

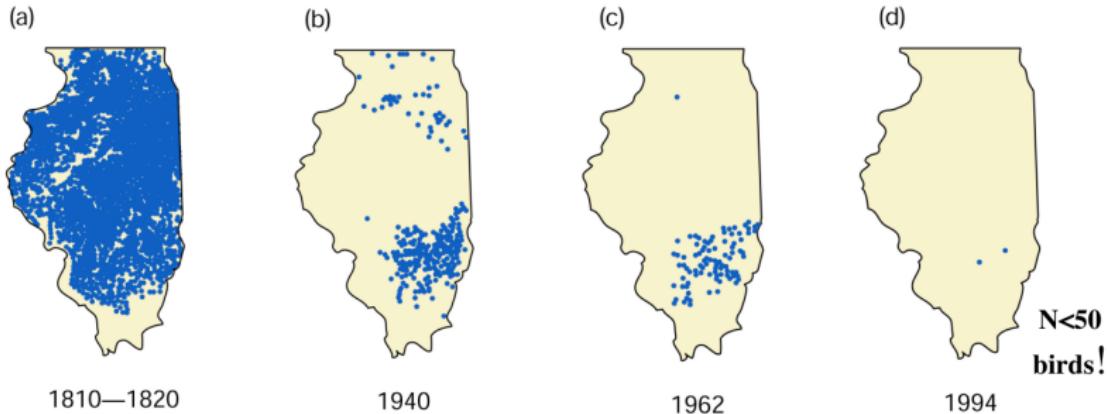
Non-random mating

## Greater prairie chicken (*Tympanuchus cupido*)



<sup>1</sup>Image: Greg Schechter, CC BY-SA 2.0.

# Greater prairie chicken (*Tympanuchus cupido*)



Habitat destruction and the shrinking range of Illinois greater prairie chickens

<sup>1</sup>Image: Freeman S. & Herron J. C. (2004). *Evolutionary analysis*. Pearson Prentice Hall.

## Non-random mating

- ▶ Violation of Hardy-Weinberg Equilibrium (HWE)
- ▶ Example: Morning glory (*Ipomoea purpurea*) pollinators have flower colour preferences
- ▶ Increases homozygosity for flower colour



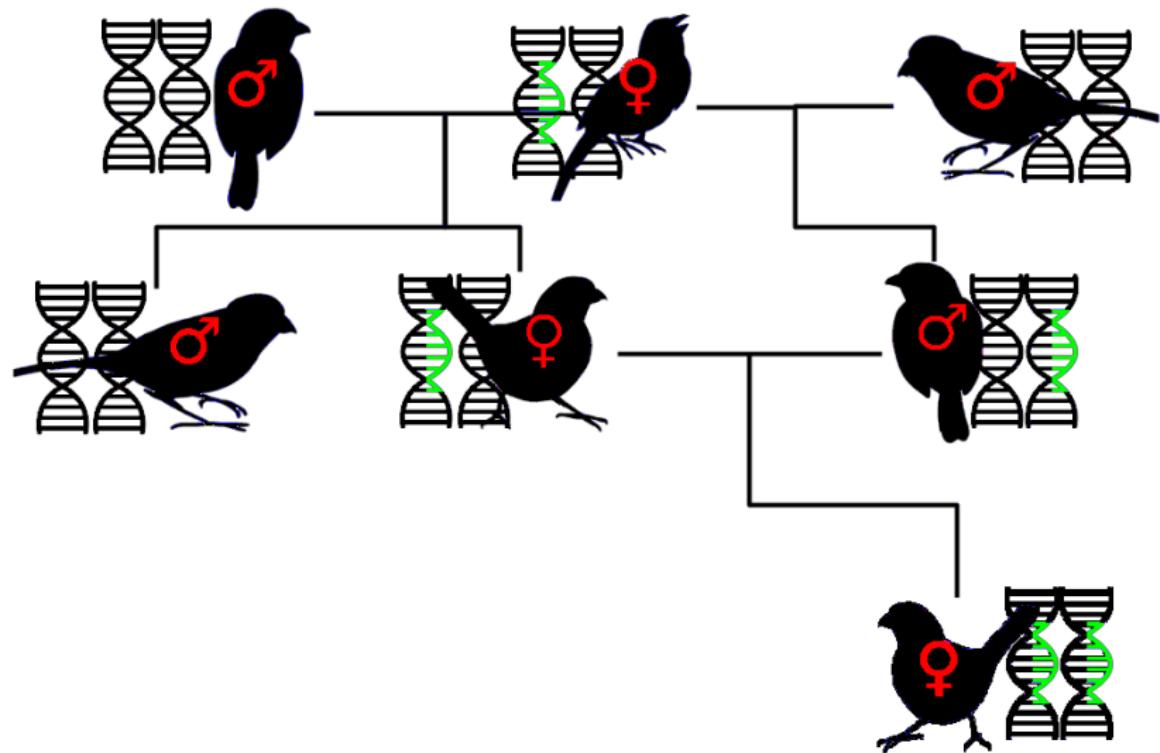
<sup>1</sup>Brown, B. A., & Clegg, M. T. (1984). Influence of flower color polymorphism on genetic transmission in a natural population of the common morning glory, *Ipomoea purpurea*. *Evolution*, 796-803. [\[Link\]](#)

