The response to selection in complex mating systems

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Dioecy



Bolitotherus cornutus Vince Formica





Silene latifolia

Complex mating systems





Gynodioecy Silene vulgaris



Alternative reproductive tactics Midshipman fish news.bbc.co.uk

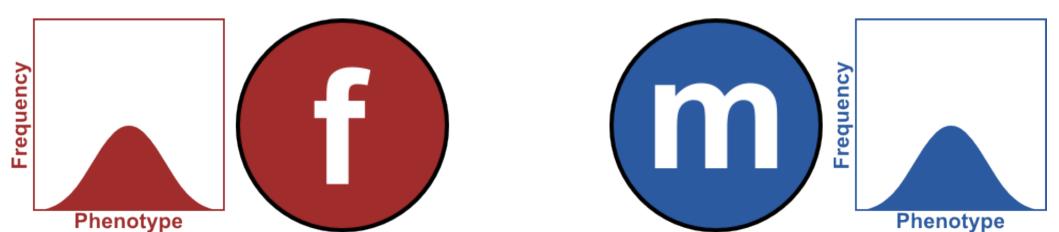


Androdioecy Caenorhabditis elegans Zeynep Altun

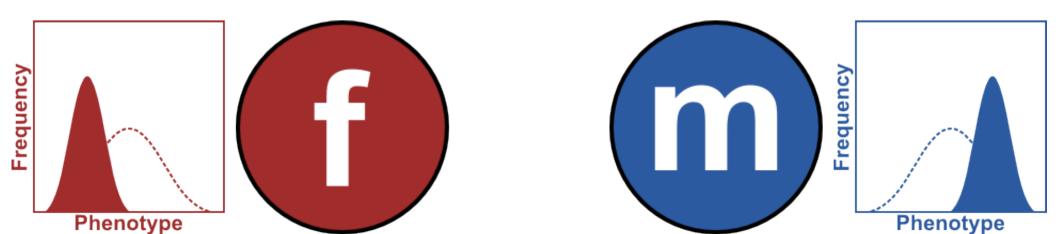


Many mating types Schizophyllum commune Doug Bowman

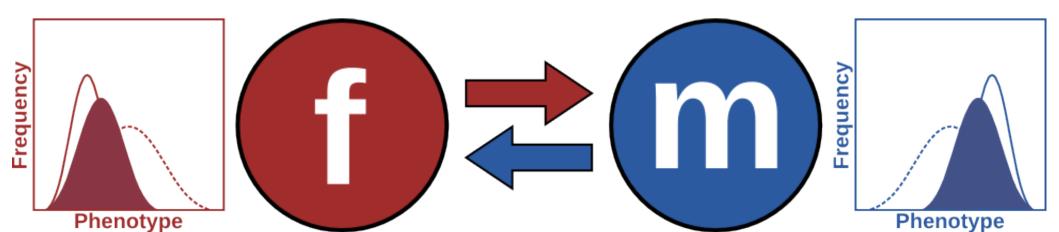
- One or more mating classes
 - Groups of individuals with different mating restrictions (e.g., sexes) or behaviors (e.g., alternative reproductive tactics)



- Selection (potentially different) within each mating class
- Response is mediated by **heritabilities**

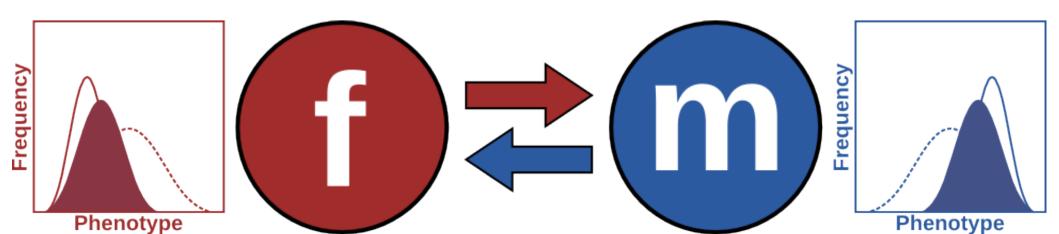


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- Allele mixing among mating classes during fertilization



