Diversity and genetic structure in selfing populations in the absence of selection
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To cite this version:
Margaux Jullien, Miguel Navascués, Joelle Ronfort, Laurène Gay. Diversity and genetic structure in selfing populations in the absence of selection. Sex uncovered: the evolutionary biology of reproductive systems, Apr 2018, Roscoff, France. 1 p., 2018. hal-02786964

HAL Id: hal-02786964
https://hal.inrae.fr/hal-02786964
Submitted on 5 Jun 2020

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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?

Simulation framework

Results

- Multilocus genotype (MLG) frequencies over time
- Single and multilocus diversity ($H_s$ and Simpson’s index, $\lambda$)
- Genetic distance between MLGs within generation ($D$, $D_{\text{max}}$)

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


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