

# Linking levels of selection with genetic modifiers

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Department of Zoology  
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@sarperotto





SOCIETY *for the* STUDY of EVOLUTION

@sse\_evolution



@sse.evolution



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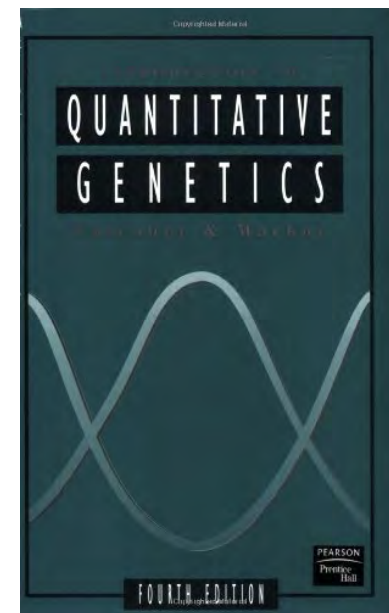
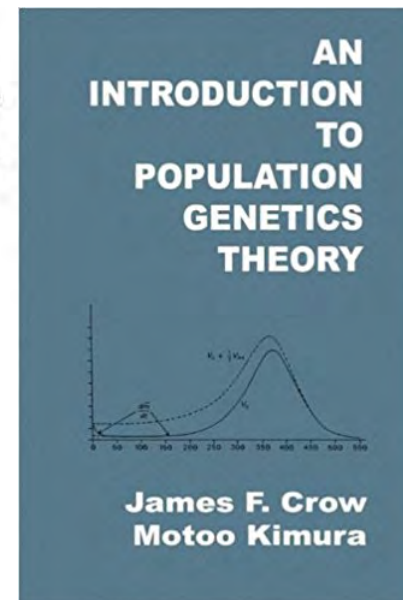
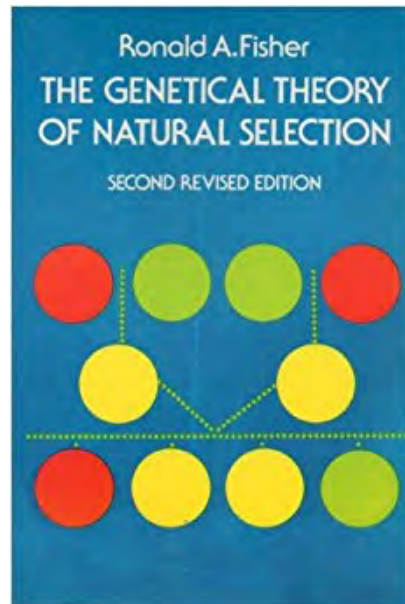
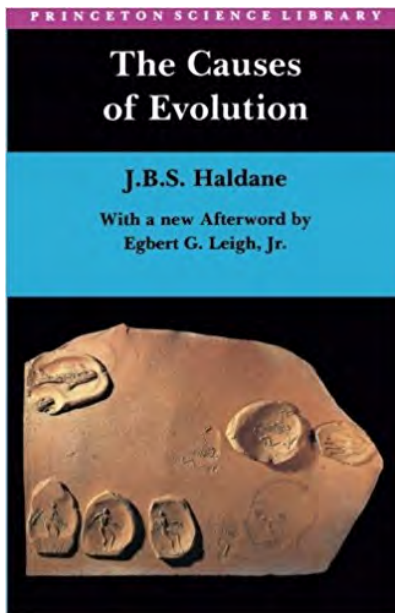
@sarperotto



# EVOLUTIONARY MODELS

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Evolution is richly underpinned by mathematical theory.



# EVOLUTIONARY THEORY

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Classical models track **genes under selection**, given:

- Mode of reproduction
- Recombination rate
- Ploidy (haploid or diploid)
- Mutation rate
- Dominance
- Life history

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$$\frac{dp}{dt} = s p(1-p)$$

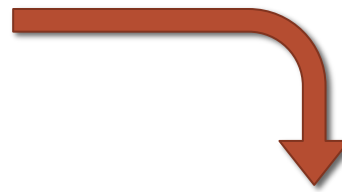
One-locus

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One-locus

$$x_1(t+1) = x_1(t) \left( \sum_{j=1}^4 x_j(t) \left( \frac{w_{1j} + w_{j1}}{2\bar{w}} \right) \right) - r D^*$$

$$x_2(t+1) = x_2(t) \left( \sum_{j=1}^4 x_j(t) \left( \frac{w_{2j} + w_{j2}}{2\bar{w}} \right) \right) + r D^*$$

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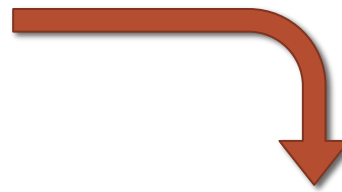
Two-locus

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One-locus

$$R = h^2 S$$

Quantitative-genetic

$$x_1(t+1) = x_1(t) \left( \sum_{j=1}^4 x_j(t) \left( \frac{w_{1j} + w_{j1}}{2\bar{w}} \right) \right) - r D^*$$

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Two-locus

# EVOLUTIONARY THEORY

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Classical models track **genes under selection**, given:

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But how do these  
features evolve?



# EVOLUTIONARY THEORY

---

Classical models track **genes under selection**, given:

- Mode of reproduction
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- Life history

How does an organism  
come to live and  
reproduce in the way  
that it does?

# MODIFIER THEORY

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# MODIFIER THEORY

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**Modifiers are just genes**, but  
they are genes that shape the very nature of an organism

# MODIFIER THEORY

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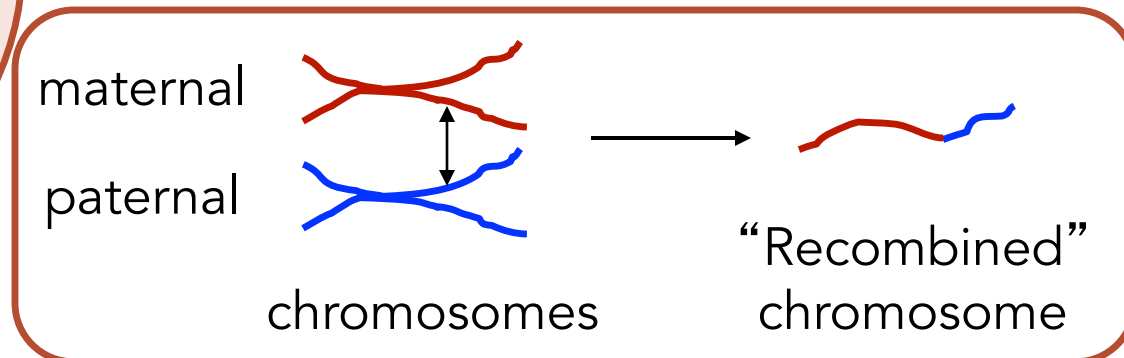
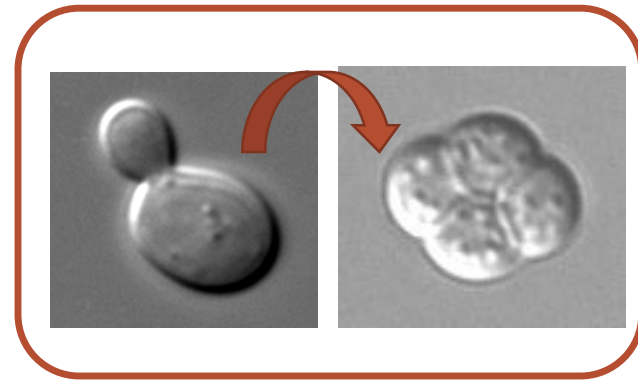
**Modifiers are just genes**, but they are genes that shape the very nature of an organism

- how it lives and reproduces
- how its genome is structured
- how its traits are inherited

# MODIFIER THEORY

**Modifiers are just genes,** but they are genes that shape the very nature of an organism

- Mode of reproduction
- Recombination rate
- Ploidy (haploid or diploid)
- Mutation rate
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# MODIFIER THEORY

---

**Modifiers models** track  
the evolutionary dynamics of genes that alter

- Mode of reproduction
- Recombination rate
- Ploidy (haploid or diploid)
- Mutation rate
- Dominance
- Life history

Helping us to answer  
**“Why do organisms  
experience evolution in  
the way that they do?”**

# MODIFIER THEORY

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- Life history

Helping us to answer  
**“Why is the biological world so diverse?”**



# MODIFIER THEORY

---

Earliest models tracked genes modifying dominance:

- Fisher (*AmNat* 1928): “it is not the mutant gene which is modified but other hereditary factors which influence the reaction of the organism to the mutant gene”
- Wright (*AmNat* 1929): “Suppose that there is another factor, **M**, which modifies the selection against the heterozygote”

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Both showed that dominance of wildtype alleles over mutant alleles could evolve, but selection was very weak (proportional to the mutation rate).

## MODIFIER THEORY

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Fisher and Wright calculated the average fitness of the new modifier across backgrounds, *ignoring genetic associations*.

## MODIFIER THEORY

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Nei (1967 *Genetics*) was the first to model the full dynamics of a modifier of recombination.

# MODIFIER THEORY

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Examples of  
modifier models

# MODIFIER THEORY

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Modifier models

Levels of selection

# MODIFIER THEORY

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Modifier models  $\longleftrightarrow$  Levels of selection

# MODIFIER THEORY

---



Modifier models  $\longleftrightarrow$  Levels of selection

**Evolutionary conflicts**



# MODIFIER THEORY

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How do modifier genes evolve when there are conflicts between what is best for the individual and what is best for the group?

- Evolution of sex
- Evolution of haploidy vs diploidy
- Evolution of sex chromosomes

# EVOLUTION OF SEX

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Among diploids, sex allows for the segregation of alleles, e.g.,  $Aa$  parents  $\rightarrow$   $AA$ ,  $Aa$ , and  $aa$  offspring.

*Can the benefits of segregation explain the evolution of sex?*

# EVOLUTION OF SEX

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Let's start by considering the conflicting levels of selection, with recurrent deleterious mutations...

# EVOLUTION OF SEX

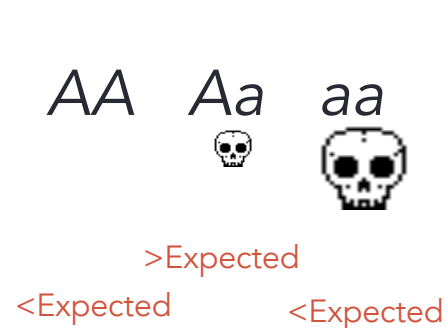
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Group level: Segregation can regenerate variance in fitness, making selection more efficient.

# EVOLUTION OF SEX

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If  $W_{Aa} > \sqrt{(W_{AA} W_{aa})}$ :  
Variance depleted by  
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# EVOLUTION OF SEX

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Group level: Segregation can regenerate variance in fitness, making selection more efficient.



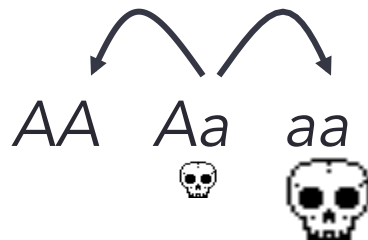
If  $W_{Aa} > \sqrt{(W_{AA} W_{aa})}$ :  
Variance depleted by  
selection  
Sex regenerates variance

Sex increases mean fitness if  $W_{Aa} > \sqrt{(W_{AA} W_{aa})}$

# EVOLUTION OF SEX

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Individual level: By breaking apart gene combinations favored by past selection, sex causes a reduction in offspring mean fitness (“segregation load”).



Sex decreases offspring fitness\*

# EVOLUTION OF SEX

---

Group level:

Increase variability

Sexuality favored:  $W_{Aa} > \sqrt{(W_{AA} W_{aa})}$



Individual level:

Avoid segregation load

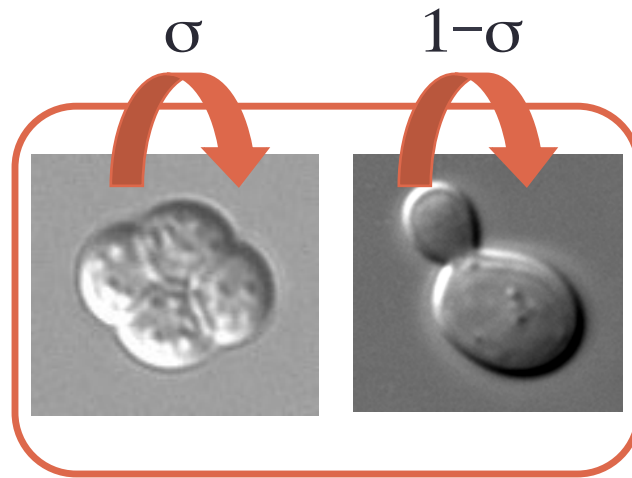
Asexuality favored



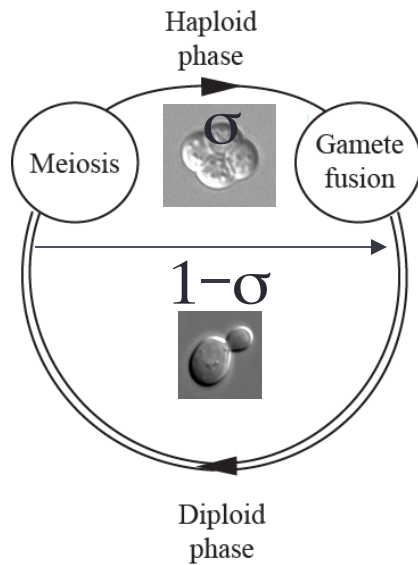
# EVOLUTION OF SEX

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**MODIFIER MODEL:** Consider a modifier that alters the probability,  $\sigma$ , that an individual reproduces sexually rather than asexually.