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Allele mixing should constrain trait adaptation in mating classes

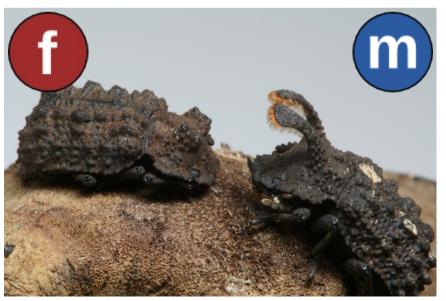


Questions

- 1. How similar are the rates of allele mixing in different mating systems?
- 2. Is adaptation more constrained in some mating classes due to allele mixing?

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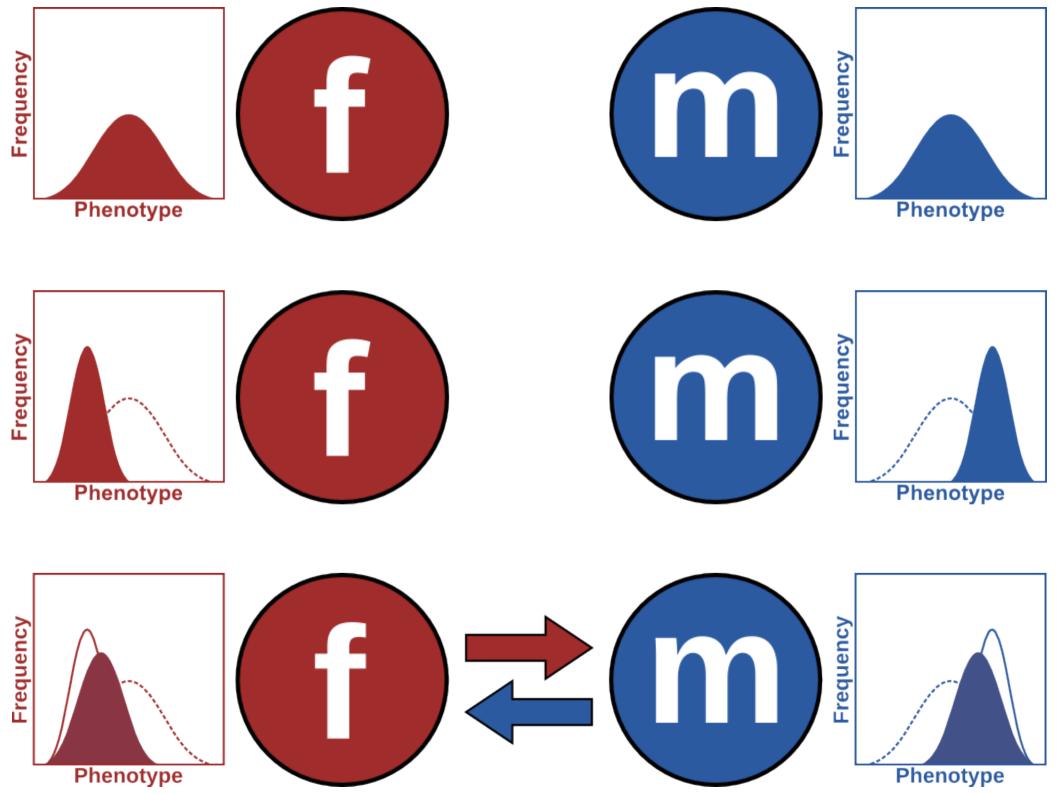
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- 2. Is adaptation more constrained in some mating classes due to allele mixing?
- Dioecy and gynodioecy

