Sex allocation in hermaphroditic metapopulations

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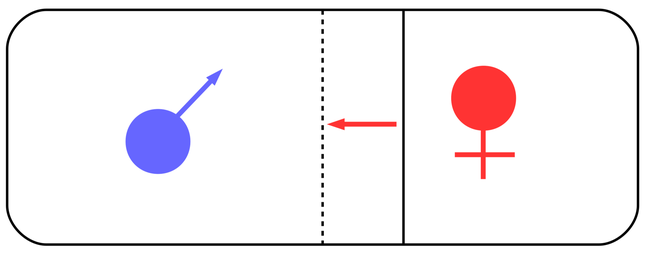
Website: https://github.com/popgenomics/quantiSex

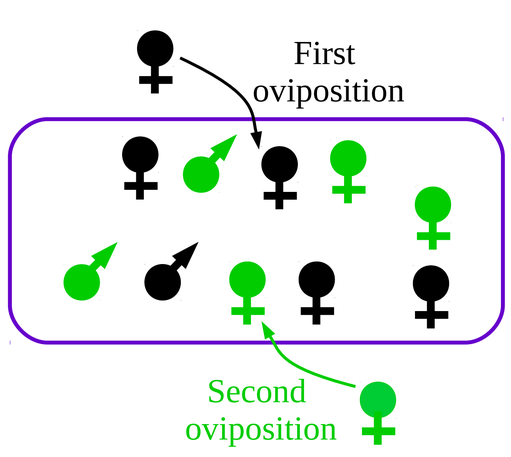
A. Sex allocation in dioecious or gonochoristic species

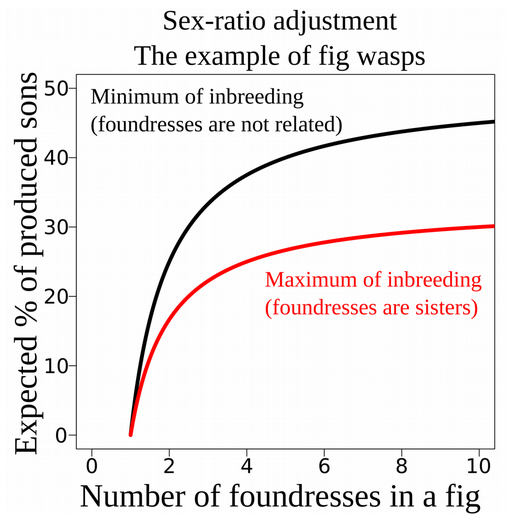
1. **Sex allocation ≈ Proportion of ♂ and ♀ produced by mothers** (weighted by the relative sex-specific cost of raising offspring).
2. **In panmictic populations ⇒ sex-ratios are balanced.**



Selection for the minority sex

3. **Non-random mating ⇒ sex-ratios are biased**.
Competitions among sons for mating (=**L**ocal **M**ate **C**ompetition) favours the selection for strategies that bias the sex-ratio towards the production of fewer ♂ and more ♀.

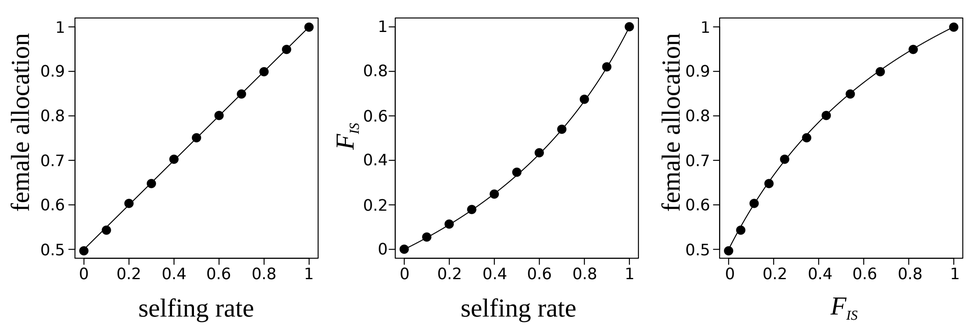




Strong LMC ⇒ bias toward daughters
Decreased LMC ⇒ production of sons closer to 50%

B. Sex allocation in demographically stable hermaphrodite (⚥) populations

1. **Sex allocation = Relative investment made to ♂ *versus* ♀ functions by ⚥ individuals.**
2. **If random mating + large dispersion ⇒** ⚥ individuals favour **equal investment in both ♂ and ♀ functions** (=50% of ♀ allocation).
3. **If limited dispersal ⇒** Sib competition ⇒ Selection for **increased investment** in the sex that shows the **smaller degree of competition** between siblings.



Relation between selfing rate in ⚥ and optimal ♀allocation.

A) $\varphi_{allocation} = \frac{1+s}{2}$ (with symetrical cost and no inbreeding depression)
B) $F_{IS} = \frac{s}{2-s}$
C) $\varphi_{allocation}$ **is difficult to measure directly from phenotypical traits**, but can be estimated by F_{IS} from neutral molecular markers.