# EVOLUTION OF SEX



$$x'_{11} = (1 - \sigma_1) \tilde{x}_{11} + \bar{\sigma} (y_1^2(1 - f) + y_1 f)$$

$$2x'_{12} = (1 - \sigma_1) 2\tilde{x}_{12} + \bar{\sigma} (2y_1 y_2 (1 - f))$$

*MAMA*

*MAMa*

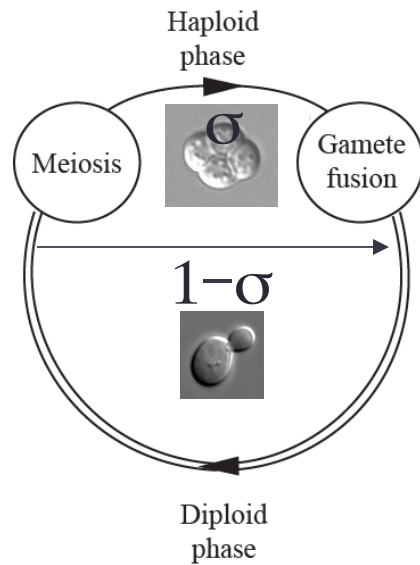
...

Diploid offspring

We track each diploid combination  
(*MAMA*, *MAMa*, ..., *mama*)

( $x_{11}, x_{12}, \dots, x_{44}$ )

# EVOLUTION OF SEX



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*MAMA*

*MAMa*

...

Asexual

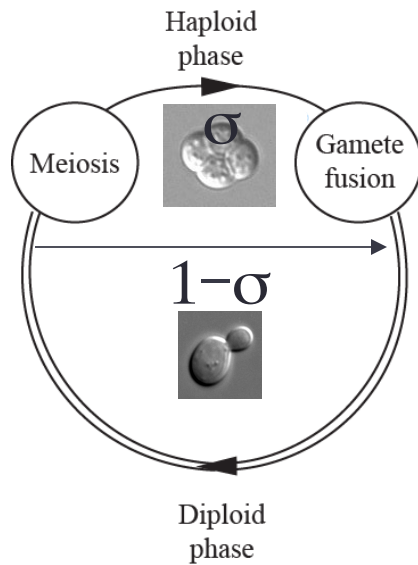
Sexual

Diploid offspring

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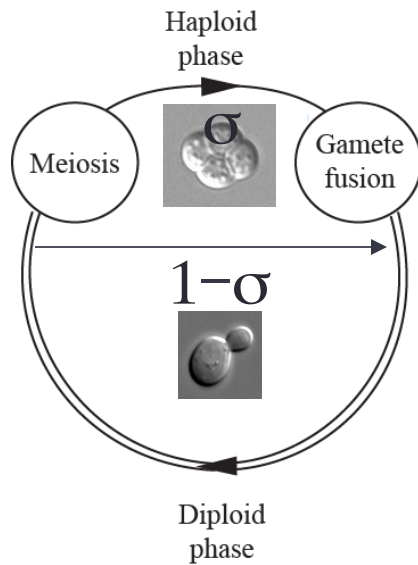
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# EVOLUTION OF SEX



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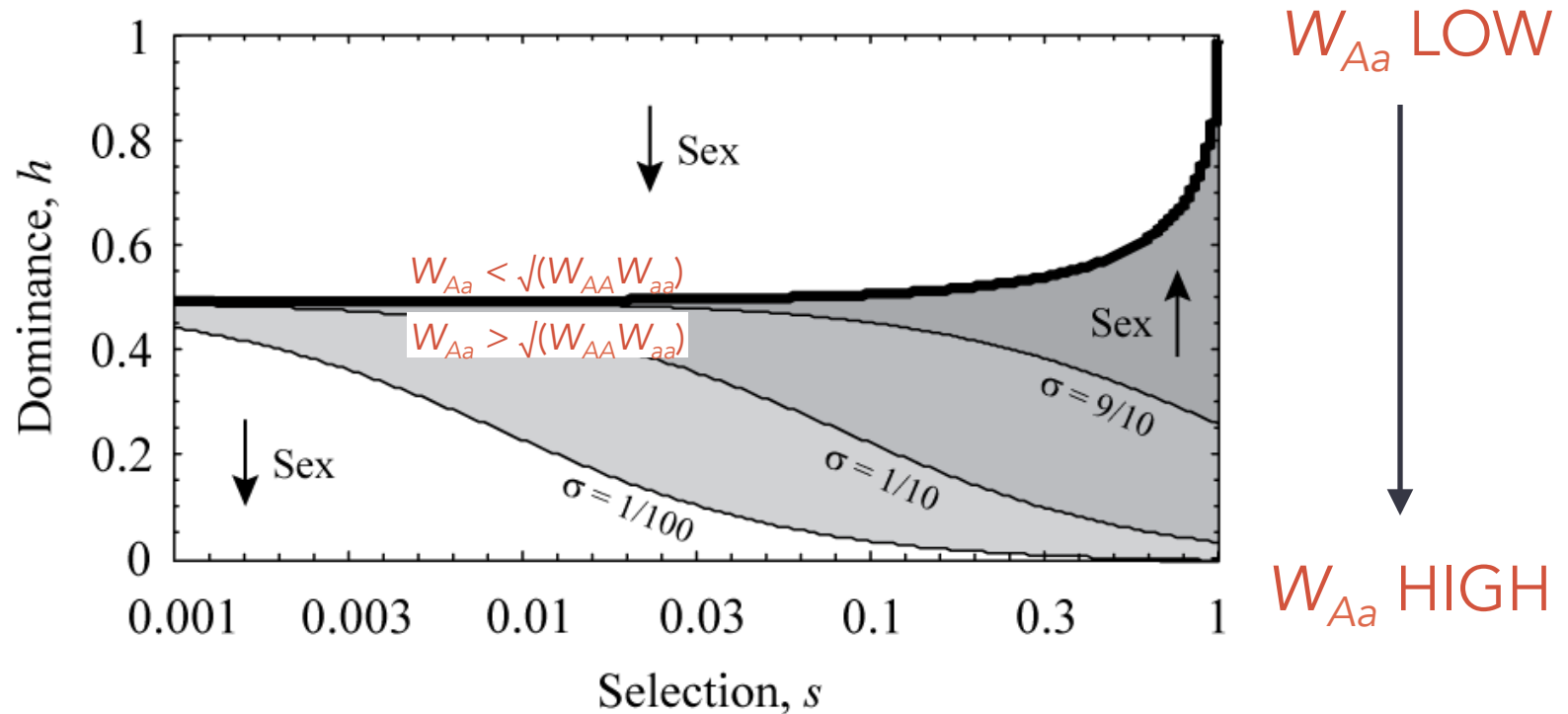
We track each diploid combination  
(*MAMA*, *MAMa*, ..., *mama*)

( $x_{11}, x_{12}, \dots, x_{44}$ )

→ Determine when new modifier alleles can spread.

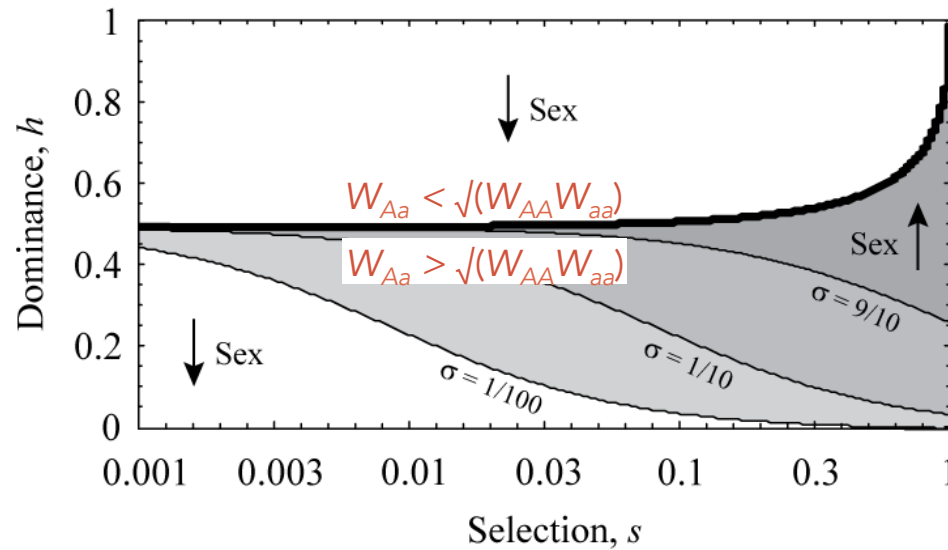
# EVOLUTION OF SEX

Modifier promoting sexuality spreads only if  $W_{Aa} > \sqrt{(W_{AA}W_{aa})}$  *and* sex & recombination are rare:

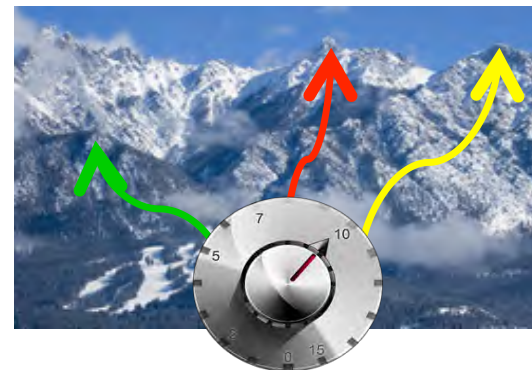


$$\begin{aligned}W_{AA} &= 1 \\W_{Aa} &= 1 - hs \\W_{aa} &= 1 - s\end{aligned}$$

# EVOLUTION OF SEX



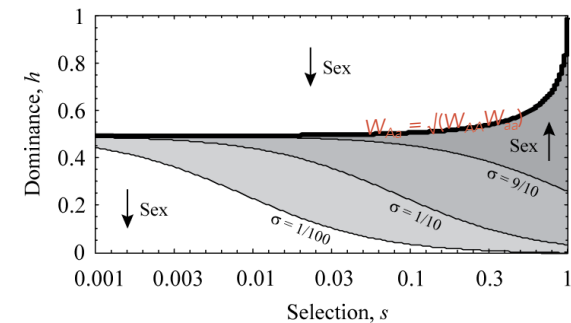
*Rate of sex/rec in population  
acts as a tuning parameter*



# EVOLUTION OF SEX

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Why do the frequencies of sex and recombination matter?



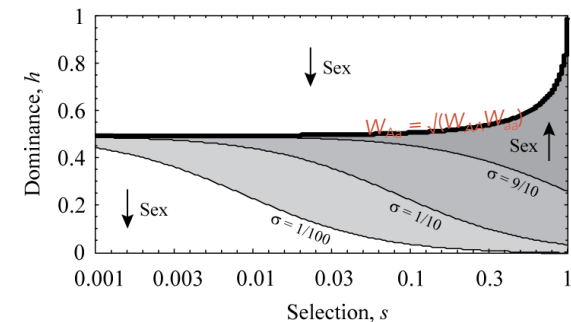


# EVOLUTION OF SEX

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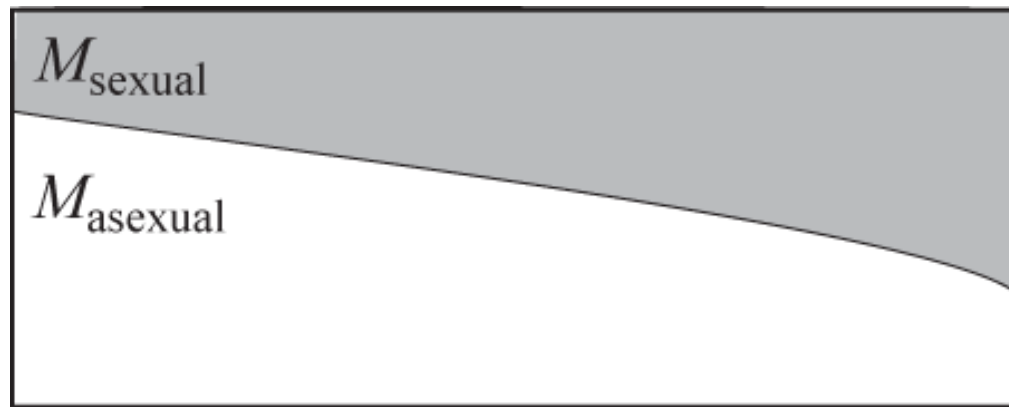
Why do the frequencies of sex and recombination matter?

The amount of genetic mixing sets the **balance** between group and individual forces acting on the modifier.