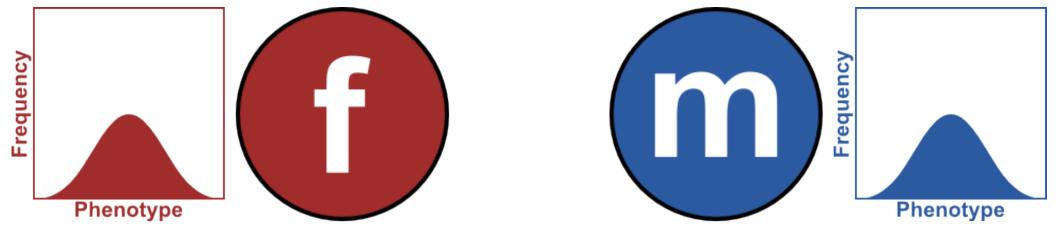


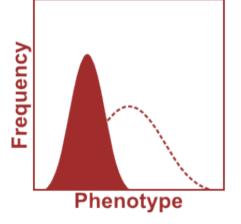


Dioecy

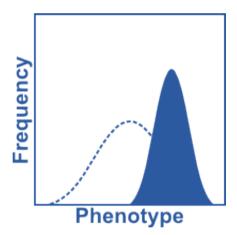
Gynodioecy

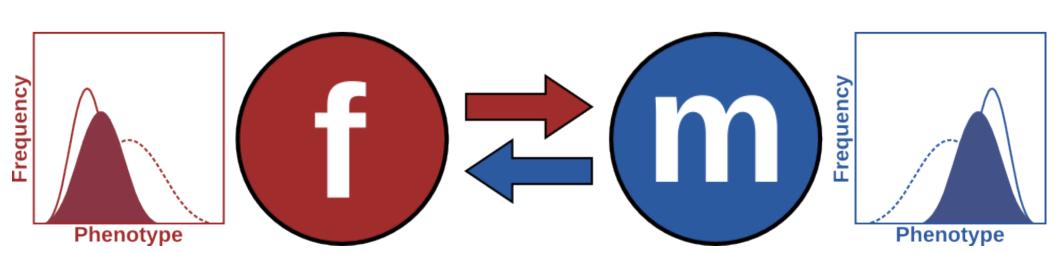






Need a common framework to describe adaptation in any mating system





- Character states: treat versions of the trait expressed in different mating classes as correlated traits
 - e.g., as though hermaphrodite body size and female body size are separate traits

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 - e.g., as though hermaphrodite body size and female body size are separate traits
- Similarity in genetic architecture is given by among-class genetic covariance, G_{hf}

Response to selection <u>within</u> a mating class

• Breeder's equation

$$\Delta \bar{x}_h = G_{hh} \beta_h$$

- *G*_{*hh*} is the additive genetic variance of the hermaphrodite character state
- β_h is the selection on the trait in hermaphrodites

Response to selection <u>within</u> a mating class

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 Selection in hermaphrodites will cause a correlated response in the female character state

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• What about allele mixing?

Between-class gene flow

- *m_i* the rate of gene flow <u>into</u> mating class *i* from other classes
- Analogous to the migration rate in spatially structured populations
- The proportion of *i* offspring whose parents are a different mating class

Response to selection

• m_h weights the influence of each class on the phenotypes of hermaphrodites next generation

$$\overline{x}_{h}^{*} = (1-m_{h})(\overline{x}_{h}+\Delta \overline{x}_{h})+m_{h}(\overline{x}_{fh}+\Delta \overline{x}_{fh})$$

Response to selection

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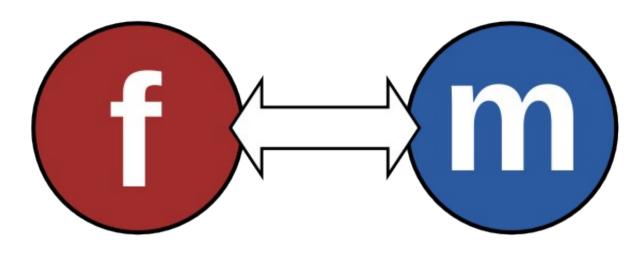
$$\overline{x}_{h}^{*} = (1 - m_{h})(\overline{x}_{h} + \Delta \overline{x}_{h}) + m_{h}(\overline{x}_{hf} + \Delta \overline{x}_{fh})$$

$$= (1 - m_{h})(\overline{x}_{h} + G_{hh}\beta_{h}) + m_{h}(\overline{x}_{hf} + G_{hf}\beta_{f})$$

