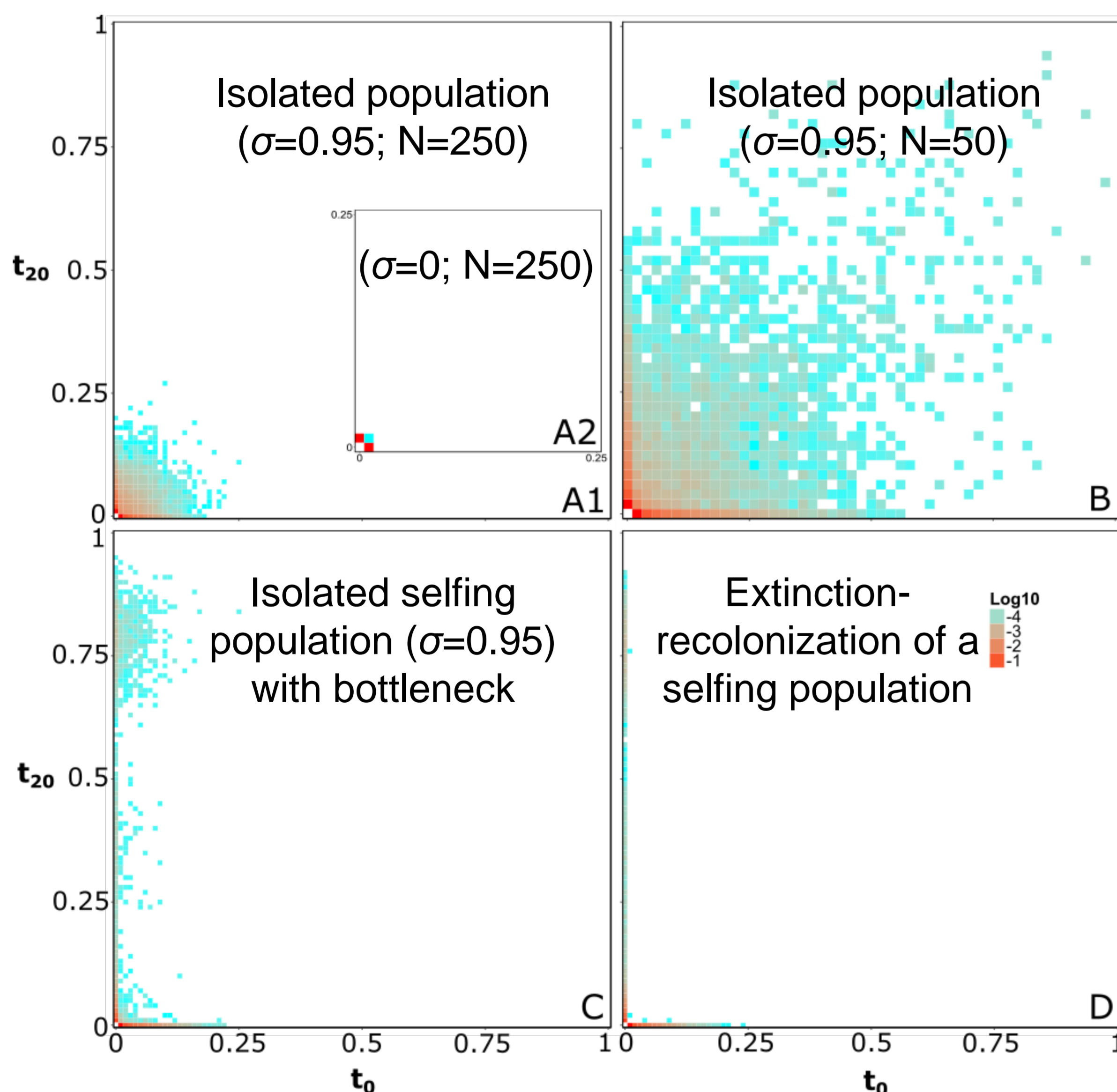
Results

Figure 2: MLG frequency spectra. The horizontal axis represents the frequency at which a MLG is found in the first sample (t_0), the vertical axis represents the frequency at which it is found in the second sample (t_{20}). The color gradient represents the $\log_{10}$ of the frequency at which each case is observed in 1000 replicates of simulations.