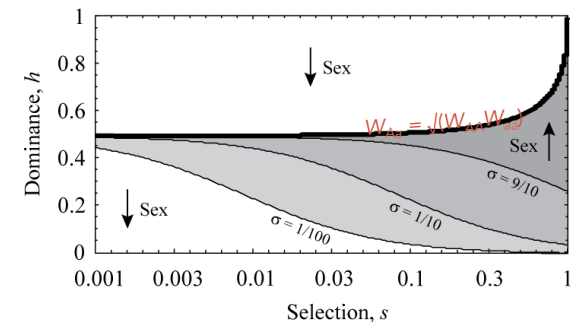
# EVOLUTION OF SEX

Without much sex/rec\*:



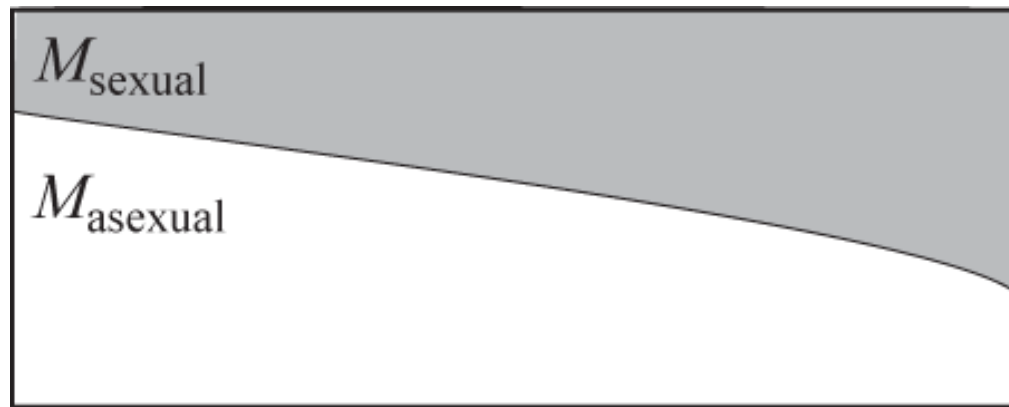
Time →

Genomes with different modifiers form almost evolutionarily separate lineages (groups).



# EVOLUTION OF SEX

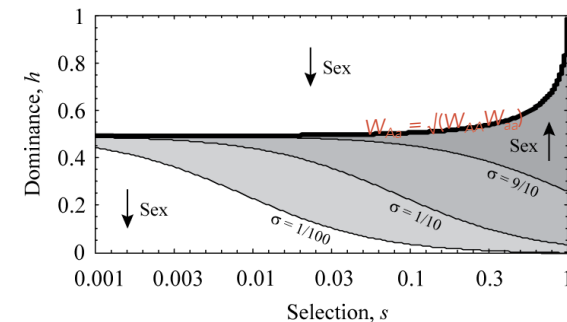
Without much sex/rec\*:



Time  $\rightarrow$

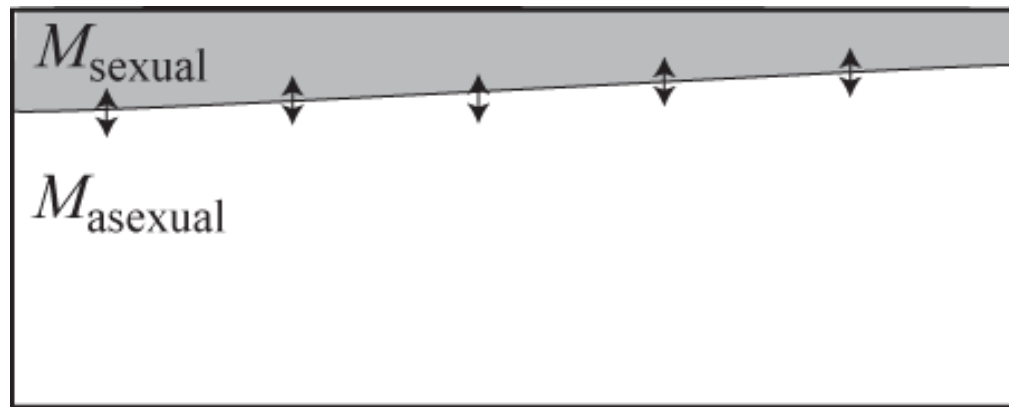
Modifiers promoting sex increase variation if  $W_{Aa} > \sqrt{(W_{AA} W_{aa})}$  & become associated with a lower mutation load.

Genetic associations build & favor sex.

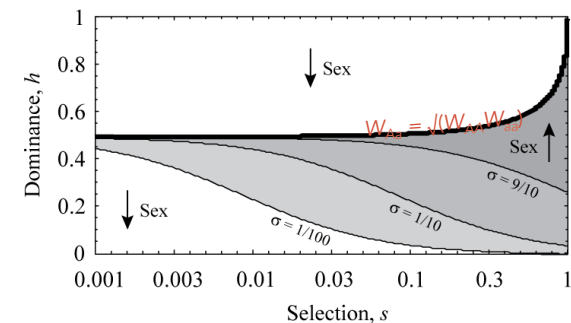


# EVOLUTION OF SEX

With frequent sex/rec<sup>\*</sup>:

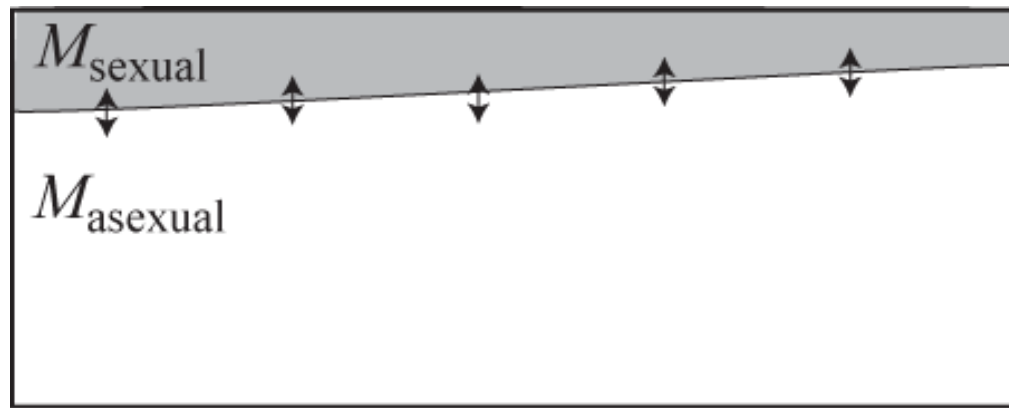


Modifiers promoting sex share genetic variants with  $M_{\text{asexual}}$  but suffer segregation load.



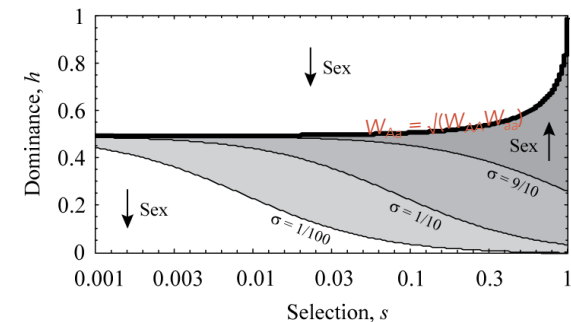
# EVOLUTION OF SEX

With frequent sex/rec\*:



Modifiers promoting sex share genetic variants with  $M_{text{asexual}}$  but suffer segregation load.

Immediate fitness effects favor asexuality.



# EVOLUTION OF SEX

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Group level:

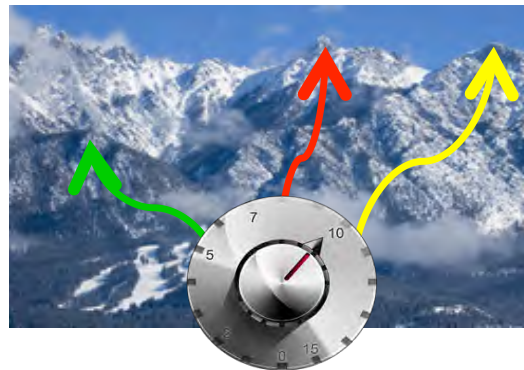
Increase variability

Sexuality favored:  $W_{Aa} > \sqrt{(W_{AA} W_{aa})}$

Individual level:

Avoid segregation

Asexuality favored



# EVOLUTION OF SEX

Analogous results are obtained when

- mutations are beneficial
- modifiers alter recombination rates
- drift acts (Hill-Robertson effects)

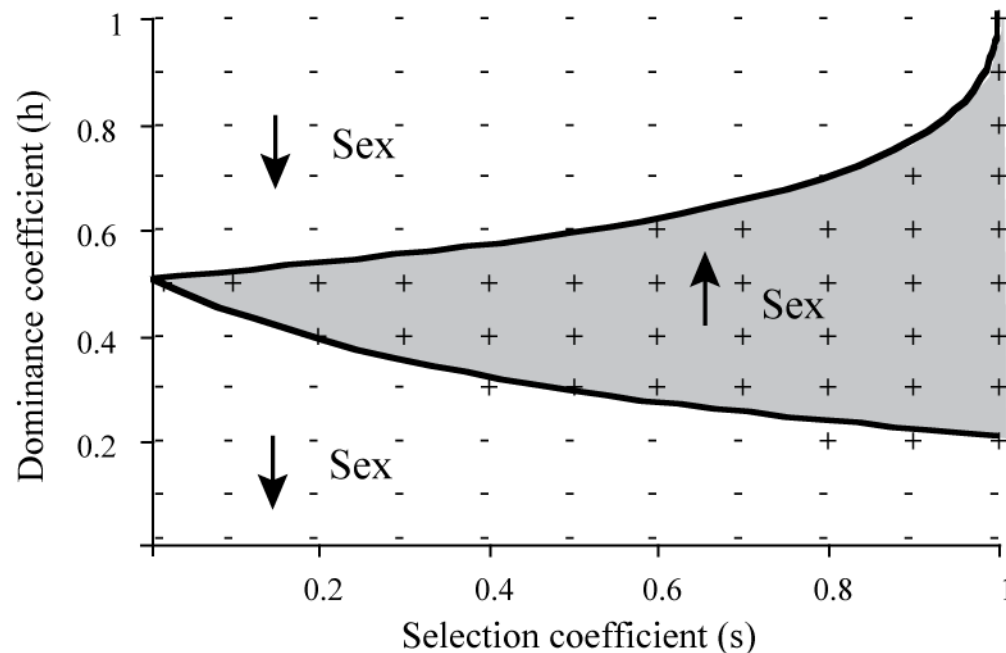
Otto 2003

Feldman et al. 1980

Barton 1995

Otto & Barton 1997

Roze & Barton 2006



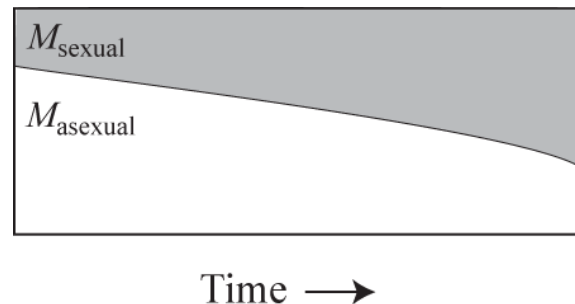
$$\begin{aligned} W_{AA} &= 1 + s \\ W_{Aa} &= 1 + hs \\ W_{aa} &= 1 \end{aligned}$$

# EVOLUTION OF SEX

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## Felsenstein & Yokoyama (1976)

“in certain cases [when linkage prevents gene flow between sub-populations] there is no sharp distinction between individual selection and group selection”