C. Questions

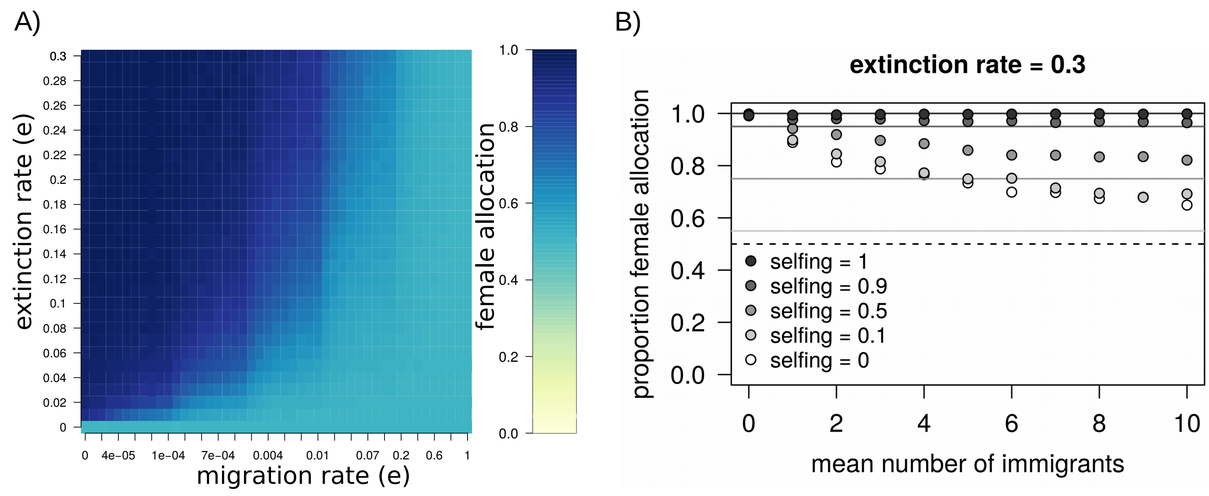
High levels of inbreeding can also emerge in outcrossers from metapopulation dynamics (local extinctions and recolonisations).

1. **How rapid must population turnover be to expect a strong biased sex allocation in a metapopulation of ⚥?**
2. **What index of inbreeding would be the best predictor of the sex allocation selected?**

D. Quantitative genetic simulations of ⚥ metapopulations

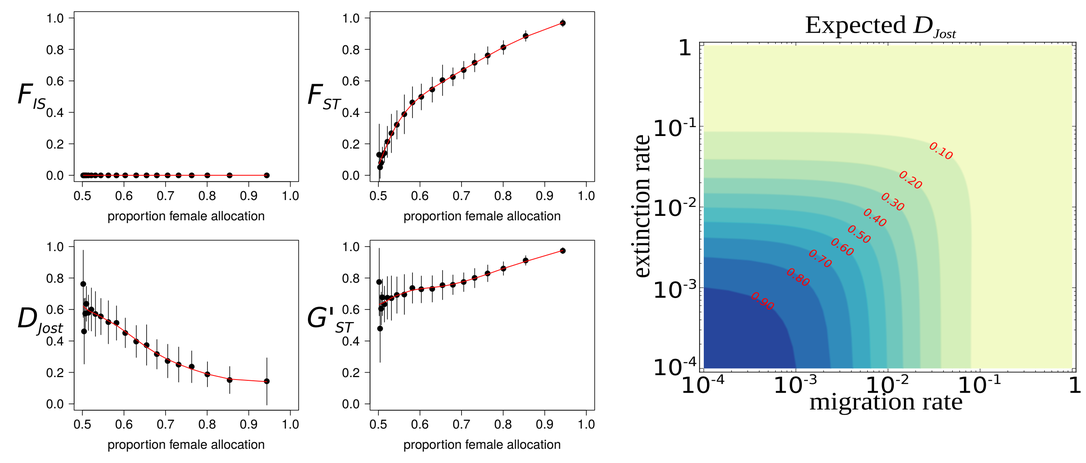
Model:

- Multi-deme metapopulation made up of ⚥.
- Sex allocation is a function of the additive effects of alleles at a single locus subject to recurrent mutations that alter the allelic effects.
- Mating within demes and seed production depends on the sex allocations of individuals.
- Demes are subject to recurrent stochastic extinction, following which their sites are recolonized through seed dispersal from the rest of the metapopulation.
- Population genetics statistics F_{ST}, F_{IS}, G'_{ST} and D_{Jost} were computed at 20 unlinked neutral loci.



- $\varphi_{allocation}$ varies from 0.5 to 1 and ↗ if: migration ↘ or extinction ↗ (**A**).
- Increased gene flow progessively ↘ the equilibrium $\varphi_{allocation}$ to values expected for single partial selfing populations (**B**).

E. Predicting $\varphi_{allocation}$ from neutral molecular markers



- **No positive association between $\varphi_{allocation}$ and (F_{IS}** (Pearson's $R^2 = 0.0006$; $p - value = 0.5494$).
- **$\varphi_{allocation}$ is most associated with F_{ST}** (Pearson's $R^2 = 0.84$; $p-value < 2.2x10^{16}$).
- New indices of differentiation G'_{ST} and D_{Jost} ↘ when migration ↗, but also when extinction ↗.
- Low D_{Jost} can thus describe two opposite situations: **no population turnover** or **extreme population turnover**.

Conclusions

1. Population **turnover should select for ♀-biased allocation** if migration is insufficiently strong to erase the genetic signatures of inbreeding brought about by colonisation.
2. In metapopulations: **F_{ST} is a much better predictor of the sex allocation selected than F_{IS}.**

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