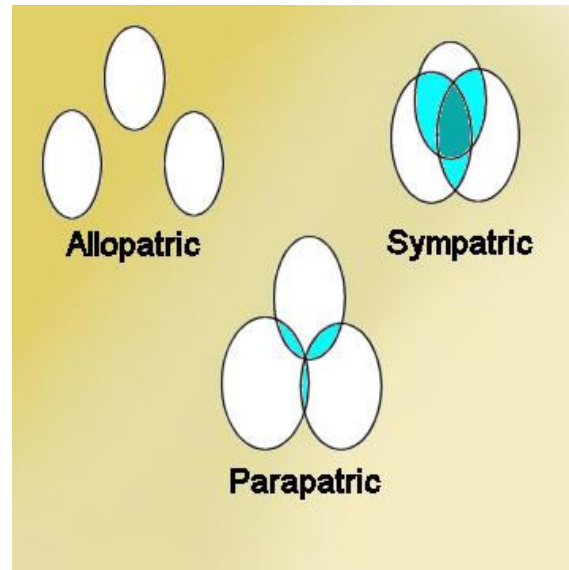


# BIOL3110 Evolutionary and Conservation Genetics



A sea of sequences to better understand the initiation of gene pools?

# Divergence despite gene flow: circumventing recombination

- Pre-zygotic

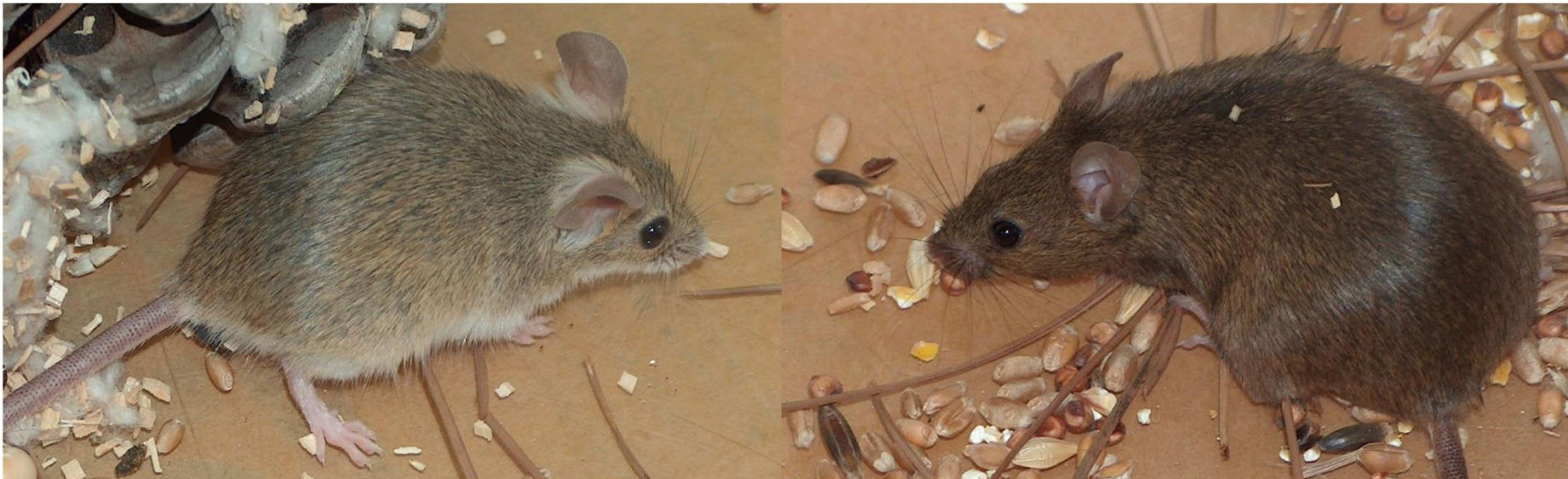
e.g. mate preference in tandem with trait under selection

- Post-zygotic isolation

e.g. lower hybrid fitness, developmental defects, less suited to environment

# 1. Post Zygotic Isolation

- Evidence that differences upon secondary contact result in genetic incompatibility  
e.g. *Mus musculus* and *M. domesticus*



Hybrid incompatibility a by-product of genetic divergence (genetic mechanisms)

- Gene duplication
- Negative epistatic interactions
- Changes in ploidy
- Chromosomal rearrangements
- Role of sex chromosomes (Haldanes rule)
- Negative mito-nuclear interactions

Extent to which involved initial divergence?