 Response depends on selection, heritabilities, and between-class gene flow

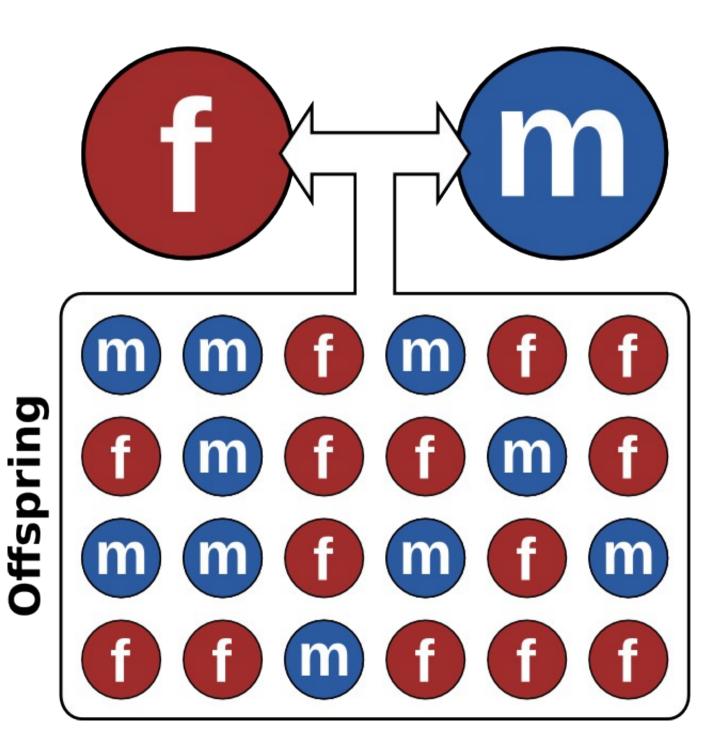
Between-class gene flow

- The proportion of *i* offspring whose parents are a different mating class
- Depends on:
 - a = Frequency of mating among classes (demography)
 - b = Class ratio resulting from each type of mating
 (genetics)