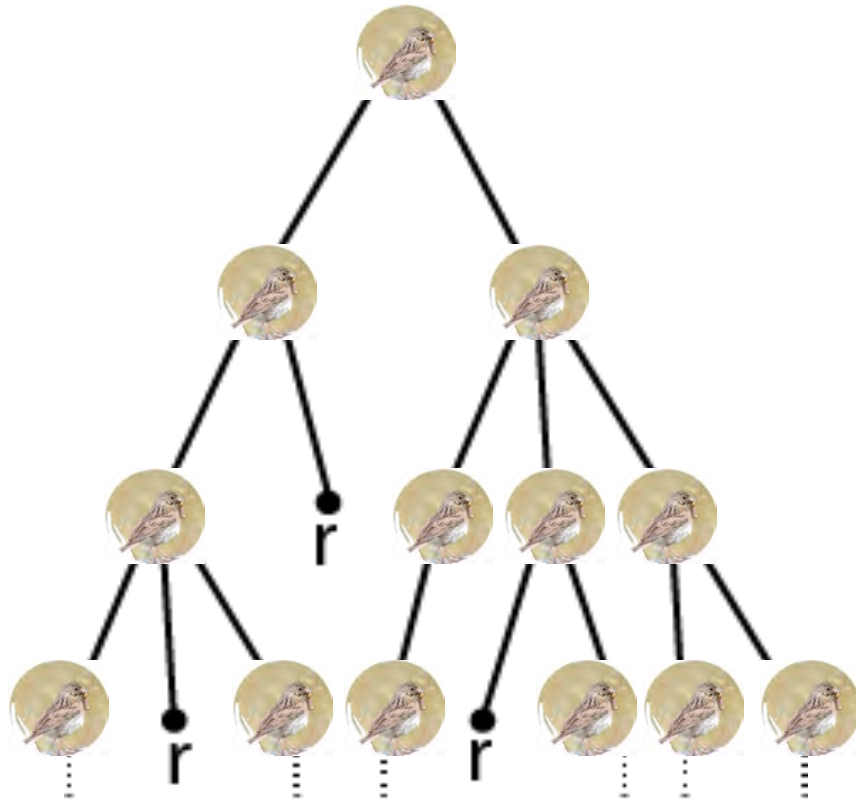




# EVOLUTION OF SEX

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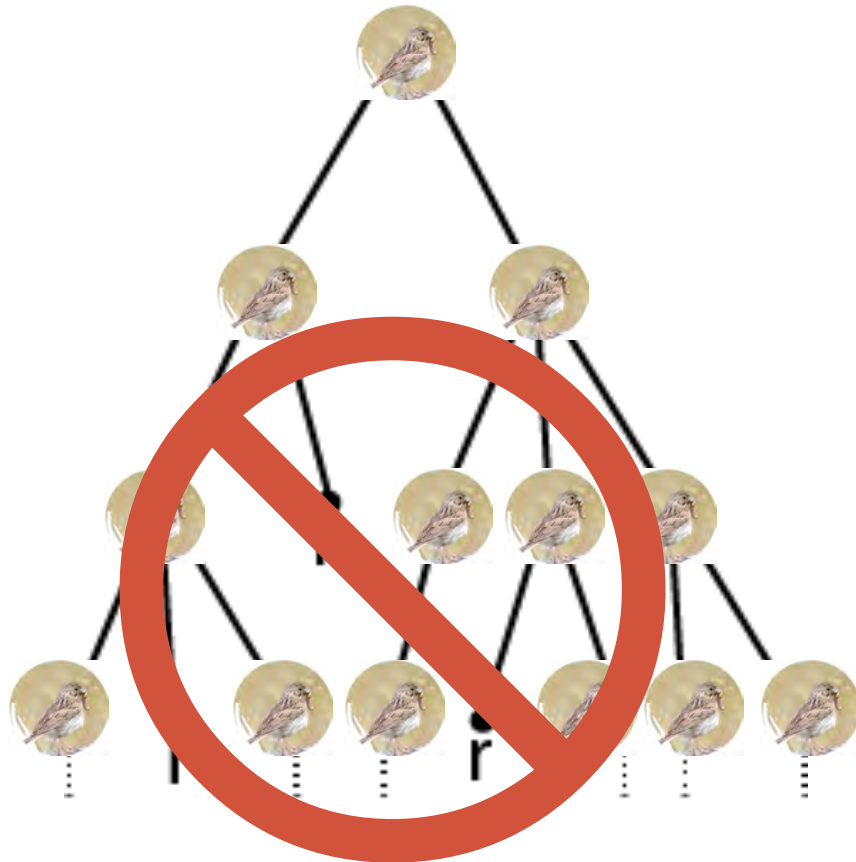
More generally, modifier models integrate **group** and **individual** selective forces.



# EVOLUTION OF SEX

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Fisher (1930)

# EVOLUTION OF SEX

---

More generally, modifier models integrate **group** and **individual** selective forces.

It may be doubted if it would be possible to point to any such character, **with the possible exception...of sexuality itself**, which could be interpreted as evolved for the specific rather than for the individual advantage.

Fisher (1930, p. 50)



# MODIFIER APPROACH

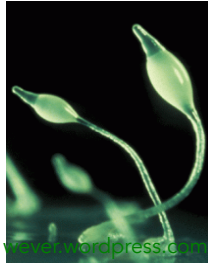
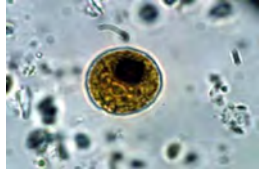
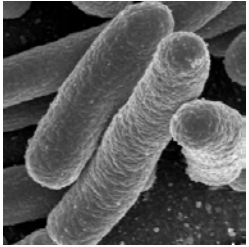
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How do modifier genes evolve when there is conflict between what is best for the individual and what is best for the group?

- Evolution of sex
- Evolution of haploidy vs diploidy
- Evolution of sex chromosomes

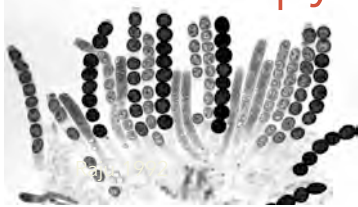
# EVOLUTION OF PLOIDY

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## Haploid

One copy of each gene



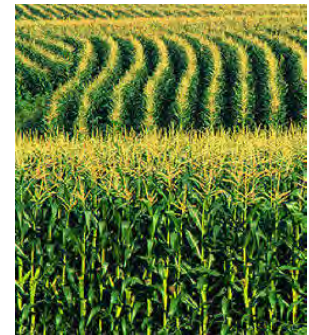
## Polyploid

Multiple copies of each gene



## Diploid

Two copies of each gene



# EVOLUTION OF PLOIDY

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Deleterious mutations are often recessive or partially so ( $h < \frac{1}{2}$ ).

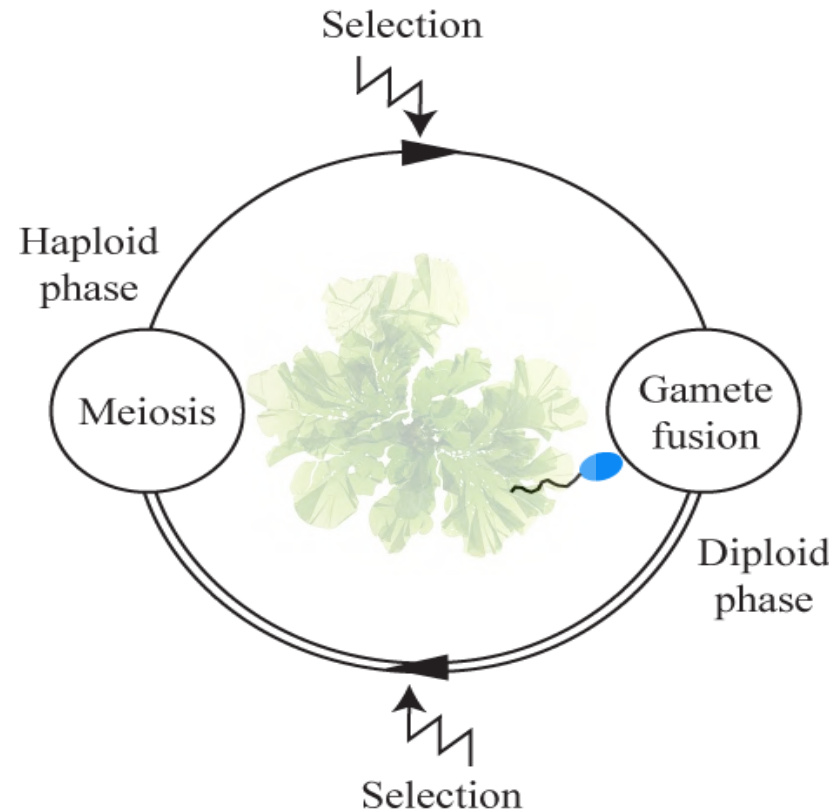
*Can the costs & benefits of expressing mutations help explain ploidy diversity?*



# EVOLUTION OF PLOIDY

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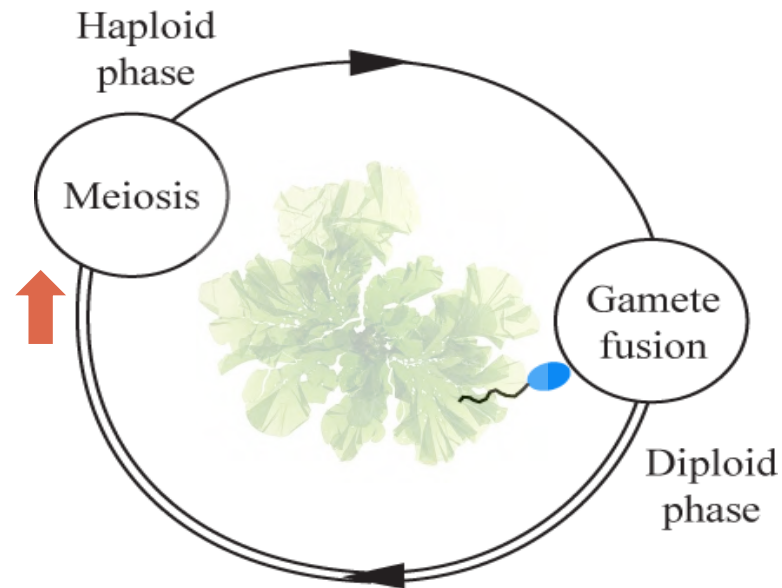
We now consider genes ("modifiers") that alter the life cycle.



# EVOLUTION OF PLOIDY

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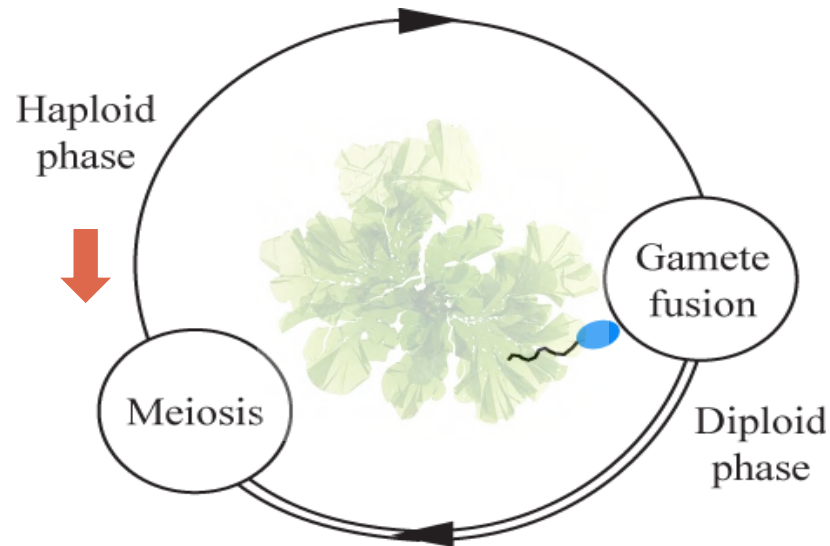




# EVOLUTION OF PLOIDY

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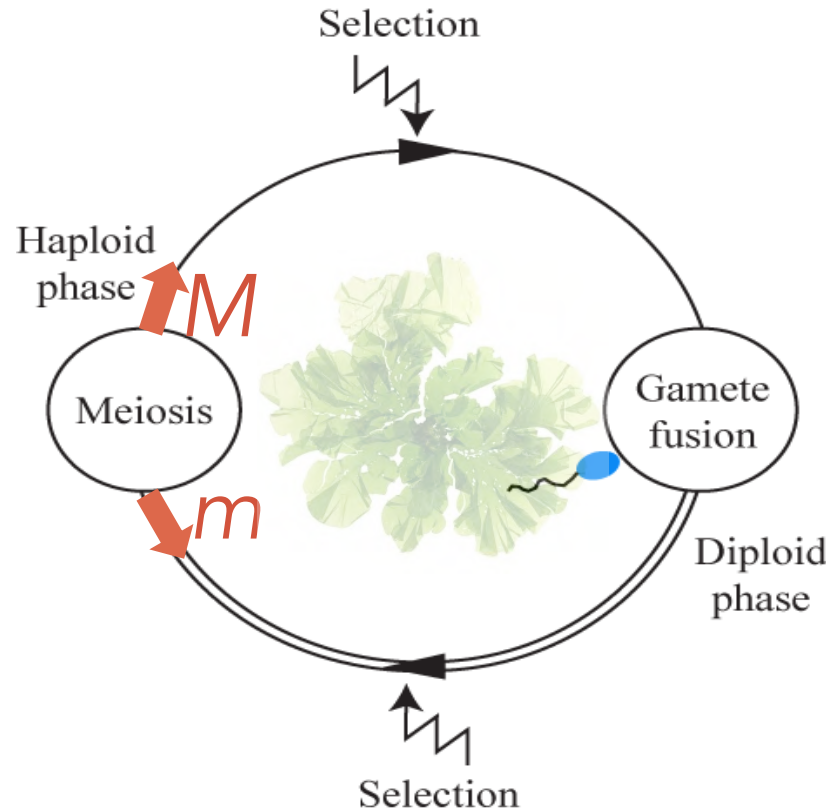
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# EVOLUTION OF PLOIDY

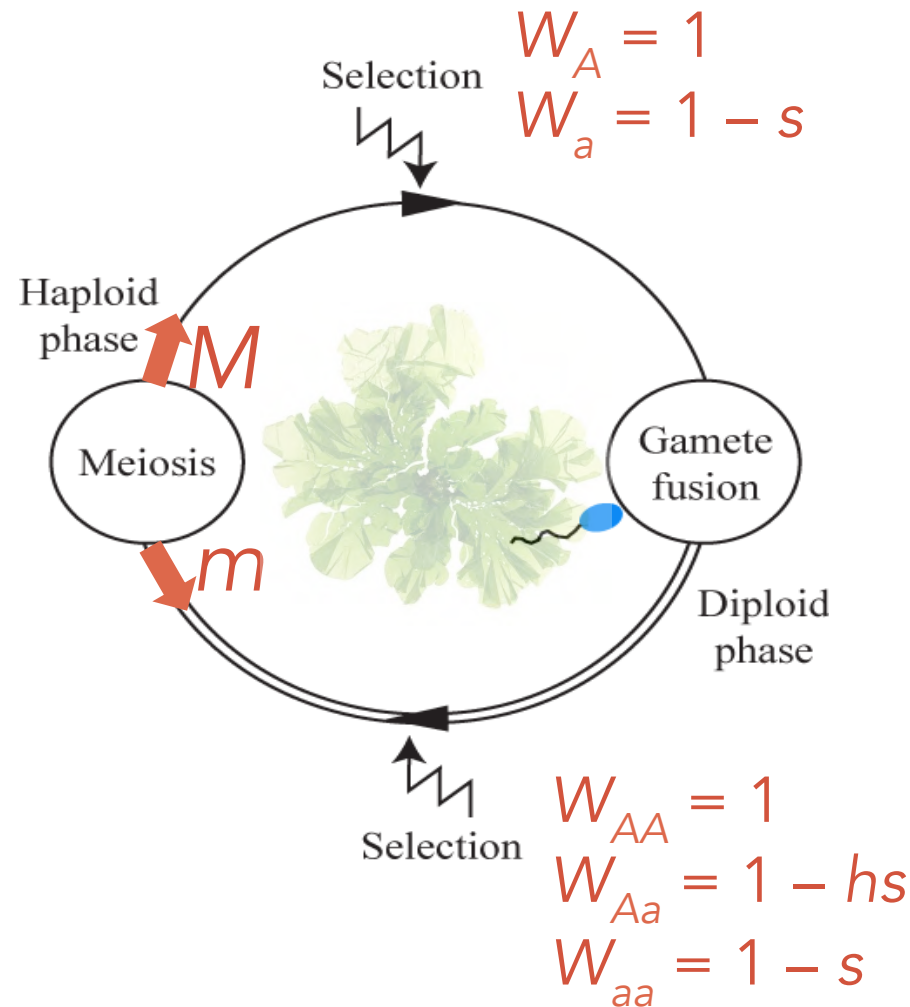
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When does  $M$   
or  $m$  spread?

