

# Migration, drift, and non-random mating

# Hardy-Weinberg conditions

- No mutation
- No selection
- No migration
- No genetic drift
- No non-random mating

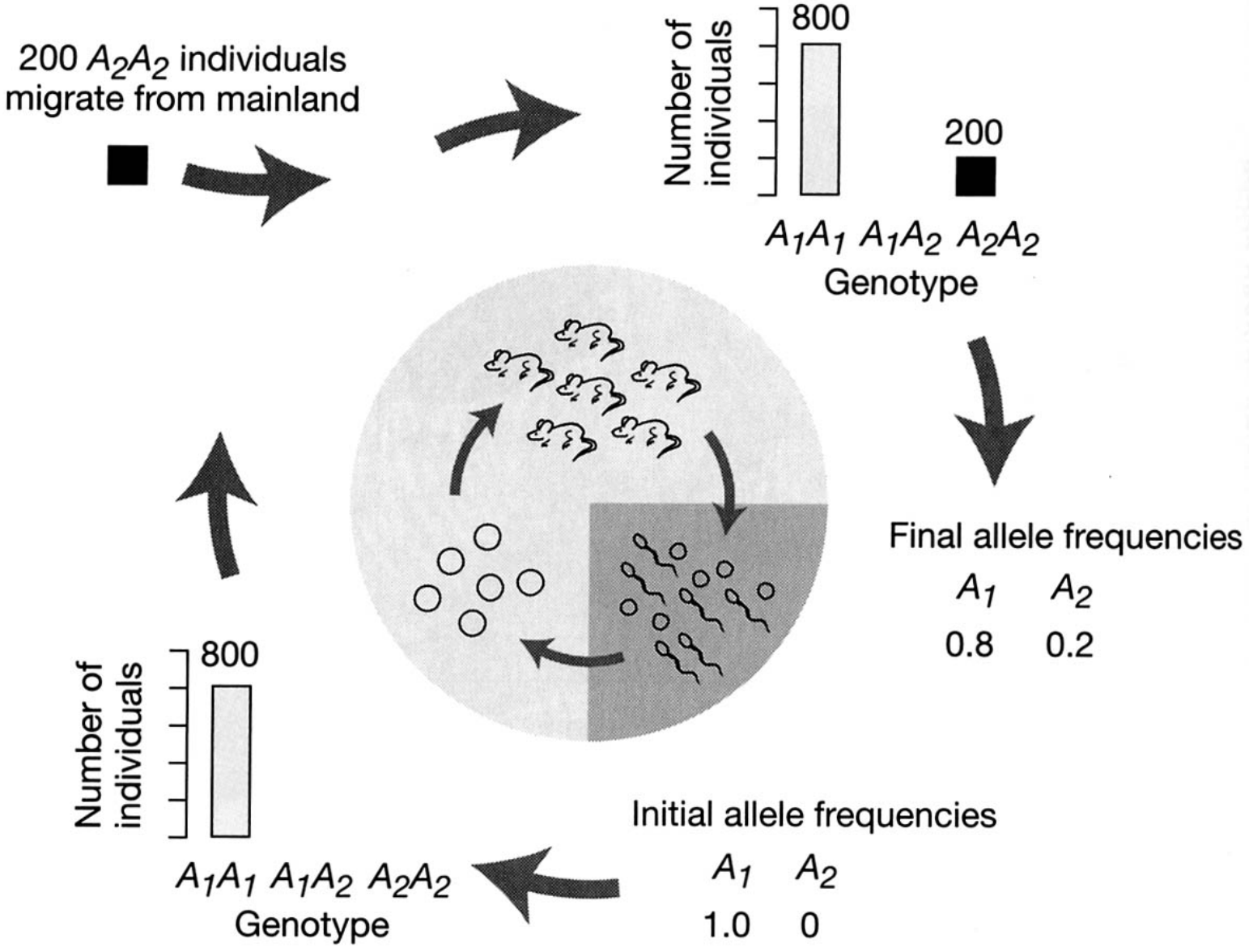
# If Hardy-Weinberg holds, then...