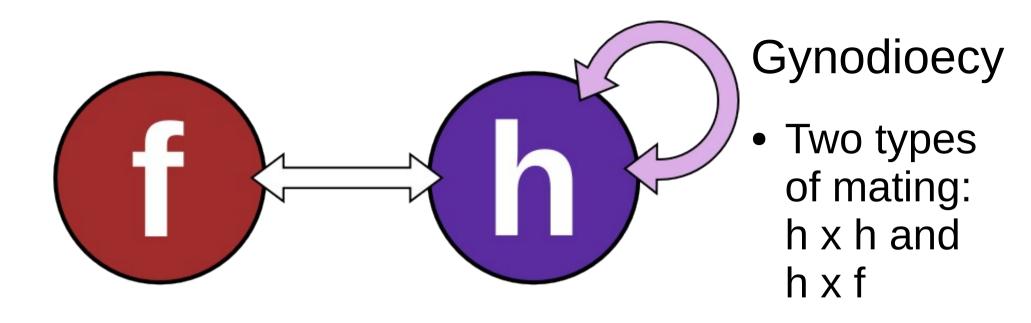
Dioecy

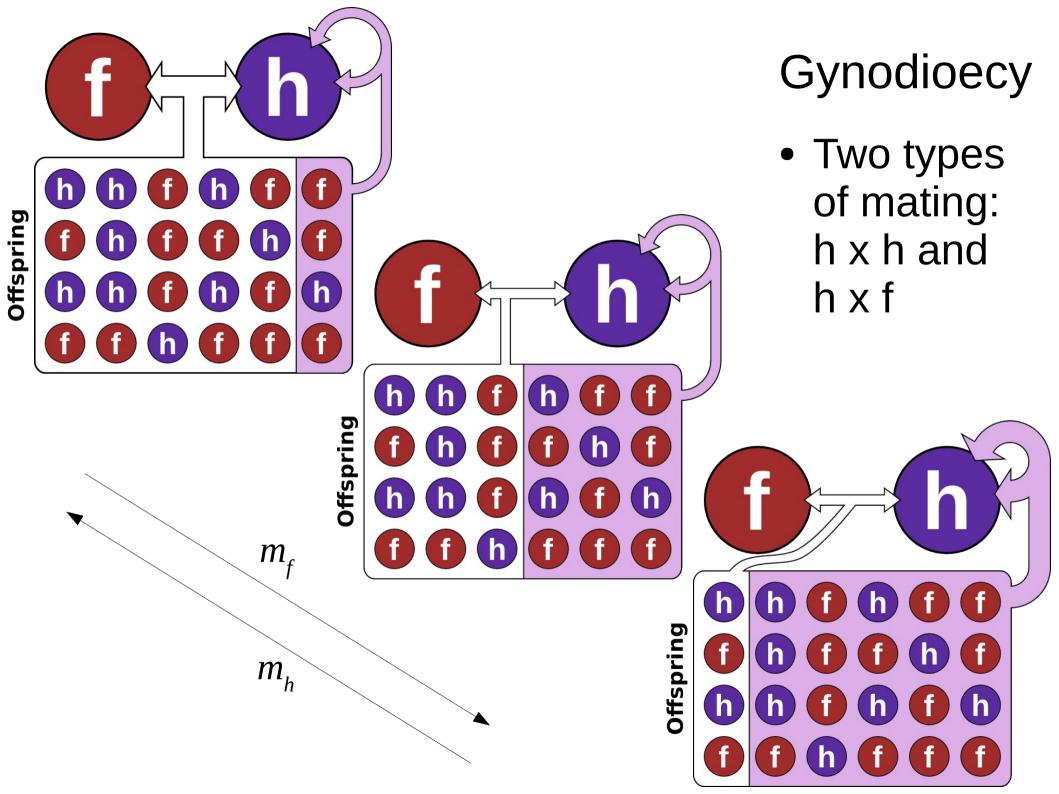
 Only one type of mating: male x female

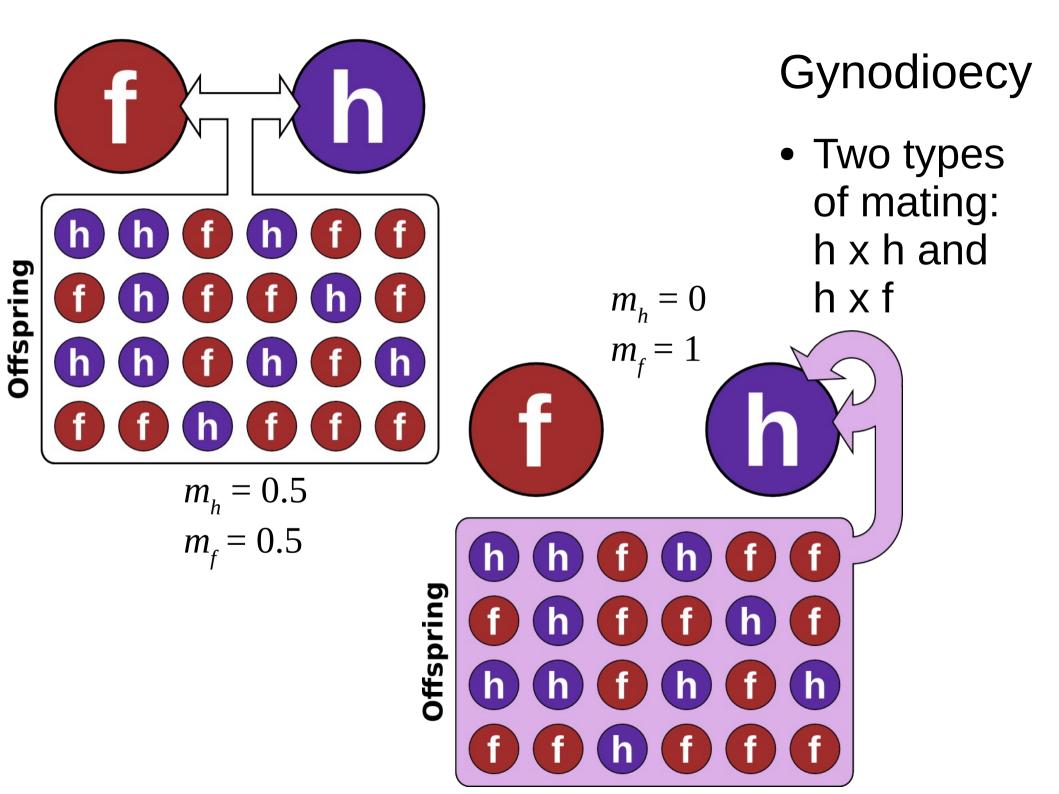


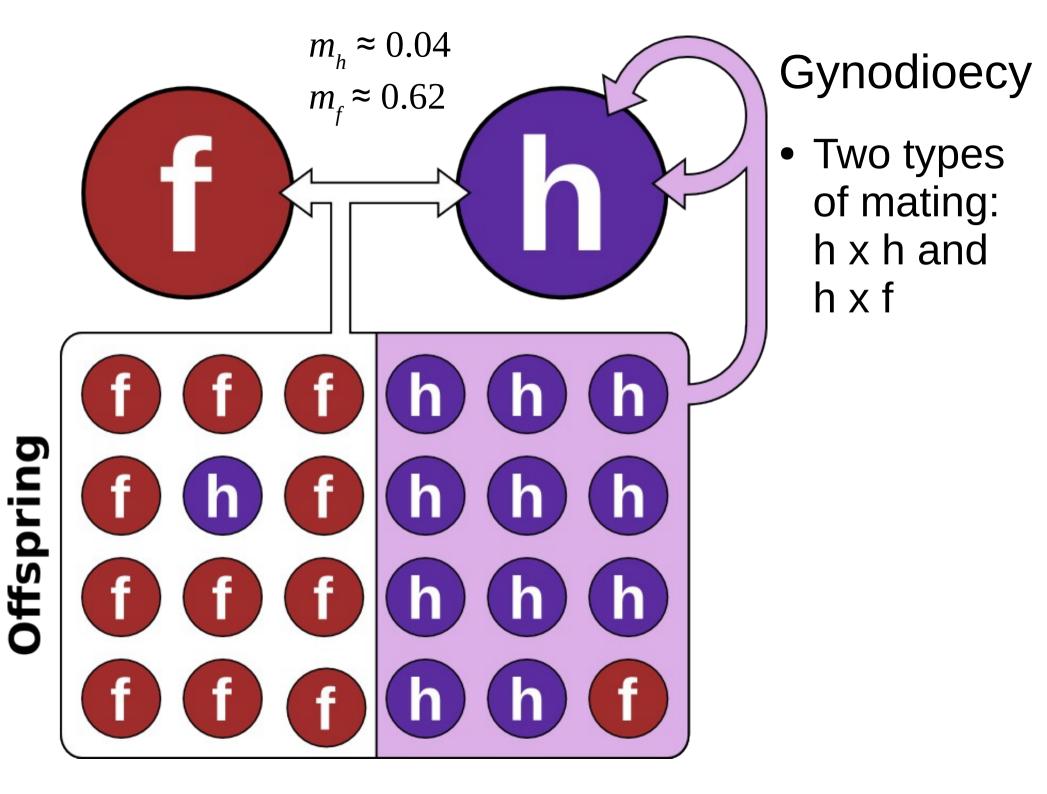
Dioecy

- Only one type of mating: male x female
- Each individual has one female and one male parent, so rates of gene flow are <u>always</u> equal
- $m_m = m_f = 0.5$