## 2. Prezygotic

e.g. of disruptive selection and habitat based (prezygotic) isolation, cichlids



● *Amphilophus citrinellus*



■ *Amphilophus zalliosus*

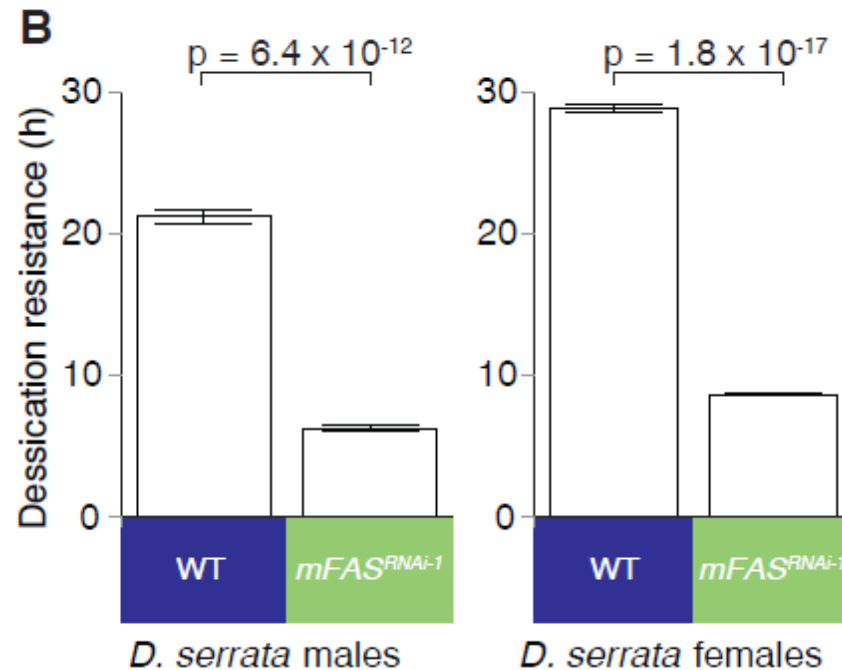
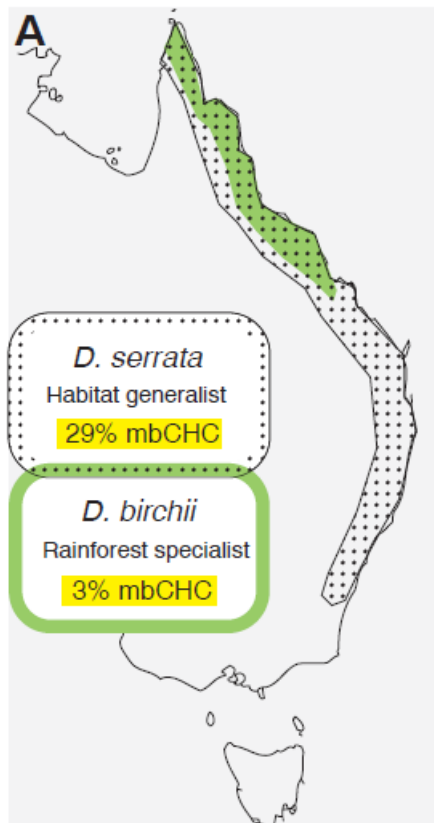
- Can be fast in which case most likely acting on standing variation.

# reducing recombination

Effects lessened when non-random mating is based on a trait under selection

- Can be 'automatic' e.g. divergent selection based on phenological traits...or
- divergent selection on mating cues associated with a trait under divergent selection

# A Single Gene Affects Both Ecological Divergence and Mate Choice in *Drosophila*



Both desiccation resistance and mate preference associated with mbCHC

# Sensory Drive - Cichlids

- Different colors
- different depths
- Assortative mating preference
- divergence much higher for opsin than neutral loci
- Strong association between color and opsin type