<sup>2</sup>Image: Public Domain

## Two types of non-random mating

1. Mating among similar or different phenotypes (affects some loci)
2. Inbreeding: mating between relatives (affects **all** loci)

## Inbreeding: mating between relatives



## The inbreeding coefficient F

- ▶ F measures the probability that the 2 alleles at a gene locus in an individual are identical-by-descent from a recent common ancestor
- ▶ Implies both alleles came from (i.e., are identical copies of) the same ancestor allele in some previous generation

## Calculating an individual's inbreeding ( $F$ ) from its pedigree

Mating type	$F$	
Self-fertilisation	1/2	(0.5)
Full-siblings	1/4	(0.25)
Half-siblings	1/8	(0.125)
First cousins	1/16	(0.0625)

Genetic drift       $\Delta F = \frac{1}{2N}$

## Inbreeding in wild populations of plants and animals

How do we estimate inbreeding  
in the absence of pedigree  
data?

## Population-level analysis of inbreeding

An average, population-level estimate of F can be calculated by comparing observed and expected heterozygote frequencies (same as  $F_{IS}$ , see later)

$$F = \frac{H_{exp} - H_{obs}}{H_{exp}}$$

- ▶  $H_{exp}$  is the expected frequency of heterozygotes *assuming* Hardy-Weinberg Equilibrium
- ▶  $H_{obs}$  is the *observed* frequency of heterozygotes in a sample

## Population-level analysis of inbreeding

Suppose we collect flowers from 100 snapdragon flowers (incomplete dominance).

- ▶ Red: 18 ( $C^R C^R$ )
- ▶ Pink: 24 ( $C^R C^W$ )
- ▶ White: 58 ( $C^W C^W$ )

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What are the frequencies of the 2 alleles?

- ▶  $\Pr(C^R) = p$
- ▶  $\Pr(C^W) = q$

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Calculate the values for p and q,

$$p = \frac{(2 \times 18) + 24}{2 \times 100} = 0.3$$

$$q = \frac{(2 \times 58) + 24}{2 \times 100} = 0.7$$

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What is expected heterozygosity ( $H_{exp}$ )?

$$H_{exp} = 2pq = 2(0.3)(0.7) = 0.42$$

What is observed heterozygosity ( $H_{obs}$ )?

$$H_{obs} = \frac{24}{100} = 0.24$$

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$$F = \frac{H_{exp} - H_{obs}}{H_{exp}}$$

$$0.43 = \frac{0.42 - 0.24}{0.42}$$

## Population-level analysis of inbreeding

$F$  is often used as a population-level inbreeding coefficient and can take on values from -1 to +1.