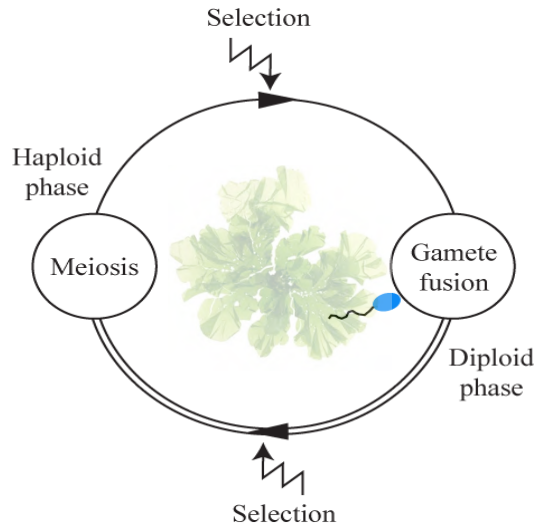


# EVOLUTION OF PLOIDY

We track each chromosome combination  
( $MA, Ma, mA, ma$ )



# EVOLUTION OF PLOIDY



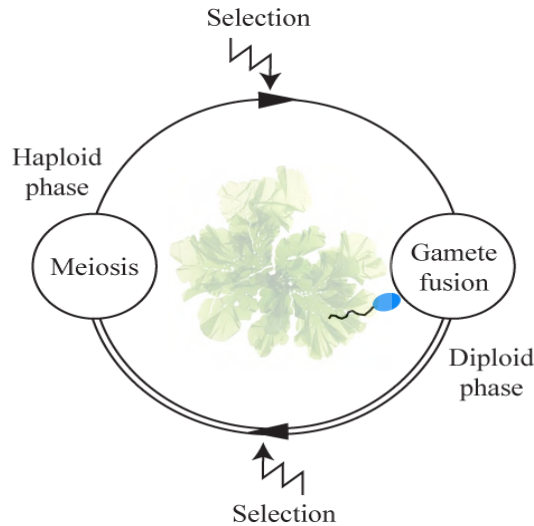
$$Tx'_1 = (1 - \frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3]$$

$$Tx'_2 = (\frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3] + (\frac{\mu_1}{2})[(1 \pm s)^{(1-d_{11})}x_1x_1 + (1 \pm hs)^{d_{11}}(1 \pm s)^{(1-d_{11})}x_1x_2 + (1 \pm s)^{(1-d_{12})}x_1x_3 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}rx_2x_3]$$

We track each  
chromosome  
combination  
( $MA, Ma, mA, ma$ )  
( $x_1, x_2, x_3, x_4$ )

Haploid selection

# EVOLUTION OF PLOIDY



$$Tx'_1 = (1 - \frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3]$$

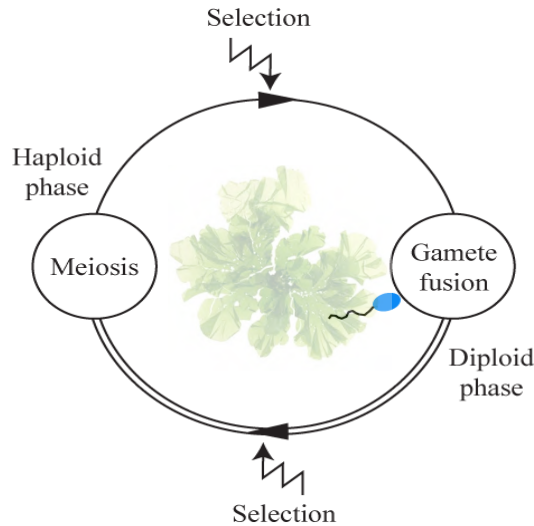
$$Tx'_2 = (\frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3] + (\frac{\mu_1}{2})[(1 \pm s)^{(1-d_{11})}x_1x_1 + (1 \pm hs)^{d_{11}}(1 \pm s)^{(1-d_{11})}x_1x_2 + (1 \pm s)^{(1-d_{12})}x_1x_3 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}rx_2x_3]$$



Gamete fusion

We track each chromosome combination  
( $MA, Ma, mA, ma$ )  
( $x_1, x_2, x_3, x_4$ )

# EVOLUTION OF PLOIDY



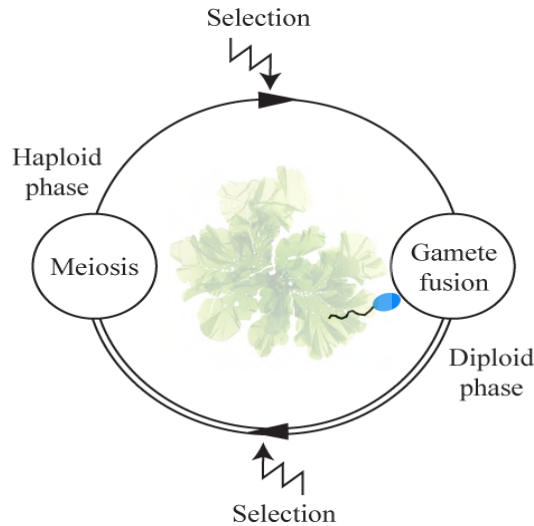
$$Tx'_1 = (1 - \frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3]$$

$$Tx'_2 = (\frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3] + (\frac{\mu_1}{2})[(1 \pm s)^{(1-d_{11})}x_1x_1 + (1 \pm hs)^{d_{11}}(1 \pm s)^{(1-d_{11})}x_1x_2 + (1 \pm s)^{(1-d_{12})}x_1x_3 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}rx_2x_3]$$

We track each  
chromosome  
combination  
( $MA, Ma, mA, ma$ )  
( $x_1, x_2, x_3, x_4$ )

Diploid selection

# EVOLUTION OF PLOIDY



$$Tx'_1 = (1 - \frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3]$$

$$Tx'_2 = (\frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3] + (\frac{\mu_1}{2})[(1 \pm s)^{(1-d_{11})}x_1x_1 + (1 \pm hs)^{d_{11}}(1 \pm s)^{(1-d_{11})}x_1x_2 + (1 \pm s)^{(1-d_{12})}x_1x_3 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}rx_2x_3]$$

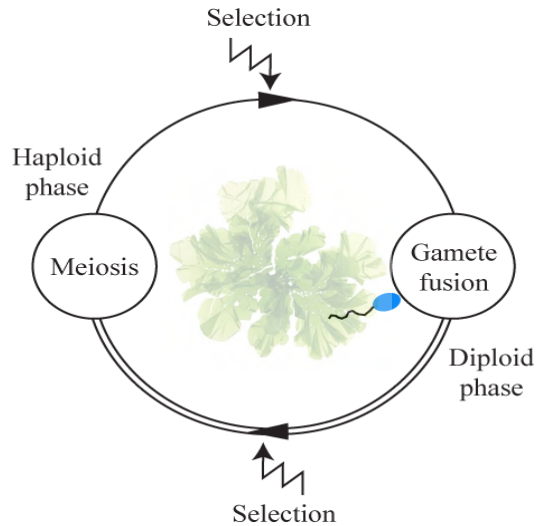


Meiosis

We track each chromosome combination  
( $MA, Ma, mA, ma$ )

( $x_1, x_2, x_3, x_4$ )

# EVOLUTION OF PLOIDY



$$Tx'_1 = (1 - \frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3]$$

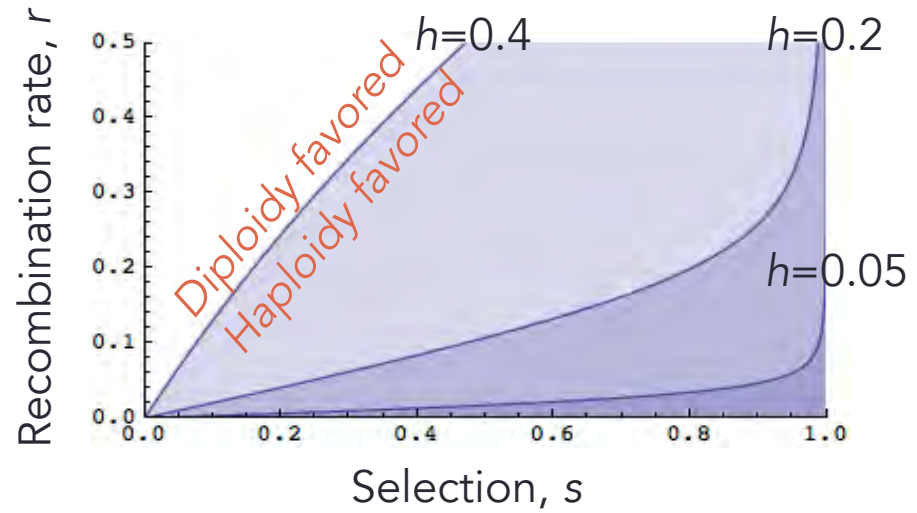
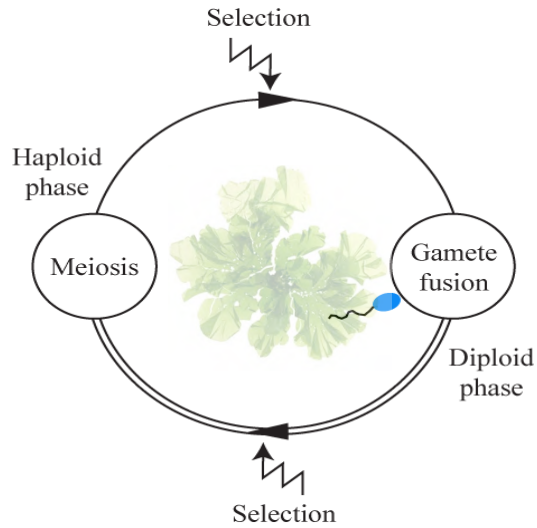
$$Tx'_2 = (\frac{\mu_2}{2})(1 - \frac{\mu_1}{2})[x_1x_1 + (1 \pm hs)^{d_{11}}x_1x_2 + x_1x_3 + (1 \pm hs)^{d_{12}}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}rx_2x_3]$$

$$(\frac{\mu_1}{2})[(1 \pm s)^{(1-d_{11})}x_1x_1 + (1 \pm hs)^{d_{11}}(1 \pm s)^{(1-d_{11})}x_1x_2 + (1 \pm s)^{(1-d_{12})}x_1x_3 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}(1 - r)x_1x_4 + (1 \pm hs)^{d_{12}}(1 \pm s)^{(1-d_{12})}rx_2x_3]$$

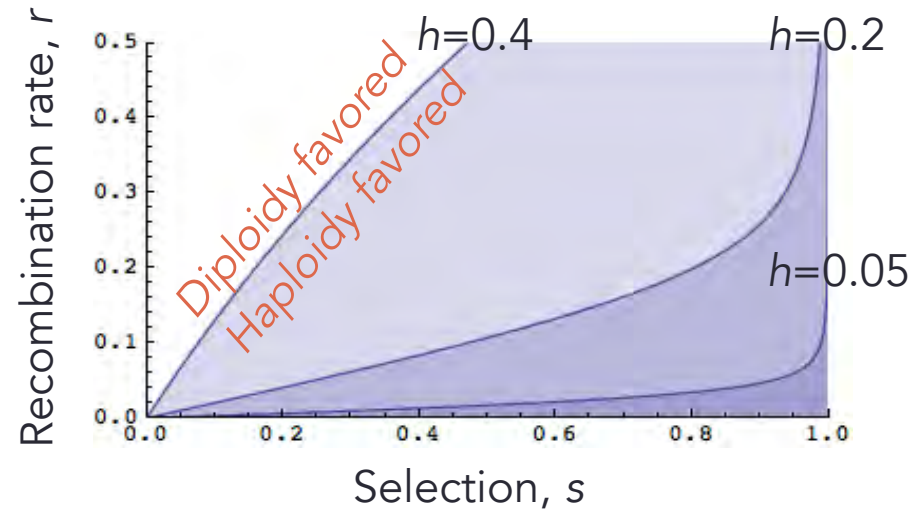
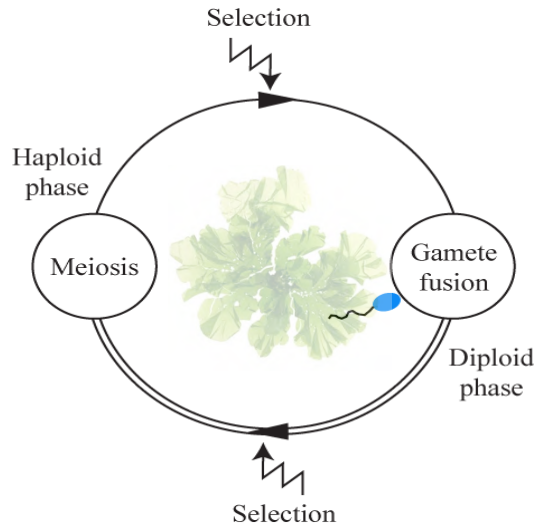
➔ Determine when new modifier alleles can spread.