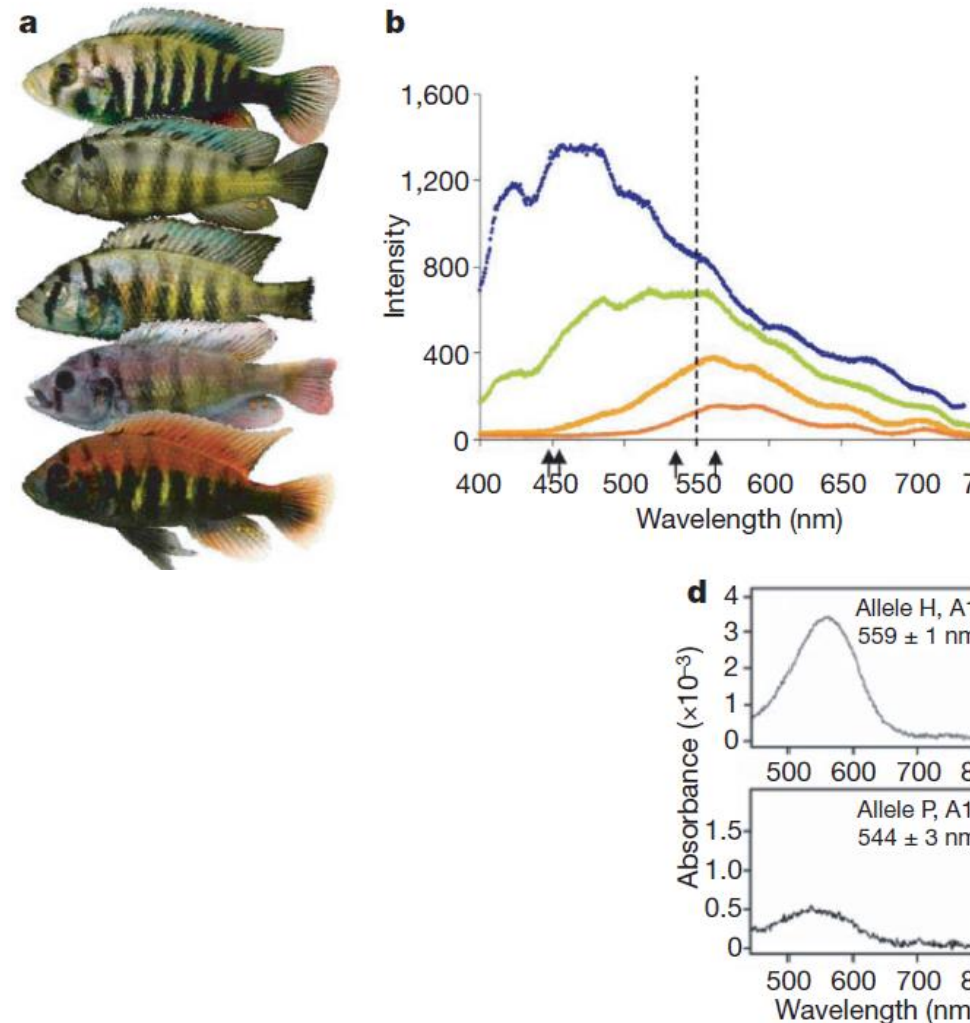
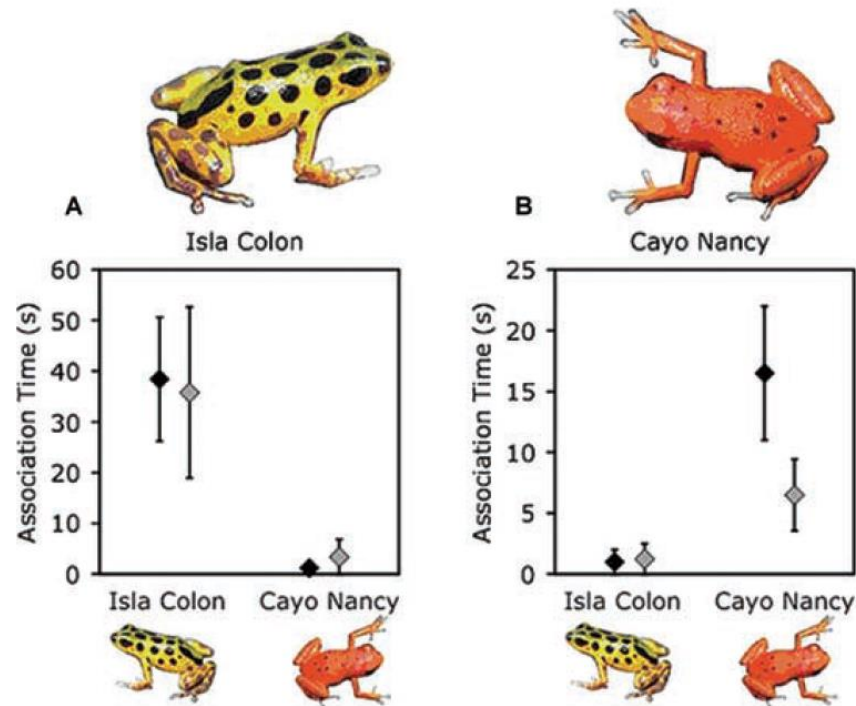