- ▶ If  $F > 0$  then there is an excess of homozygotes and a deficit of heterozygotes relative to HW equilibrium genotype frequencies.
- ▶ If  $F = 0$  then the observed genotype frequencies are in accord with HW equilibrium genotype frequencies.
- ▶ If  $F < 0$  then there is an excess of heterozygotes and a deficit of homozygotes relative to HW equilibrium genotype frequencies.

## Four Sources of Excess Homozygosity

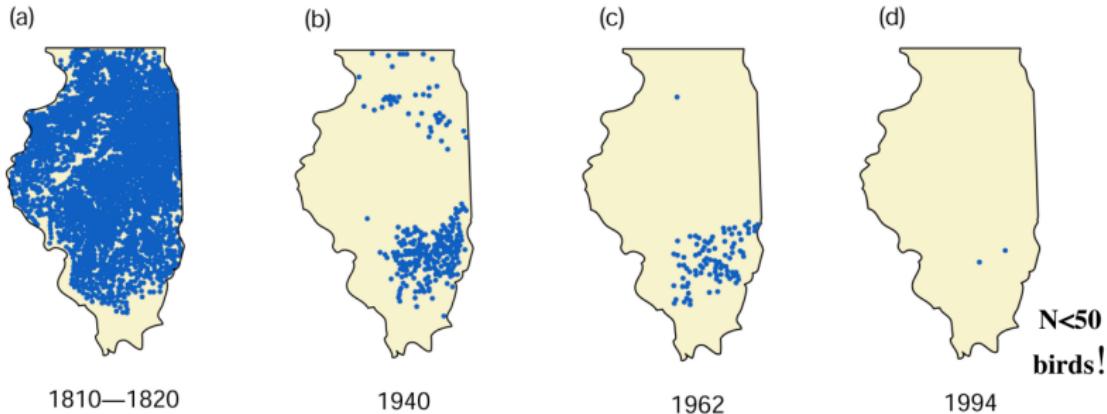
1. Inbreeding between close relatives
2. Random genetic drift in finite populations
3. Heterozygote disadvantage
4. Positive assortative mating among like phenotypes

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<sup>1</sup>Image: Greg Schechter, CC BY-SA 2.0.