- No allele frequency change
  - $p$  = frequency of allele A
  - $q$  = frequency of allele a
- Genotype frequencies follow from  $p^2 + 2pq + q^2$

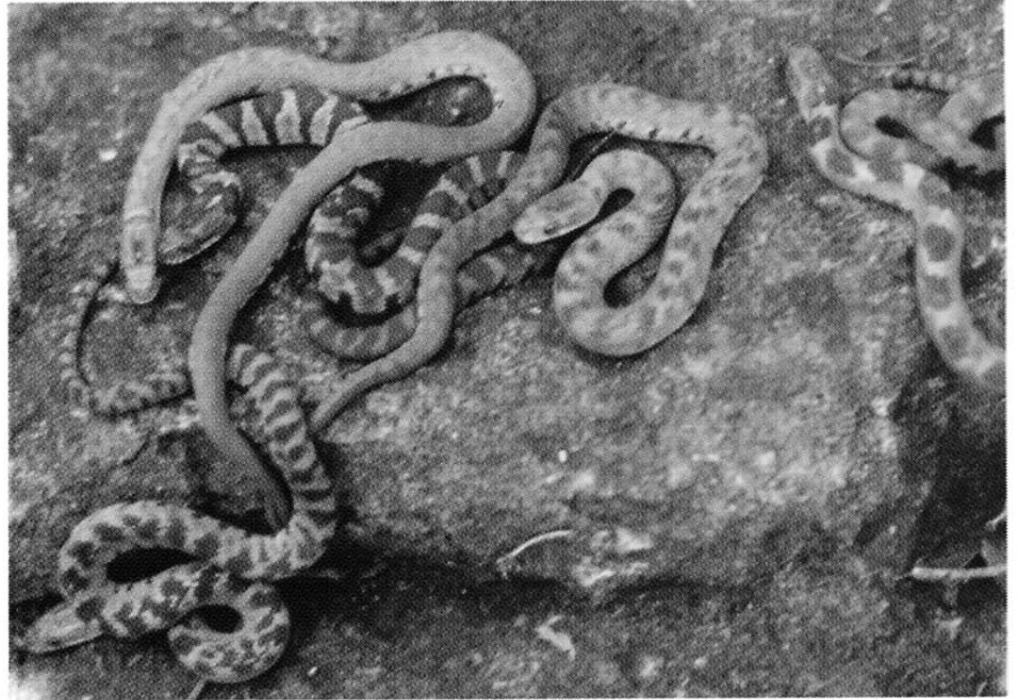
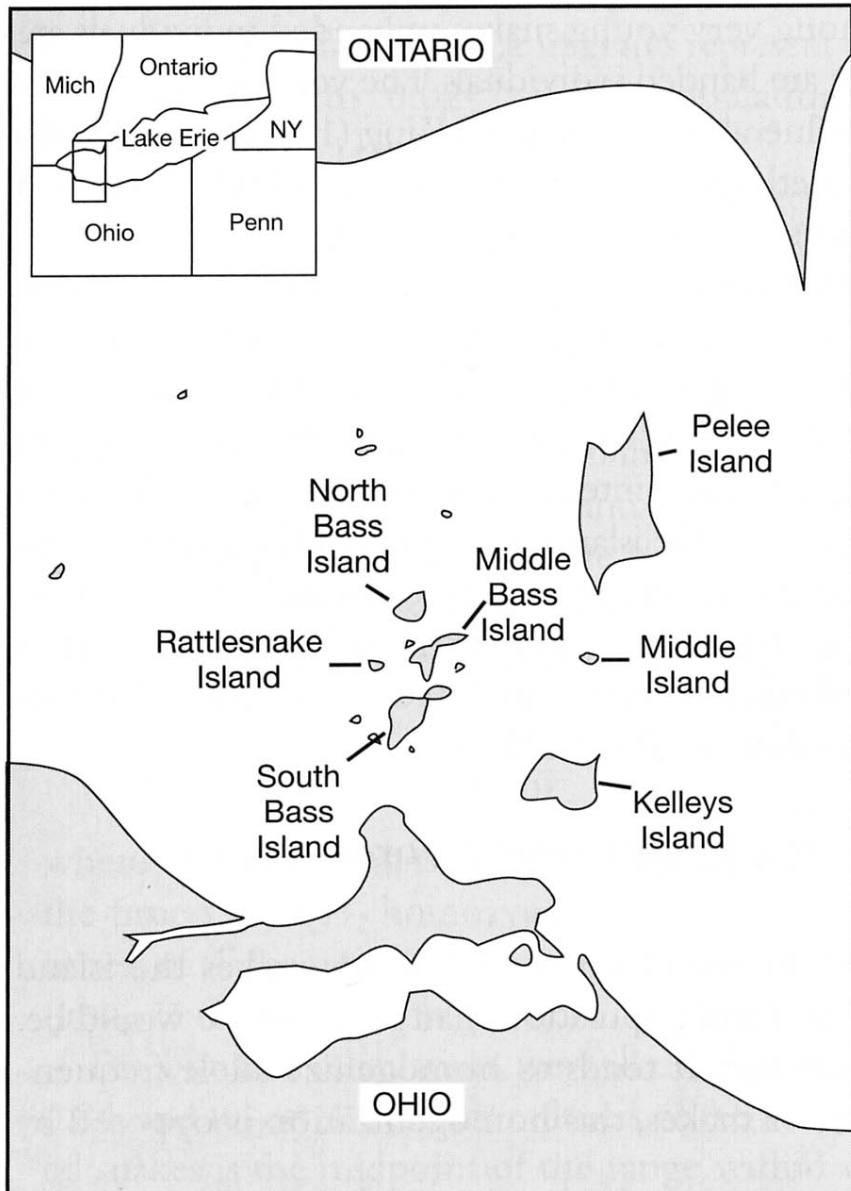
# Migration