Figure 1 | Male phenotypes, light gradients and *LWS* opsin absorbance

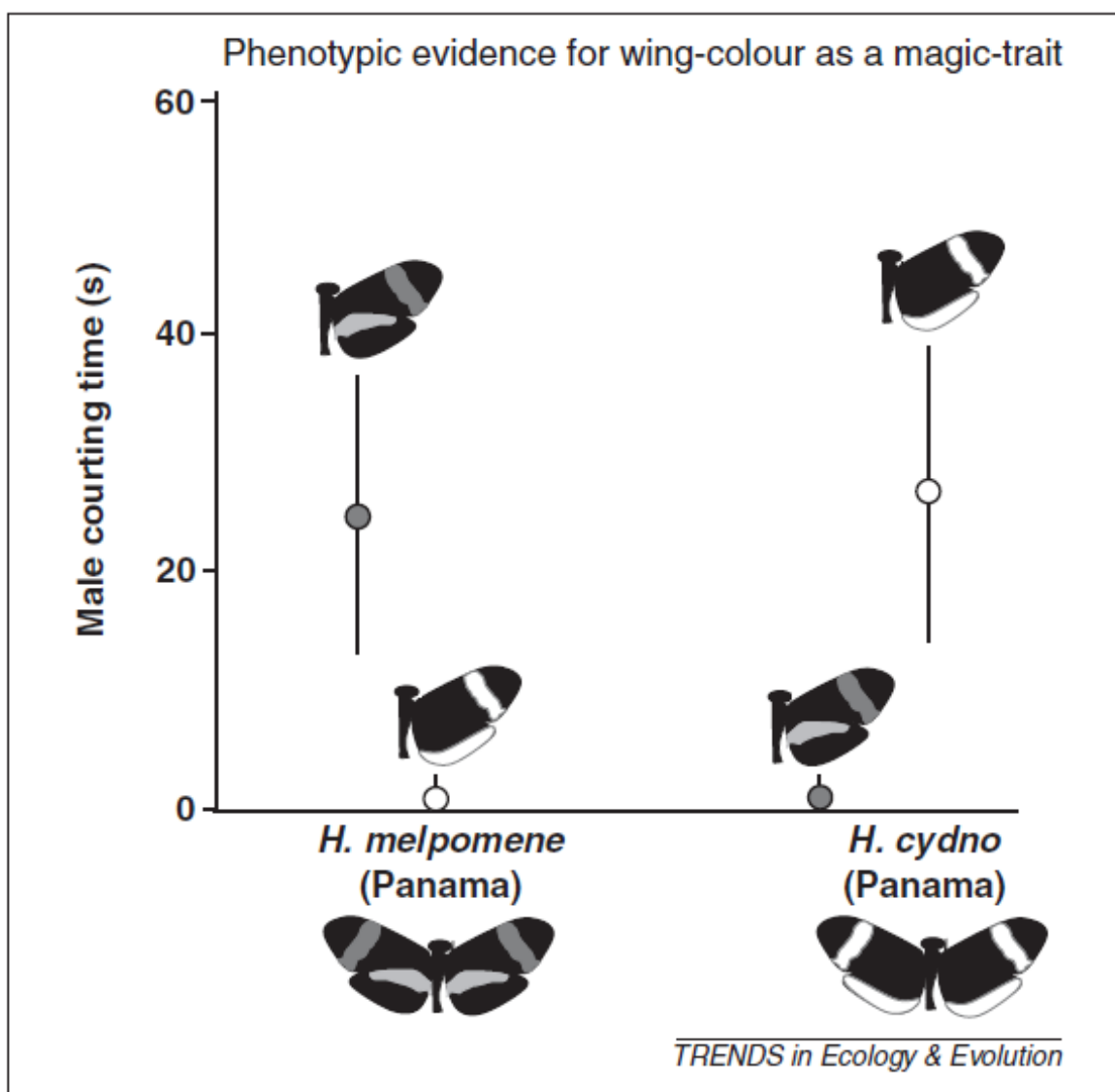


# Poison Dart Frog



**Figure 1.** Mean association times for female subject frogs from (A) Isla Colon and (B) Cayo Nancy. Darkened symbols represent blue-light trials and gray symbols represent white light trials. Vertical bars illustrate standard errors.

Assortative mating and ecologically important trait: aposematicism



Same with  
*Heliconius*  
butterflies.....

**Figure 2.** An example of a magic trait. Mimetic color-patterns in *Heliconius* butterflies are under divergent selection to adapt to different models and these color patterns also affect mate choice such that individuals prefer to mate with individuals of the same color-pattern. Shown here is the mean ( $\pm$  95% confidence intervals) time spent courting live females in 10-minute trials. Similar results were observed using paper color-pattern models. Adapted with permission from Macmillan Publishers Ltd: Nature [22].