Between-class gene flow

1. How similar are the rates of allele mixing in different mating systems?

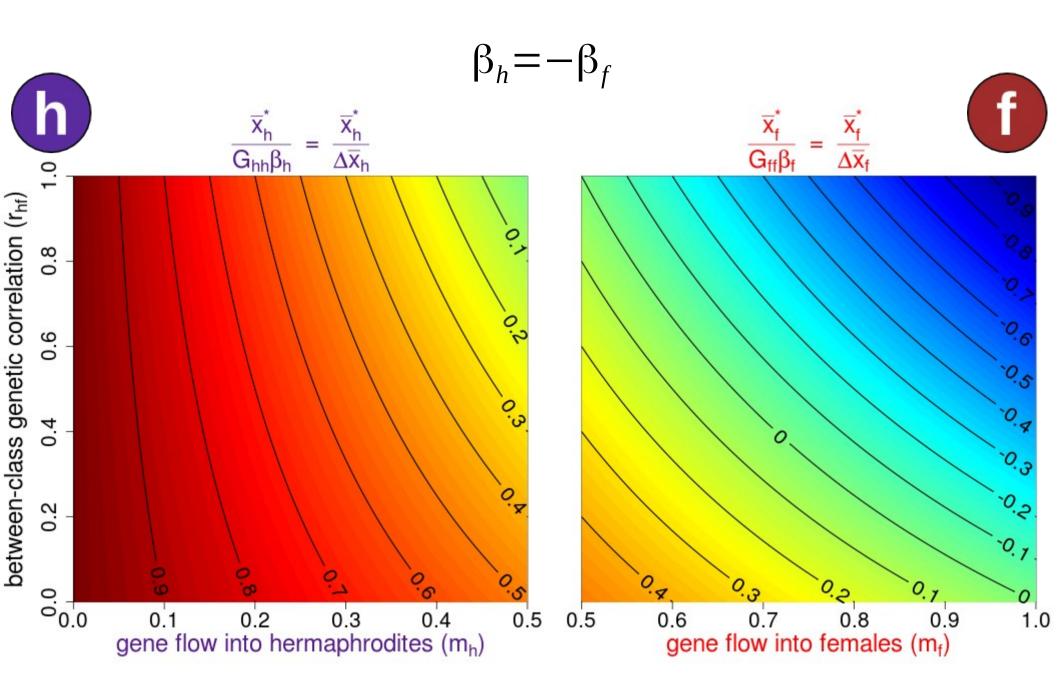
- $0 \le m_h \le 0.5$
- $0.5 \le m_f \le 1$
- But the specifics will depend on the population (a) demography and (b) genetics