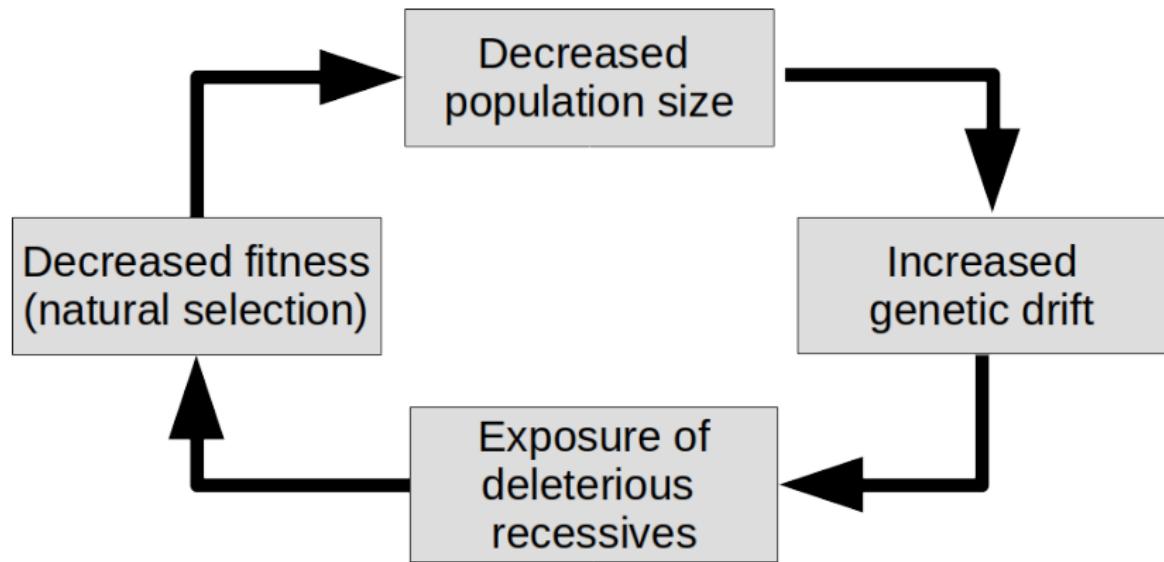
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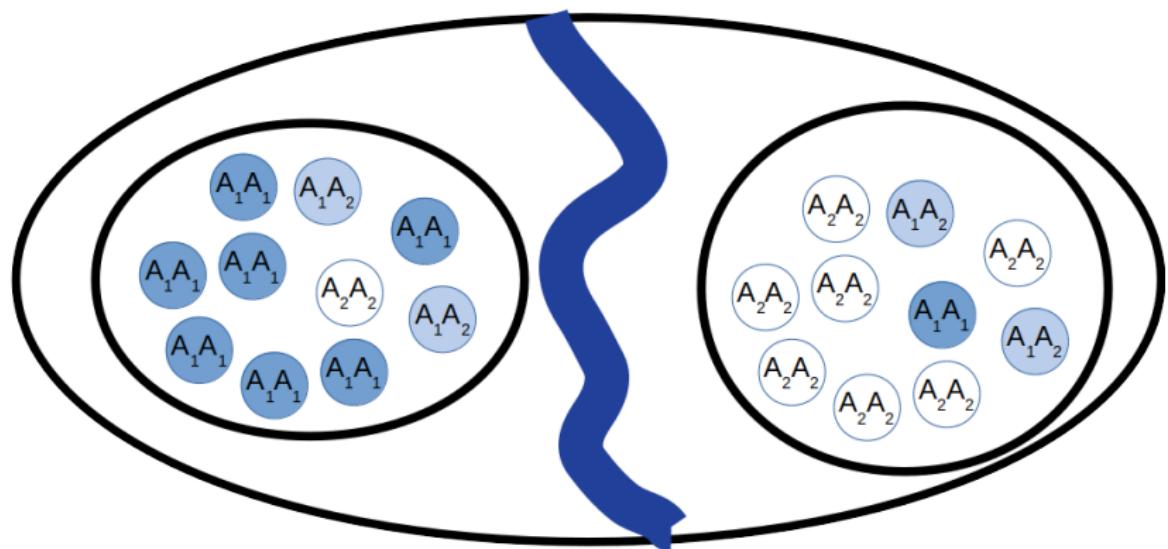
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## Conservation genetics



This feedback loop between small population size, the expression of inbreeding depression, and reduced fitness, has been termed an extinction vortex

# Population subdivision and F coefficients



## Population subdivision and F coefficients

If we want to sample a population, but it is *actually* 2 subdivided populations, such that random mating is only within sub-populations, we get fewer heterozygotes than expected.

Genotype	$A_1A_1$	$A_1A_2$	$A_2A_2$
Subpopulation 1	64	32	4
Subpopulation 2	4	32	64
Total	68	64	68

This deficiency of heterozygotes due to subdivision is called the **Wahlund effect**.

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<sup>1</sup>Halliburton R. (2004). Introduction to population genetics.  
Pearson/Prentice Hall.

## Population subdivision and F coefficients

Average deviation in heterozygosity *just due to subdivision,*

$$F_{ST} = \frac{H_T - H_S}{H_T}.$$

In the above equation,

- ▶  $H_T$  is the *expected* heterozygosity of the whole population (ignoring any subdivision)
- ▶  $H_S$  is the average of expected heterozygosities across all subpopulations

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## Population subdivision and F coefficients

We can also look at  $F_{IS}$ , the average deviation within a sub-population ( $H_I$  is the mean of observed heterozygosities over all sub-populations),

$$F_{IS} = \frac{H_S - H_I}{H_S}.$$

And we can look at  $F_{IT}$ , the overall deviation in heterozygosity in the total population,

$$F_{IT} = \frac{H_T - H_I}{H_T}.$$

This last one is not used as often.

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