How are adaptive loci and those involved in premating isolation maintained in the face of recombination?

- Close to centromere
- Located on an inversion
- Physical Linkage
- Pleiotropy
- Facilitated by sexual selection....or
- Condition dependant mate choice (based on pre-existing cues)
- Misidentified reinforcement

# Pleiotropy or close linkage?

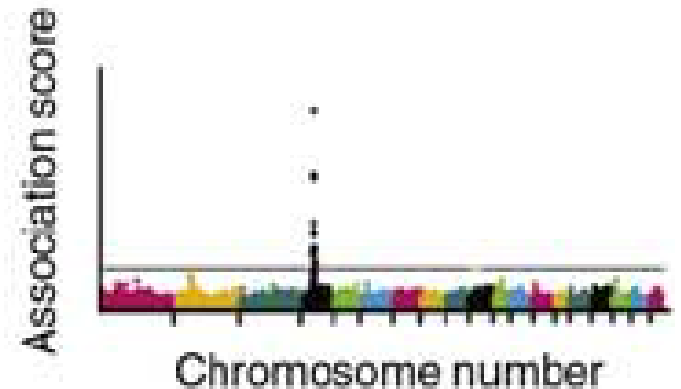
- Already a number of candidate genes to investigate. NGS of targeted regions.

e.g.

- MHC (parasite resistance/mate choice)
- Wing color and mate choice map to same gene in butterflies

# Location of regions under selection?

- Genome wide association studies with current 'model' organisms
- Three spine stickle back
- Heliconius
- Trout, white fish
- Arabidopsis
- Drosophila



Need a linkage map

# A few needs/challenges

- Genomes of many model organisms are not completely annotated
- Need better data bases describing gene function (gene ontology project)
- Need data base of ecological associations
- Divergence in gene regulation a challenge e.g. difficulties in measuring transcript abundance.

A sea of sequences to better  
understand the initiation of separate  
gene pools?

‘drowning in data’ will be a major  
selective pressure over the next few  
years....

# Brief Summary

Final Exam:

35 multiple choice or 'quiz type' questions

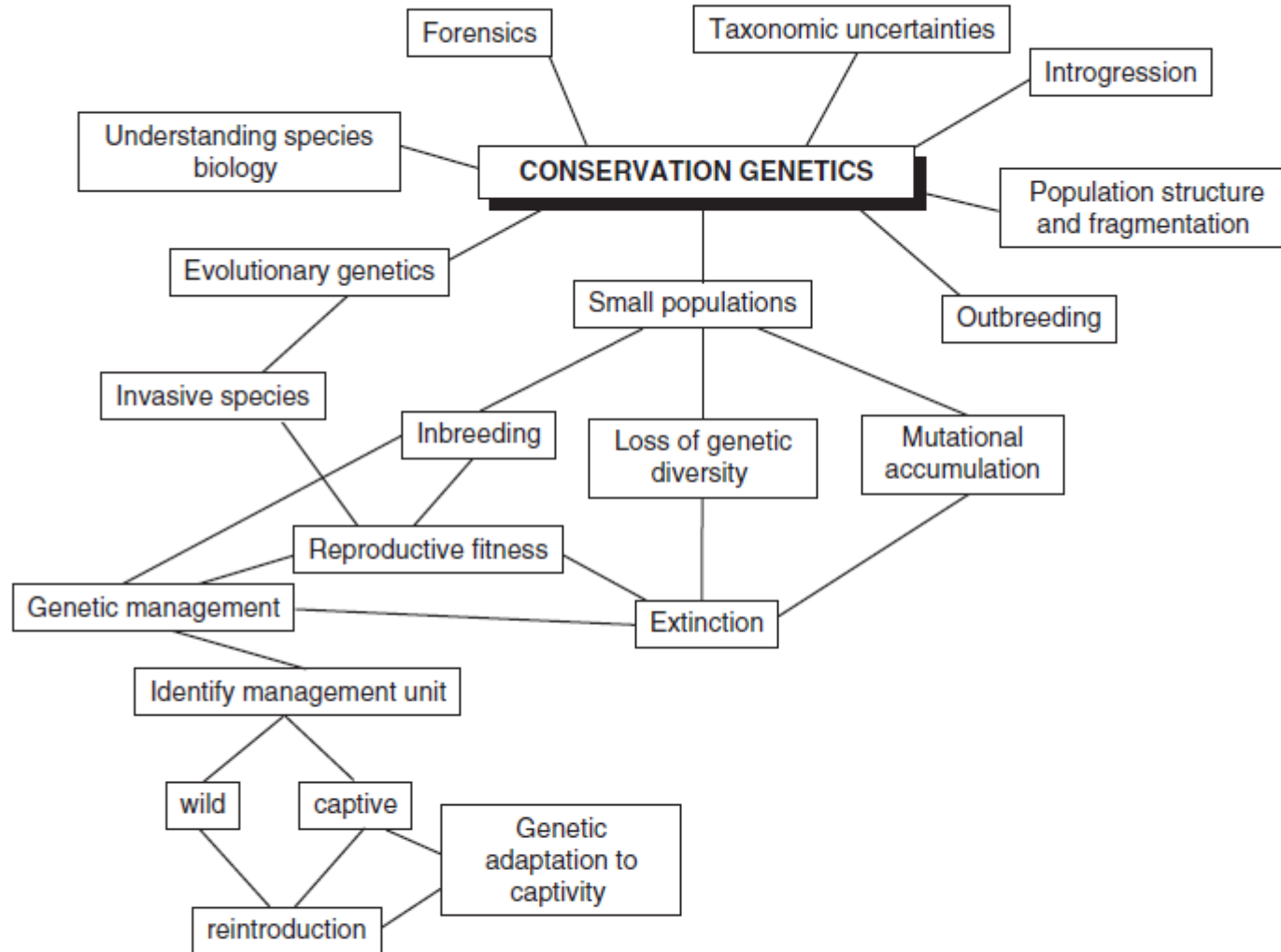
2 hours + 30 minutes

14<sup>th</sup> June commencing at 2pm

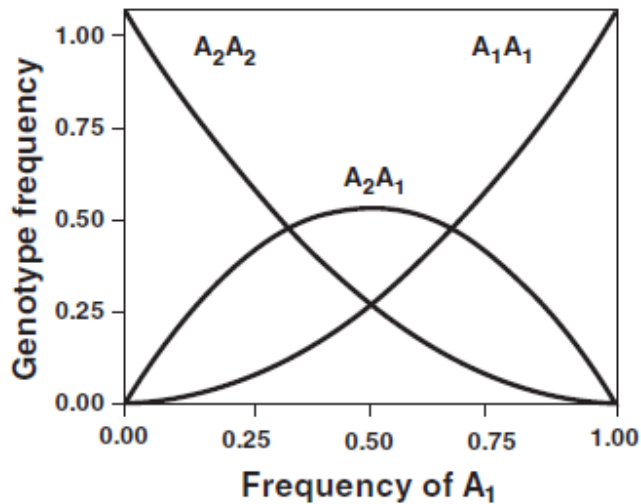
Online

Open Book





**Fig. 1.3** Structure and content of conservation genetics.



**Fig. 4.1** Relationship between genotype frequencies and allele frequencies in a population in Hardy-Weinberg equilibrium.

Use expected genotype frequencies to:

- Estimate allele frequencies
- Estimate  $H_e$
- Evaluate for deviations from HWE
- Calculate F statistics

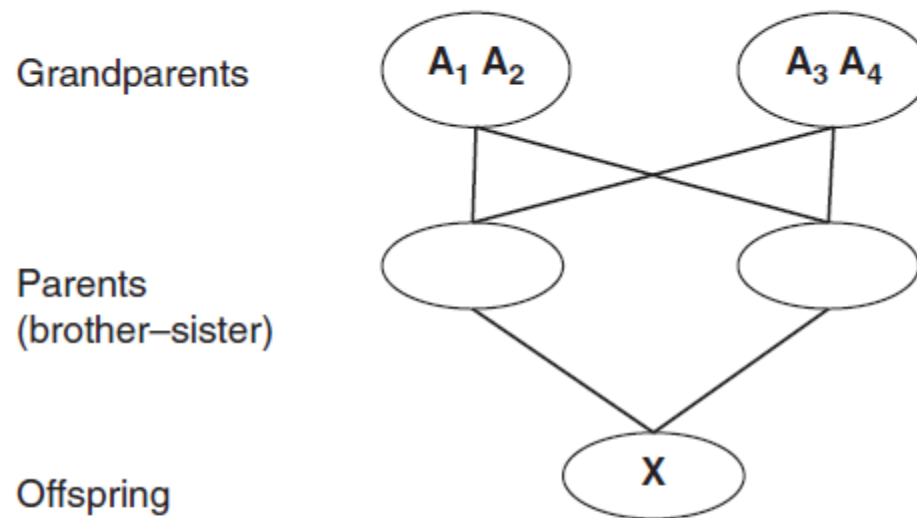
$$F_{IS} = 1 - \frac{H_I}{H_S} \quad (14.4)$$

$$F_{ST} = 1 - \frac{H_S}{H_T} \quad (14.5)$$

$$F_{IT} = 1 - \frac{H_I}{H_T} \quad (14.6)$$

where  $H_I$  is the observed heterozygosity averaged across all population fragments,  $H_S$  is the expected heterozygosity averaged across all population fragments and  $H_T$  is the expected heterozygosity for all populations, treated as a whole (equivalent to  $H_e$ ).