# EVOLUTION OF PLOIDY



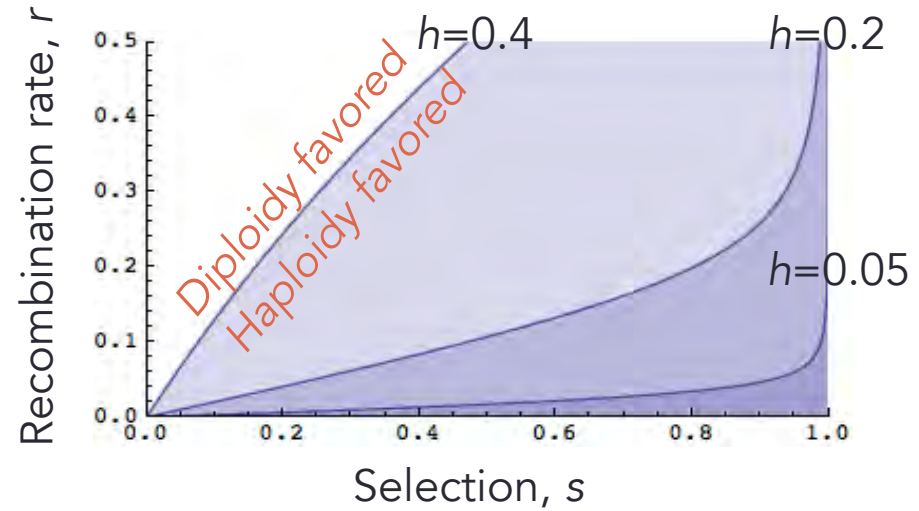
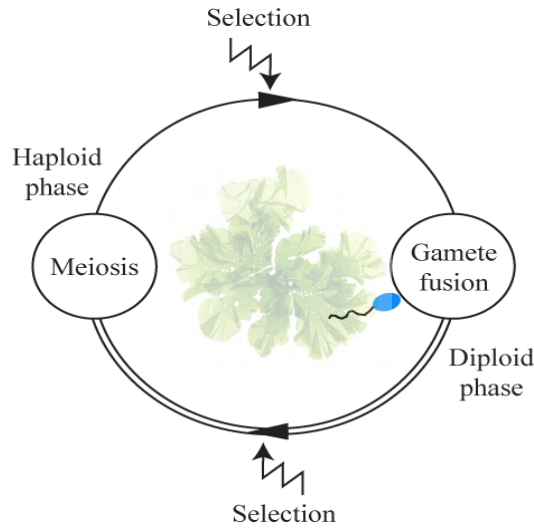
# EVOLUTION OF PLOIDY



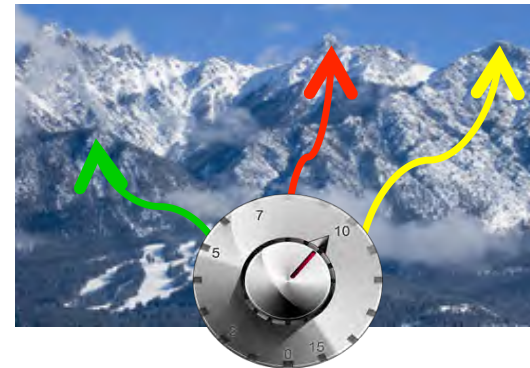
Haploid life cycles favored when organisms are primarily asexual, tend to mate with relatives, or have low rates of recombination.

Diploid life cycles favored when exchange is common.

# EVOLUTION OF PLOIDY



*Rate of sex/rec in population  
again acts as a tuning parameter*



Otto & Goldstein (1992)  
Otto & Marks (1996)  
Otto & Gerstein (2008)

# EVOLUTION OF PLOIDY

---

The amount of genetic mixing sets the **balance** between group and individual forces acting on the modifier.



# EVOLUTION OF PLOIDY

---

Group level: Selection is more efficient when mutations are fully revealed in haploids.



Misako Inaoka, *Green-pin Bird*

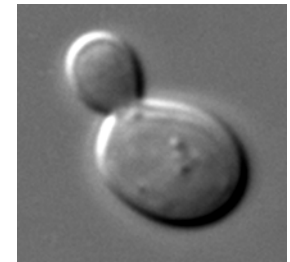
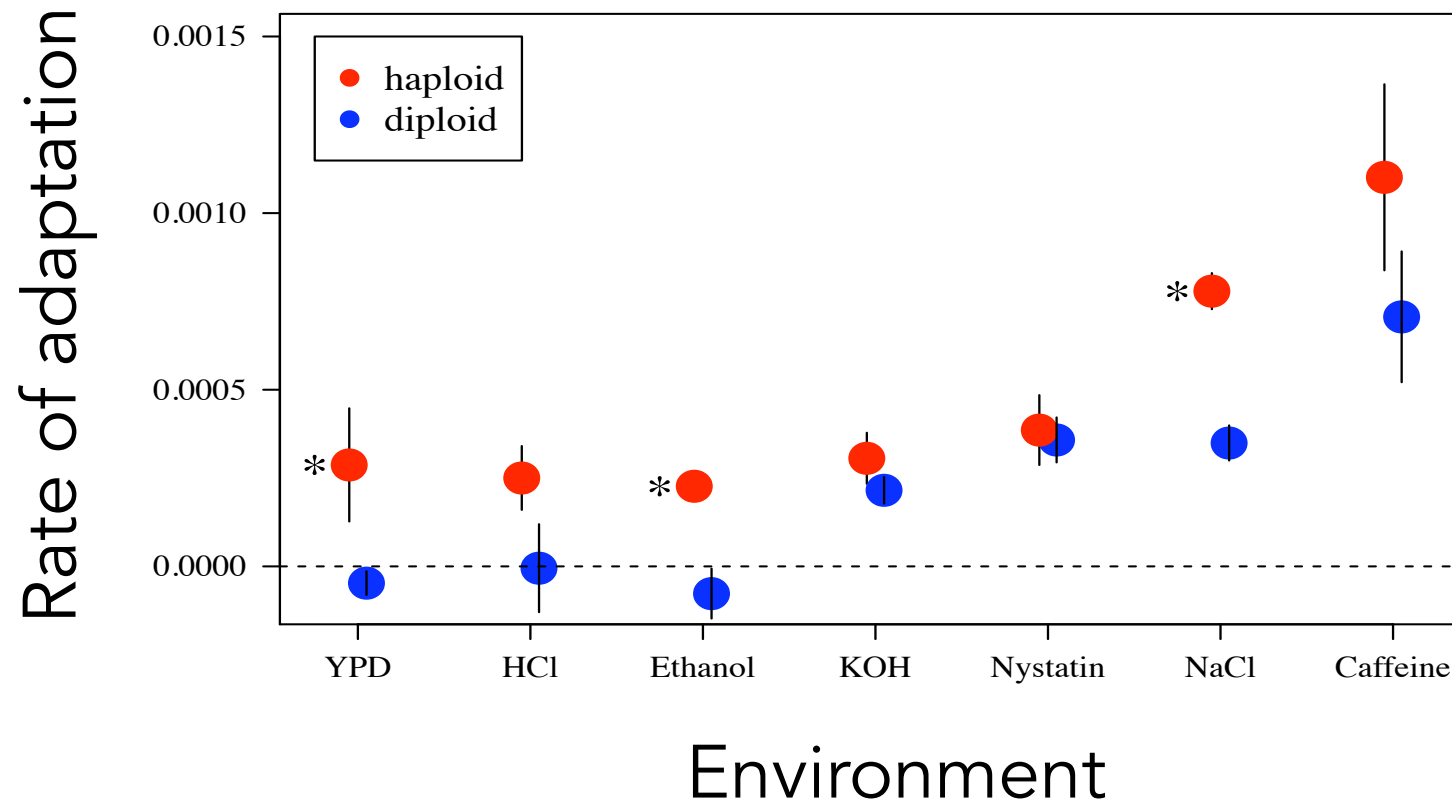


Haploidy always favored

Haploid load =  $\mu$    Diploid load =  $2\mu$

# EVOLUTION OF PLOIDY

**Example:** Selection purges deleterious alleles and hastens the spread of beneficial alleles more rapidly in haploid yeast

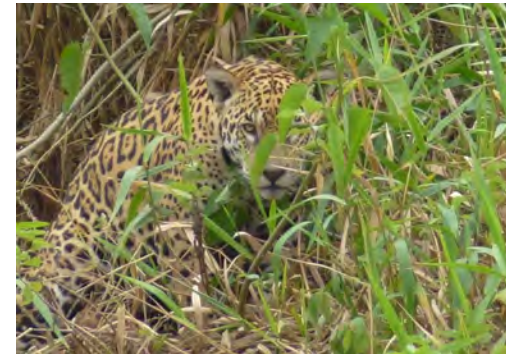


# EVOLUTION OF PLOIDY

---



Individual level: Any individual is better off as a diploid if it can mask deleterious mutations.



Diploidy favored if  $h < 1/2$

# EVOLUTION OF PLOIDY

---

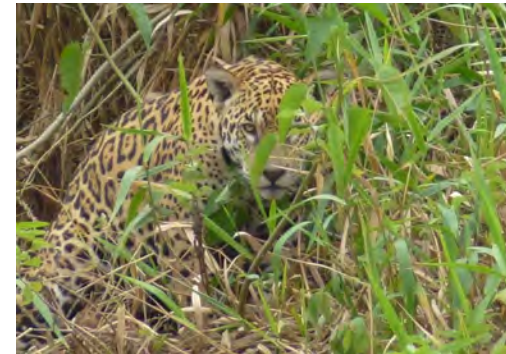
Group level: Selection is more efficient when mutations are fully revealed in haploids.



Misako Inaoka, Green-pin Bird



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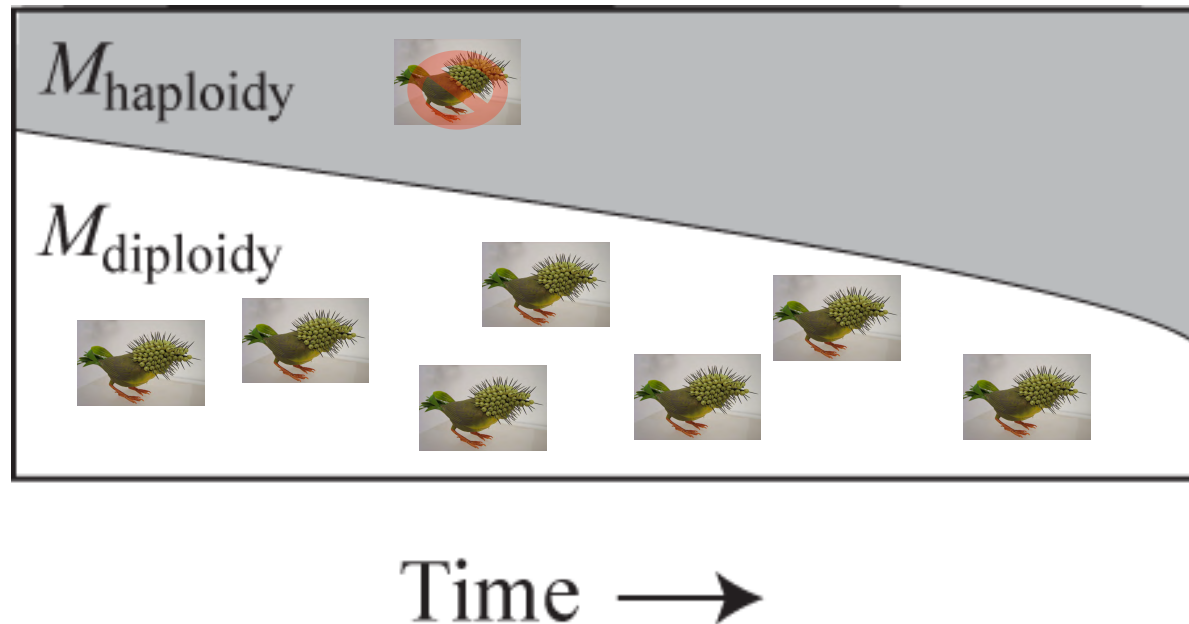
Haploid load =  $\mu$  Diploid load =  $2\mu$