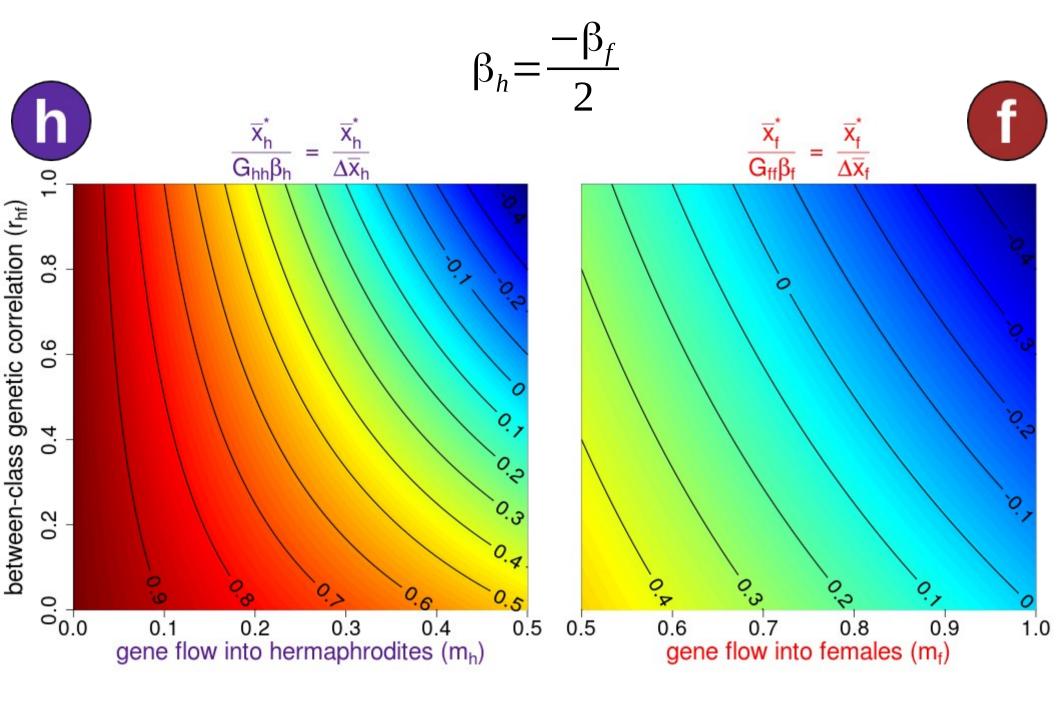
Between-class gene flow

1. How similar are the rates of allele mixing in different mating systems?

- $0 \leq m_h \leq 0.5$
- $0.5 \le m_f \le 1$

• How does this affect constraint for each class?





Constraints due to gene flow

2. Is adaptation more constrained in some mating classes due to allele mixing?

- Compared to dioecy
 - Trait evolution in females is <u>more</u> constrained by gene flow
 - Trait evolution in hermaphrodites is <u>less</u> constrained by gene flow

Implications

- Can use character state approach to compare multiple mating systems
- Adaptation in complex mating systems: rates of gene flow matter too, not just trait correlations
- The response to selection within one mating class may be a poor predictor of evolution

Acknowledgements

- Laura Galloway
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Between-class gene flow

$$m_{i} = \frac{\# \text{"migrant" gametes into i}}{\# \text{ gametes into i}}$$
$$= \frac{\sum_{j \neq i} \overline{W}_{j} m_{ij}}{\overline{W}_{i} (1 - m_{i}) + \sum_{j \neq i} \overline{W}_{j} m_{ij}}$$

- *m*_{ji} = the proportion of gametes produced by *i* parents which end up in *j* offspring
- *m*._{*i*} = the proportion of gametes produced by *i* parents which end up in another mating class

Between-class gene flow

- m_{ji} = the proportion of gametes produced by *i* parents which end up in *j* offspring
- *m*._{*i*} = the proportion of gametes produced by *i* parents which end up in another mating class
- For gynodioecy:

$$m_{hf} = b_{hxf}$$

 $m_{fh} = a(1-b_{hxh})+(1-a)(1-b_{hxf})$

Gene flow into hermaphrodites

$$m_{h} = \frac{(1-a)b_{hxf}}{2b_{hxf} + a(1+a)(b_{hxh} - b_{hxf})}$$

• If all mating is between hermaphrodites, a = 1

$$m_h = \frac{0}{2b_{hxf} + 2(b_{hxh} - b_{hxf})} = 0$$

If hermaphrodites always mate with females,
 a = 0

$$m_{h} = \frac{b_{hxf}}{2b_{hxf} + 0(b_{hxh} - b_{hxf})} = \frac{b_{hxf}}{2b_{hxf}} = \frac{1}{2}$$

• The version of the trait expressed in a single mating class

Locus		Additive			Breeding	
		effects			value	
A ₁ A ₂		α ₁	+	α2	=	Xm



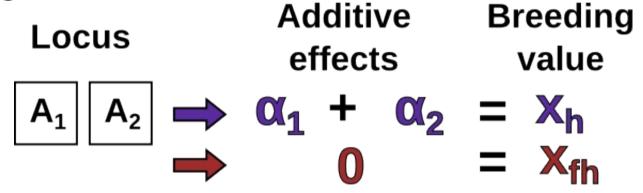
• The version of the trait expressed in a single mating class

Locus	Additive effects	Breeding value	
$ \begin{bmatrix} A_1 \\ A_2 \end{bmatrix} \Longrightarrow $		$= X_m$	
	U	— ^fm	

• *x_{fm}*: female character state carried by males



• The version of the trait expressed in a single mating class





• The version of the trait expressed in a single mating class

Locus	Additive	Breeding value	
	effects		
$ A_1 A_2 \Longrightarrow$	$\alpha_1 + \alpha_2$	$= X_h$	
	0	= X _{fh}	

• The similarity between character states is given by G_{hf} , the additive genetic covariance

Future directions

- Other mating systems
- Assumes gene flow is independent of phenotype
- Need predictions of variance evolution to predict longer term evolution
- Are gene flow and selection related?