## Full-sib mating



$$F_X = \Pr(X = A_1 A_1 \text{ or } A_2 A_2 \text{ or } A_3 A_3 \text{ or } A_4 A_4) \\ = 1/16 + 1/16 + 1/16 + 1/16 = 1/4$$

**Fig. 12.2** Inbreeding coefficients for individuals resulting from self-fertilization and full-sib mating.

5. We obtained the following gamete frequencies for 80 individuals. What is the value of linkage disequilibrium (D) for this sample? Would you conclude that there is linkage between alleles at these two loci?

	$A_1B_1$	$A_1B_2$	$A_2B_1$	$A_2B_2$	
Frequency	0.220	0.300	0.400	0.080	1.000

Answer:

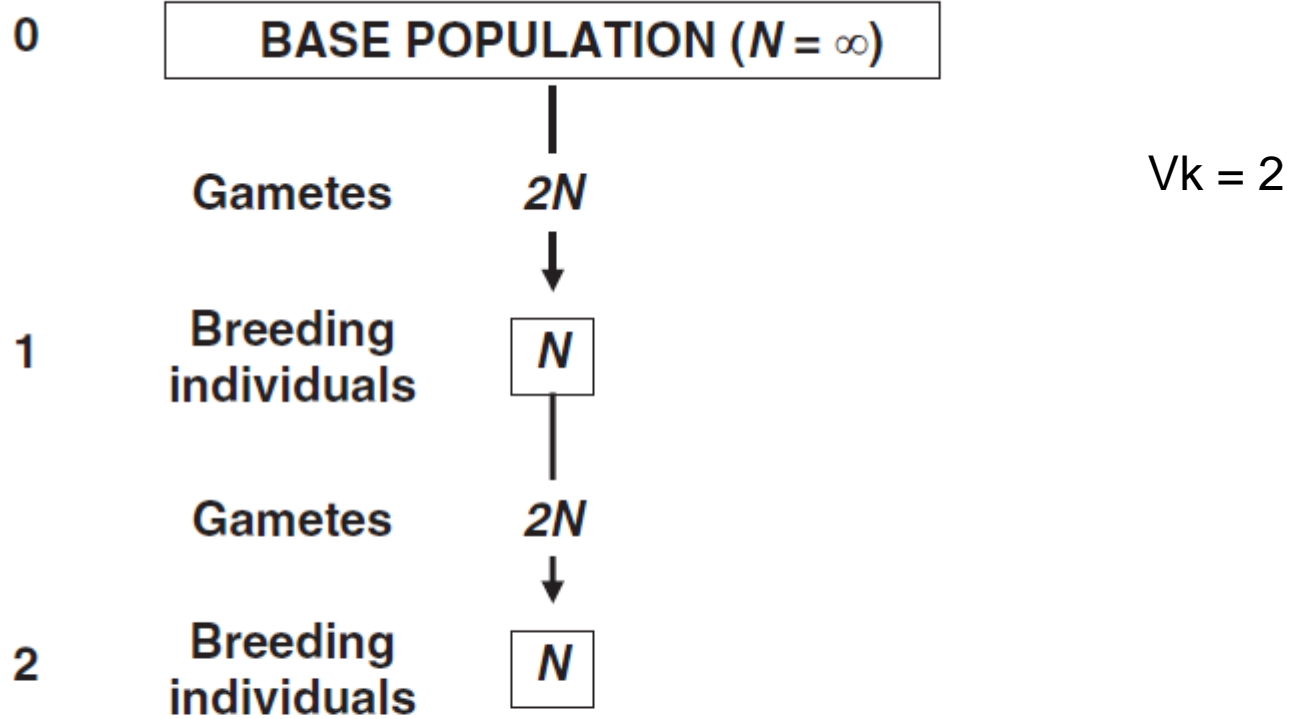


	$A_1B_1$	$A_1B_2$	$A_2B_1$	$A_2B_2$
Observed frequency	$r$	$s$	$t$	$u$
	0.220	0.300	0.400	0.080

$$D = (r \times u) - (s \times t)$$

$$\begin{aligned}
 D &= (0.22 \times 0.08) - (0.3 \times 0.4) \\
 &= 0.0176 - 0.12 \\
 &= \mathbf{-0.1024}
 \end{aligned}$$

**Generation**



**Fig. 8.8** Idealized population. From the very large base population a sample of  $N$  adults is taken and this population is maintained as a random mating, closed population with constant number of parents in each generation.