# EVOLUTION OF PLOIDY

---

With little genetic mixing:



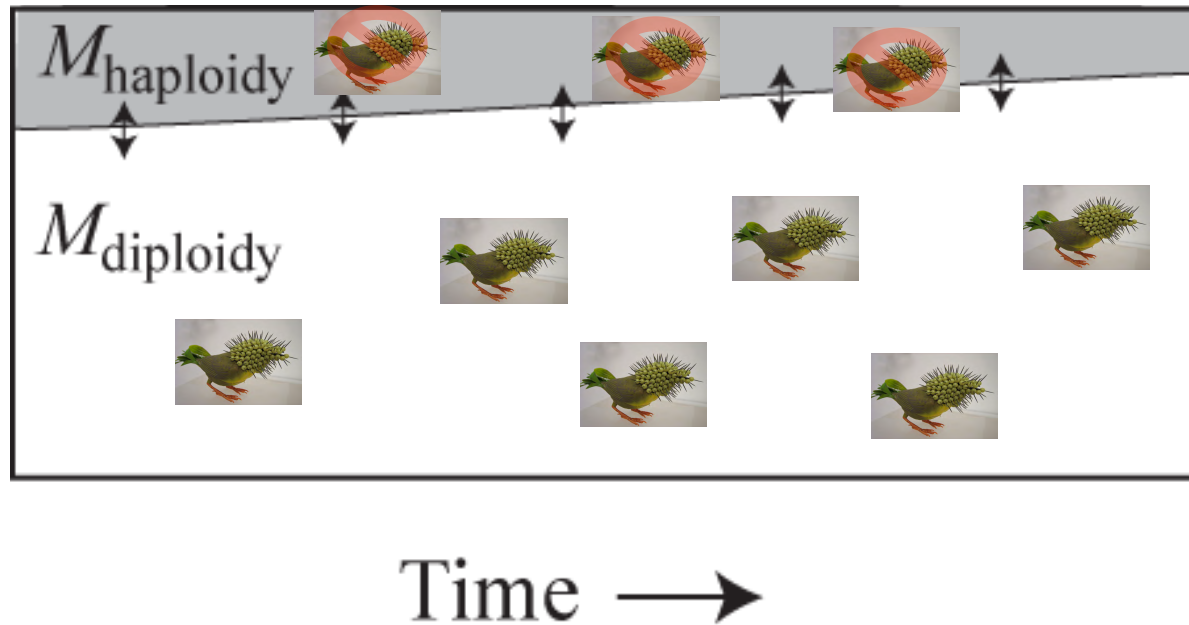
Genes promoting haploidy purge deleterious mutations, producing more fit lineages.

*Haploidy favored*

# EVOLUTION OF PLOIDY

---

With frequent genetic mixing:



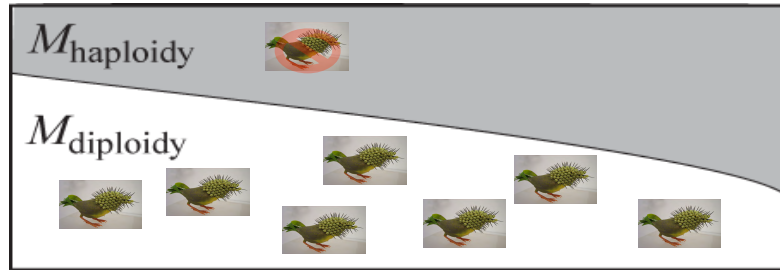
Mutations are largely masked in diploids but passed onto and exposed in haploids.

*Diploidy favored*

# EVOLUTION OF PLOIDY

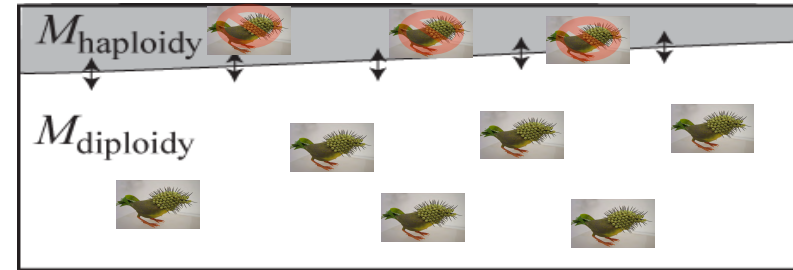
Group level: Purging

Low mixing → *Haploidy*



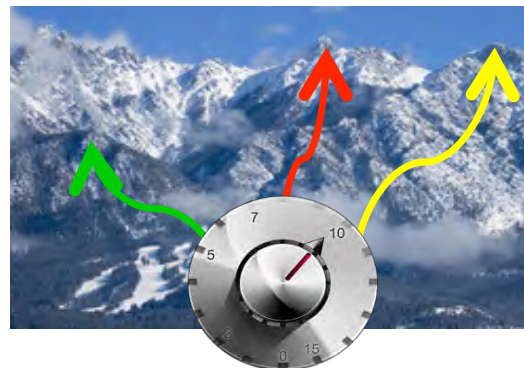
Individual level: Masking

High mixing → *Diploidy*



Low mixing ← → High mixing

Genetic mixing



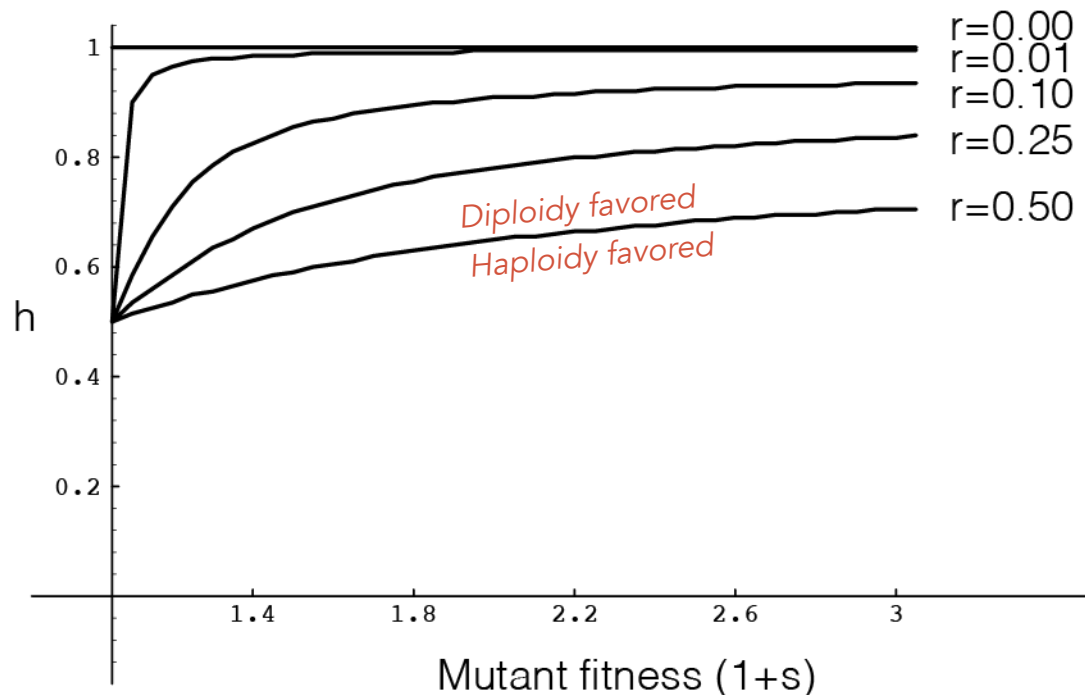
# EVOLUTION OF PLOIDY

Analogous results are obtained when

- mutations are beneficial
- haploids & diploids have intrinsic differences

Otto 1994

Scott & Rescan 2017



$$\begin{aligned} W_{AA} &= 1 + s \\ W_{Aa} &= 1 + hs \\ W_{aa} &= 1 \end{aligned}$$

# MODIFIER APPROACH

---

How do modifier genes evolve when there is conflict between what is best for the individual and what is best for the group?

- Evolution of sex
- Evolution of haploidy vs diploidy
- Evolution of sex chromosomes

# EVOLUTION OF SEX CHROMOSOMES

---

One of the first modifier models explored the tendency for recombination to decrease between two sex determining genes on a sex chromosome.

- Nei 1969



# EVOLUTION OF SEX CHROMOSOMES

---

The force favoring linkage – selection against intersexes – is an example of *epistasis* creating a strong **recombination load**.



# EVOLUTION OF SEX CHROMOSOMES

---

More generally, when different alleles benefit males and females (“sexually antagonistic selection”), tighter linkage is favored between that locus and the sex determining region.

Fisher 1931, Rice 1987,  
Charlesworth & Charlesworth 1980,  
Lenormand 2003





# EVOLUTION OF SEX CHROMOSOMES

---

Group level: Tight linkage keeps alleles that work well together in male and female descendants.



Tighter linkage favored

# EVOLUTION OF SEX CHROMOSOMES

---

Group level: Tight linkage keeps alleles that work well together in male and female descendants.



Tighter linkage favored



Individual level: Tight linkage keeps alleles that work well together in offspring.



Tighter linkage favored

# EVOLUTION OF SEX CHROMOSOMES

---

Group level: Tight linkage keeps alleles that work well together in male and female descendants.



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Individual level: Tight linkage keeps alleles that work well together in offspring.



Tighter linkage favored

# EVOLUTION OF SEX CHROMOSOMES

---

But is the loss of recombination on sex chromosomes inevitable?



# EVOLUTION OF SEX CHROMOSOMES

---

But is the loss of recombination on sex chromosomes inevitable?

Theoretically: No

Modifier models indicate that increased recombination can sometimes be favored.





# EVOLUTION OF SEX CHROMOSOMES

---

But is the loss of recombination on sex chromosomes inevitable?

Theoretically: No



Modifier models indicate that increased recombination can sometimes be favored.

What??

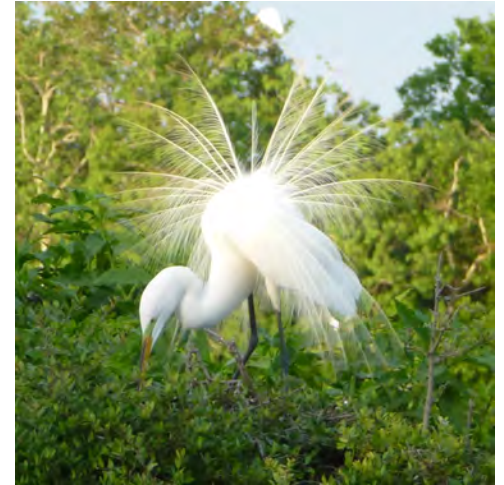


# EVOLUTION OF SEX CHROMOSOMES

---

Step back:

While we focus on male and female individuals, these do not breed true.



# EVOLUTION OF SEX CHROMOSOMES

---

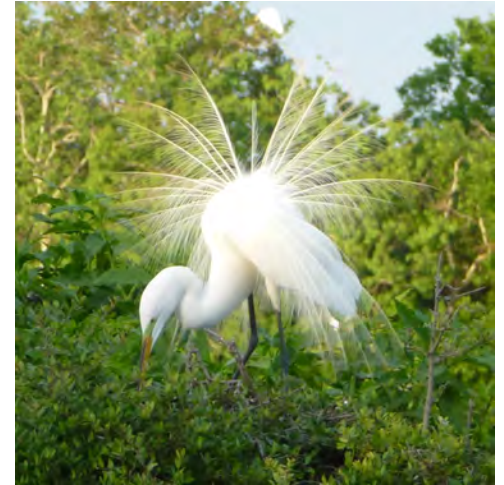
Step back:

While we focus on male and female individuals, these do not breed true.

Consider instead the chromosomes:

- X in females
- X in males
- Y

The sexual three-some



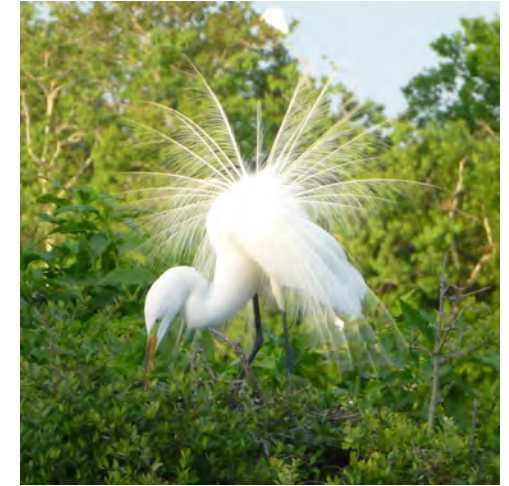


# EVOLUTION OF SEX CHROMOSOMES

---

With some forms of selection, the allele that is beneficial in females ("a") can also be favored on the Y.

- X in females: a ↑
- X in males: a ↓
- Y in males: a ↑



(Overdominance in males or sexually antagonistic selection with the female-beneficial allele also favored in pollen/sperm.)

# EVOLUTION OF SEX CHROMOSOMES

---

With some forms of selection, the allele that is beneficial in females ("a") can also be favored on the Y.

- X in females: a ↑
- X in males: a ↓
- Y in males: a ↑



When the same allele is favored in females and on the Y,  
fathers that recombine produce fitter daughters.