- Not seasonal movement
  - E.g. birds
- Movement of alleles from one population to another
  - Called ‘gene flow’
- Makes populations more similar to each other

# Migration



# *Nerodia sipedon*



# Selection on banding pattern

- Mainland
  - Banded snakes favored (dappled light)
- Islands
  - Unbanded snakes favored
    - Barren limestone basking surfaces
- Banded alleles on island persist due to migration from mainland

# Migration of alleles

- Changes allele frequencies
- Can alter genotype frequencies
- Makes populations more similar



# Measuring genetic similarity of populations

- $F_{st}$  statistic ranges from 0 to 1
- Measures variation among subpopulations relative to the total variation ( $s$  and  $t$ )
- $F_{st}$  high, then subpopulations pretty distinct
- $F_{st}$  low, subpopulations homogenous

# *Silene dioica* Swedish islands

- Colonize young island
  - Genes that get to any specific island mostly a matter of chance
- Pollination by insects
  - Over time, genes get spread from island to island (migration of alleles)
- Die off through ecological succession
  - Old populations survivors stochastic

# Giles and Goulet, 1997

(a)



(b)

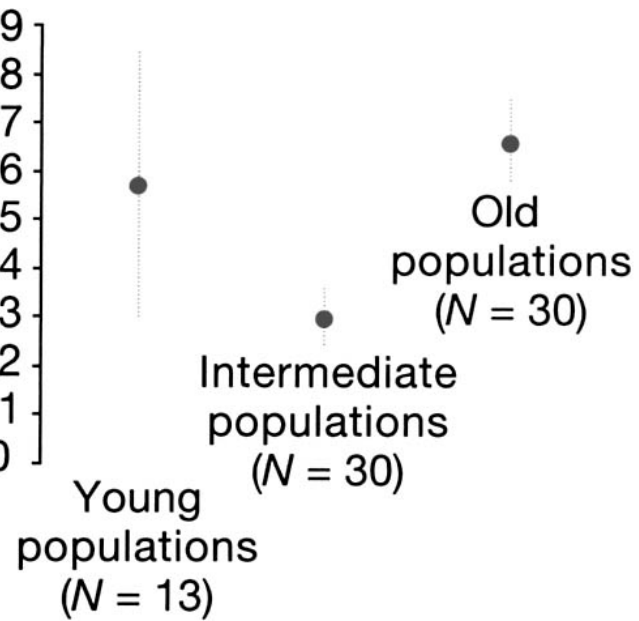
Variation in allele frequencies  
among populations ( $F_{ST}$ )

0.09  
0.08  
0.07  
0.06  
0.05  
0.04  
0.03  
0.02  
0.01  
0

Young  
populations  
( $N = 13$ )