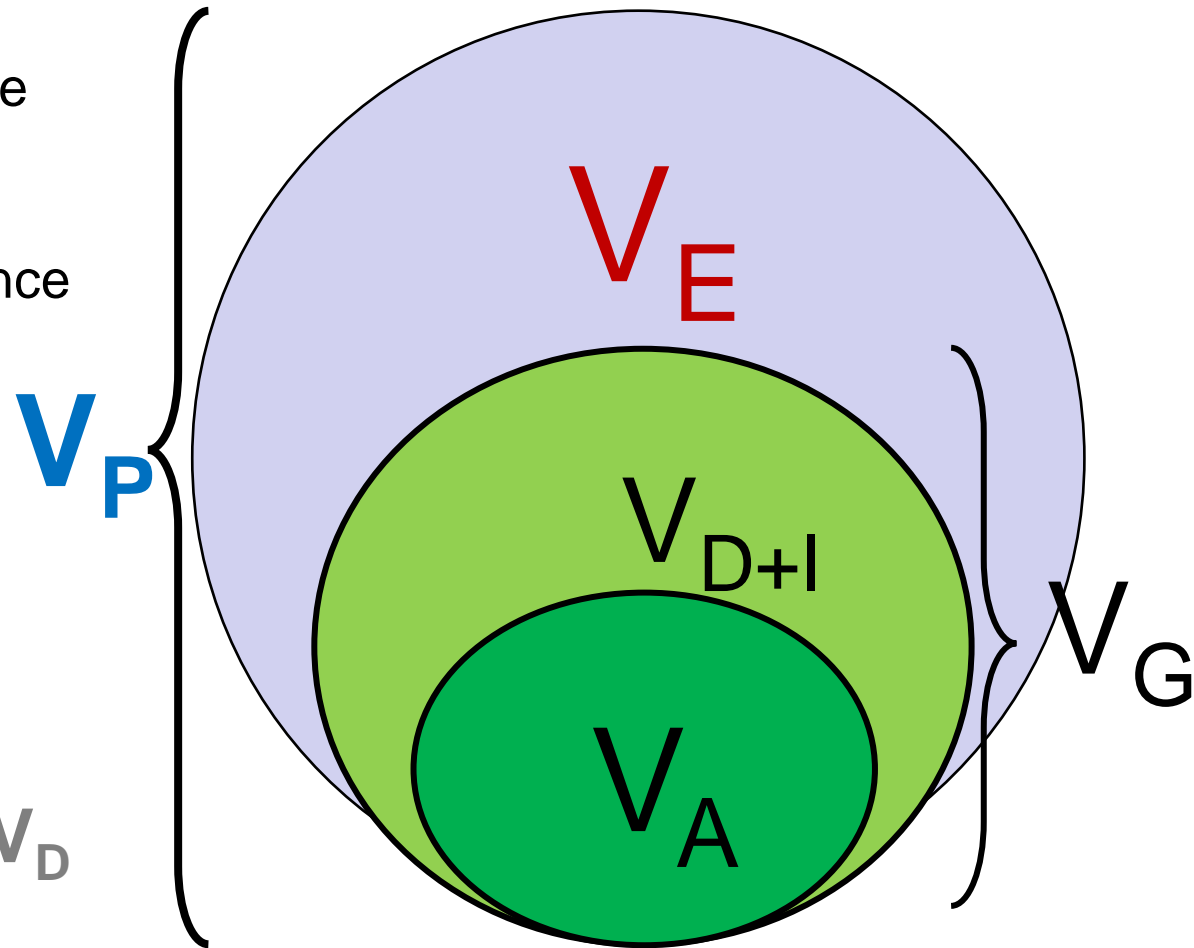
# Types of Genetic Variance

$V_P$  = Phenotypic Variance  
 $V_E$  = Environmental Variance  
 $V_D$  = Dominance Variance  
 $V_I$  = Epistatic Variance  
 $V_A$  = Additive Genetic Variance

$$V_G = V_A + V_I + V_D$$

$$V_P = V_E + V_G$$

$$V_P = V_E + V_A + V_I + V_D$$



$$R = h^2S$$