1  
1  
0

$$\frac{1 + M_{aa} - 2F_{aa}M_{aa}}{2(1 + M_{aa} - F_{AA} - F_{aa}M_{aa})}$$

$$\frac{1 + M_{aa} - 2F_{aa}M_{aa}}{(1 + M_{aa})^2 - 2(F_{aa} + F_{AA})M_{aa}}$$

0

Unlinked modifier

$$F_{AA} = 0.75$$

$$F_{Aa} = 1$$

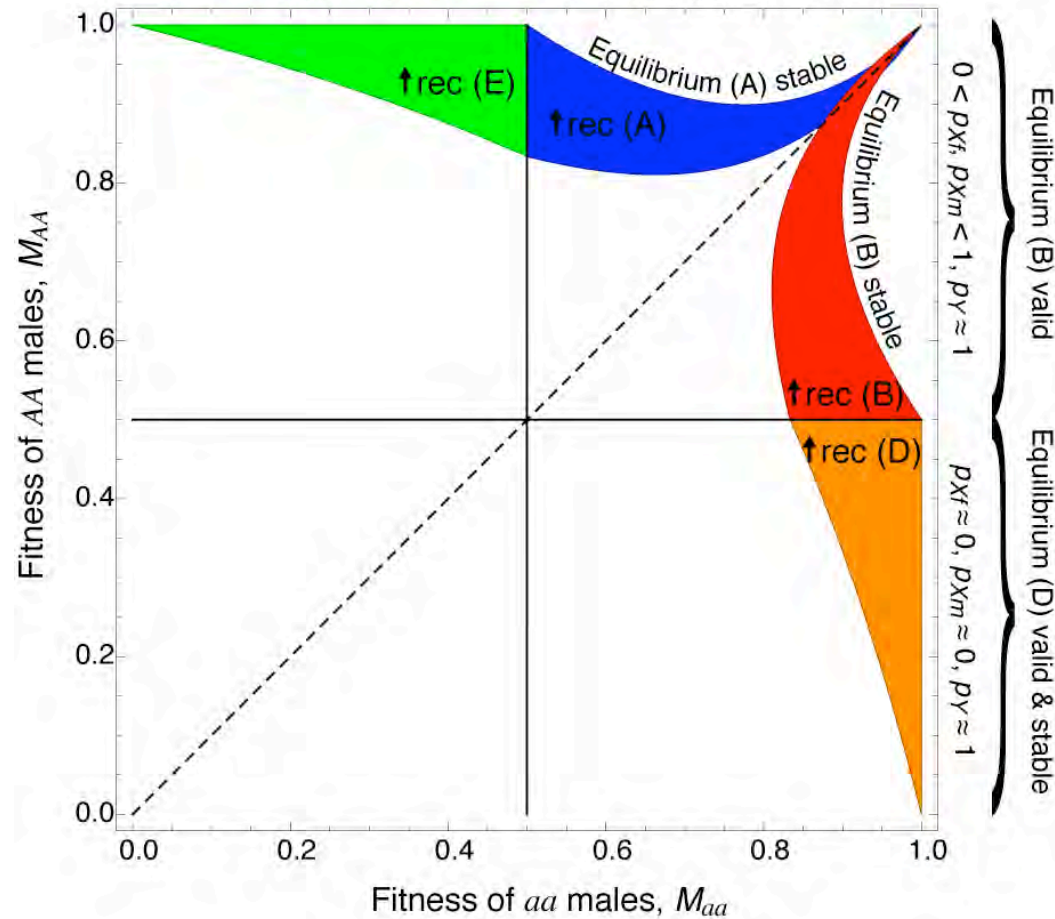
$$F_{aa} = 0.75$$

Equilibrium (E) valid & stable

Equilibrium (A) valid

$$p_{Xf} \approx 1, p_{Xm} \approx 1, p_Y \approx 0$$

$$0 < p_{Xf}, p_{Xm} < 1, p_Y \approx 0$$



$$\frac{1 + M_{AA} - 2F_{aa}}{2(1 + M_{AA} - F_{aa} - F_{AA}M_{AA})}$$

$$\frac{M_{AA} + M_{AA}^2 - 2F_{aa}M_{AA}}{(1 + M_{AA})^2 - 2(F_{aa} + F_{AA})M_{AA}}$$

1

0  
0  
1

0

(

$$F_{aa} = 0.75$$

1

1



# EVOLUTION OF SEX CHROMOSOMES

---

Group level: Tight linkage keeps alleles that work well together in male and female descendants.



Tighter linkage favored

Individual level: Tight linkage keeps alleles that work well together in offspring.



Tighter linkage favored



# EVOLUTION OF SEX CHROMOSOMES

---

Group level: Tight linkage keeps alleles that work well together in male and female descendants.



Tighter linkage favored



Individual level: Looser linkage allows fathers to produce fitter daughters.



Looser linkage favored

# EVOLUTION OF SEX CHROMOSOMES

Group level: Specialization

♀ beneficial alleles with X

♂ beneficial alleles with Y

Tight linkage favored

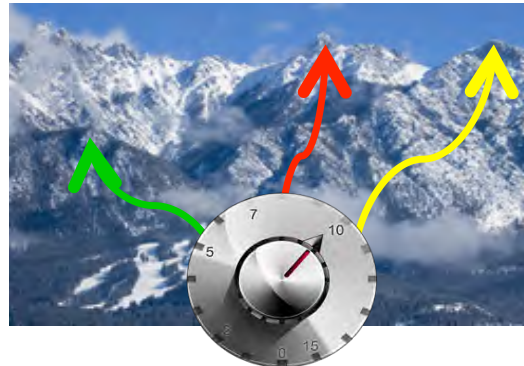
Chromosome level: Sharing

♀ beneficial alleles from Y to X

Recombination favored

Tightly  
Linked  
modifier

Loosely  
Linked  
modifier



# EVOLUTION OF SEX CHROMOSOMES

## Group level: Specialization

## Chromosome level: Sharing

♀ beneficial alleles with X

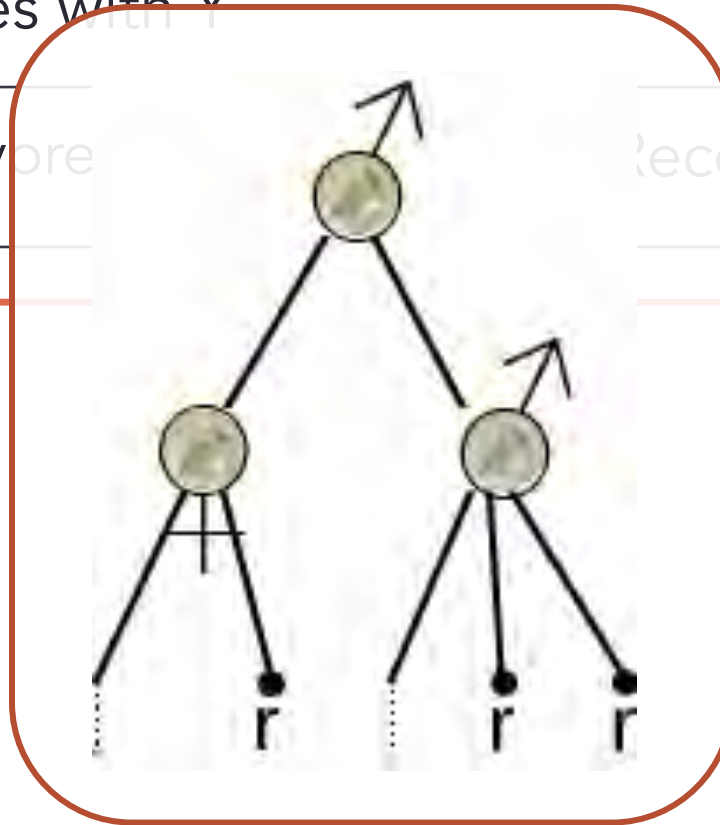
♂ beneficial alleles with Y

♀ beneficial alleles from Y to X

# Tight linkage fav

recombination favored

Tightly  
Linked  
modifier



Loosely  
Linked  
modifier



# MODIFIER THEORY

---



Modifier models  $\longleftrightarrow$  Levels of selection

Balance

Insight

Inspiration

Simplification

# MODIFIER THEORY

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SOCIETY *for the* STUDY of EVOLUTION

**Mutation rate:** Fidelity vs responsiveness [Gillespie 1981]

**Epigenetics:** Mutability vs stability [Furrow & Feldman 2005]

**Migration:** Local adaptation vs kin competition [Billiard & Lenormand 2005]

**Mating system:** Inbreeding vs outbreeding depression [Epinat & Lenormand 2009]

**Phenotypic canalization:** Responsiveness vs stability [Kawecki 2000]

**Mating preferences:** Natural vs sexual selection [Kirkpatrick 1982]

**Species boundaries:** Conspecific vs heterospecific matings [Banks et al. 2012]

# Summary

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Modifier models shift our perspective...

- from “what is best” to “what can evolve”
- from genes that affect fitness to genes that mold how an organisms lives and reproduces

# Summary

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- Group-level (long-term) evolutionary forces most important with tight linkage and low levels of sex
- Individual-level (short-term) evolutionary forces more important with frequent genetic mixing

➔ Modifier models find the balance



# Summary

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A modifier approach adds to the richness of our understanding of evolution, by detailing how genes evolve that mold the very nature of inheritance...

and how the features of the organism & its environment alter the outcome to help account for the diversity of life on this planet.



# Acknowledgments



Marc Feldman



Nick Barton



Joe Felsenstein





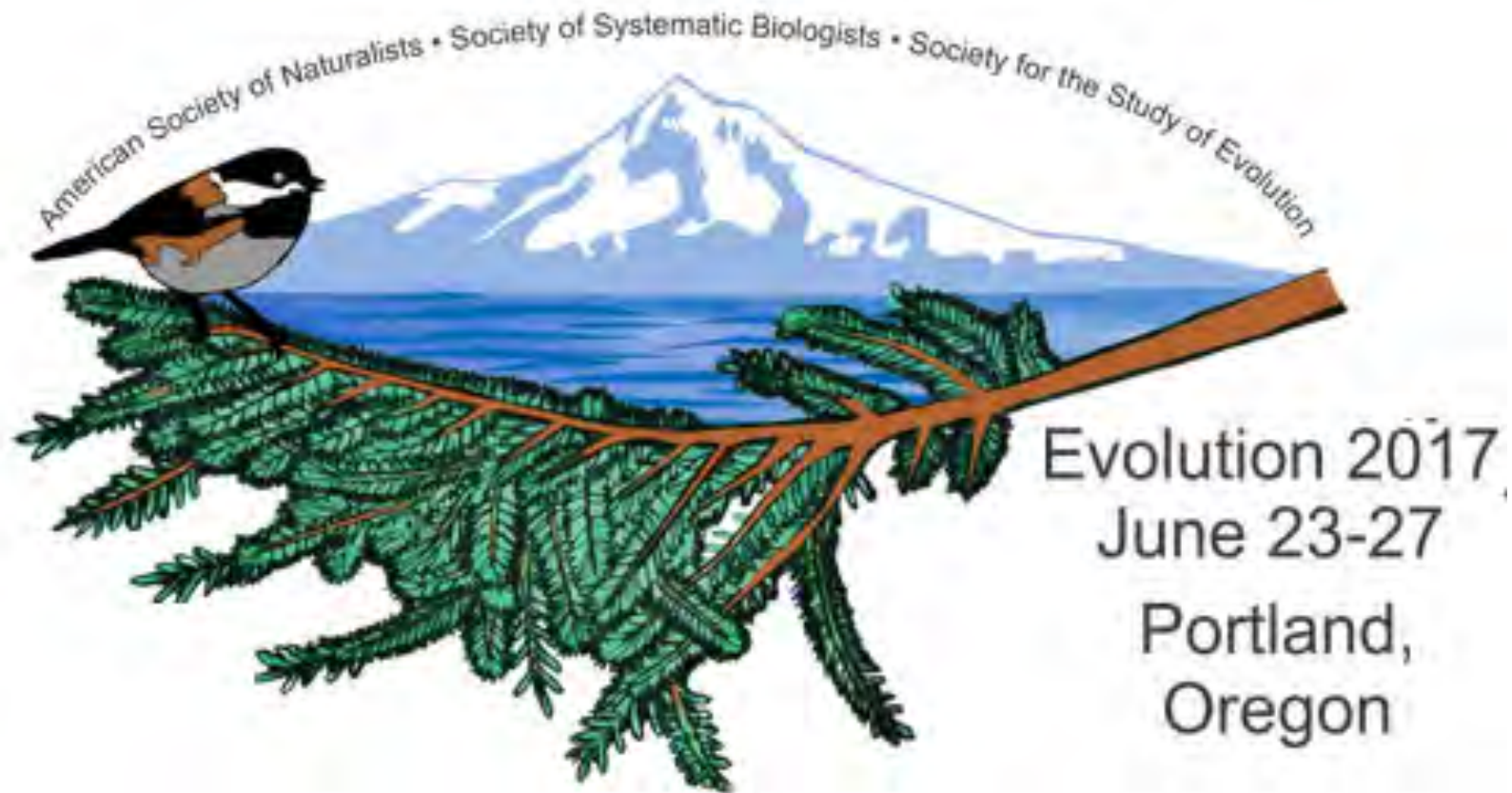
Aleeza  
Gerstein



Michael  
Scott



Alirio  
Rosales



**Howard Rundle**

**Meeting Organizing  
Committee**

**Mitch Cruzan**