➢ Selfing results in repeated MLGs that are maintained over time
➢ Only small population size or strong population bottlenecks lead to one predominant MLG
➢ Extinction-recolonization completely changes the MLG composition of the population over time

➢ For a fixed effective population size (corrected for the selfing rate[2]), monolocus diversity is similar but distributed between MLGs as shown by increasing D_{max} with selfing
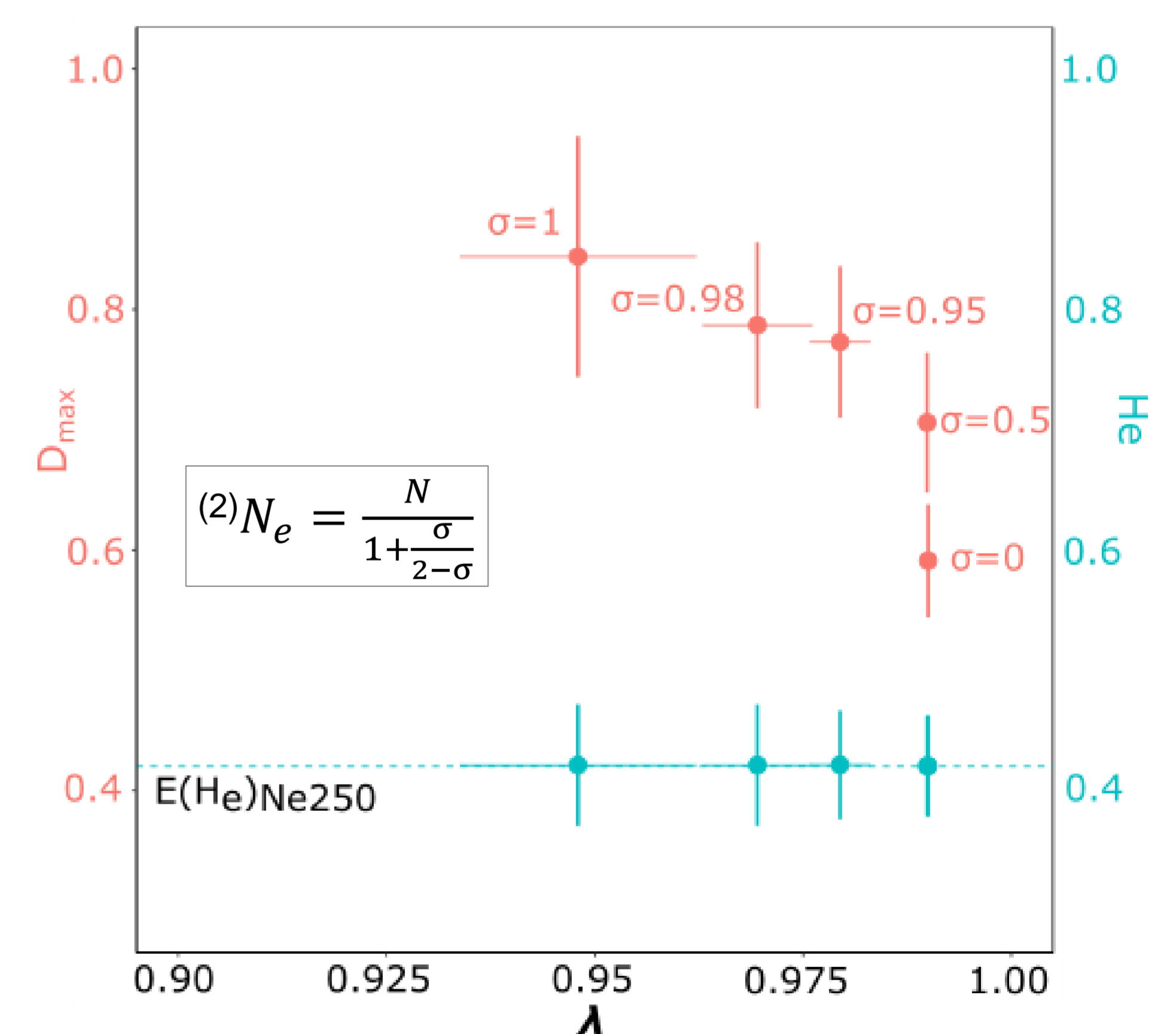
$$^{(2)}N_e = \frac{N}{1+\frac{\sigma}{2-\sigma}}$$

Figure 3: Maximum distance between MLGs (D_{max}), single (H_e) and multilocus diversity (λ) in populations with increasing selfing rate but equivalent drift levels

Our simulations show that neutral processes combined with predominant selfing can result in populations composed of a few selfing "lineages" differentiated from one another, as observed in natural populations. Demographic events exacerbate the effects of selfing on MLG diversity and create temporal stochasticity of the population composition. This simulation framework and diversity statistics can be used to infer populations' demographic parameters (Approximate Bayesian Computation, ongoing).

References

Allard, R. W. 1975. "The Mating System and Microevolution." *Genetics* 79 Suppl (June): 115–26.

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