Intermediate  
populations  
( $N = 30$ )

Old  
populations  
( $N = 30$ )



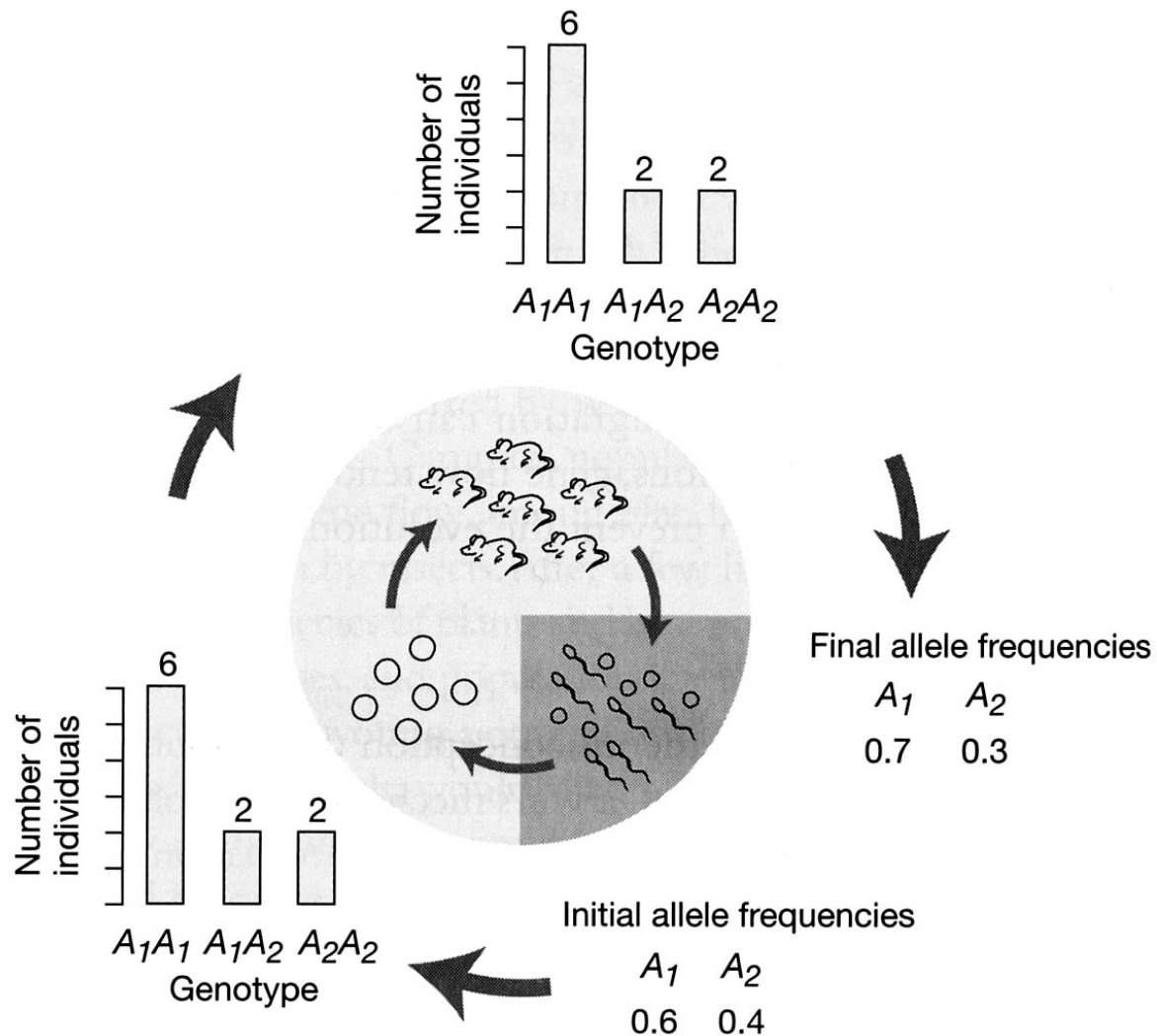
# Genetic drift

- In Giles and Goulet's study, what accounts for the high  $F_{st}$  values for young populations?
- Chance founder events
  - Populations drawn from small potential pool

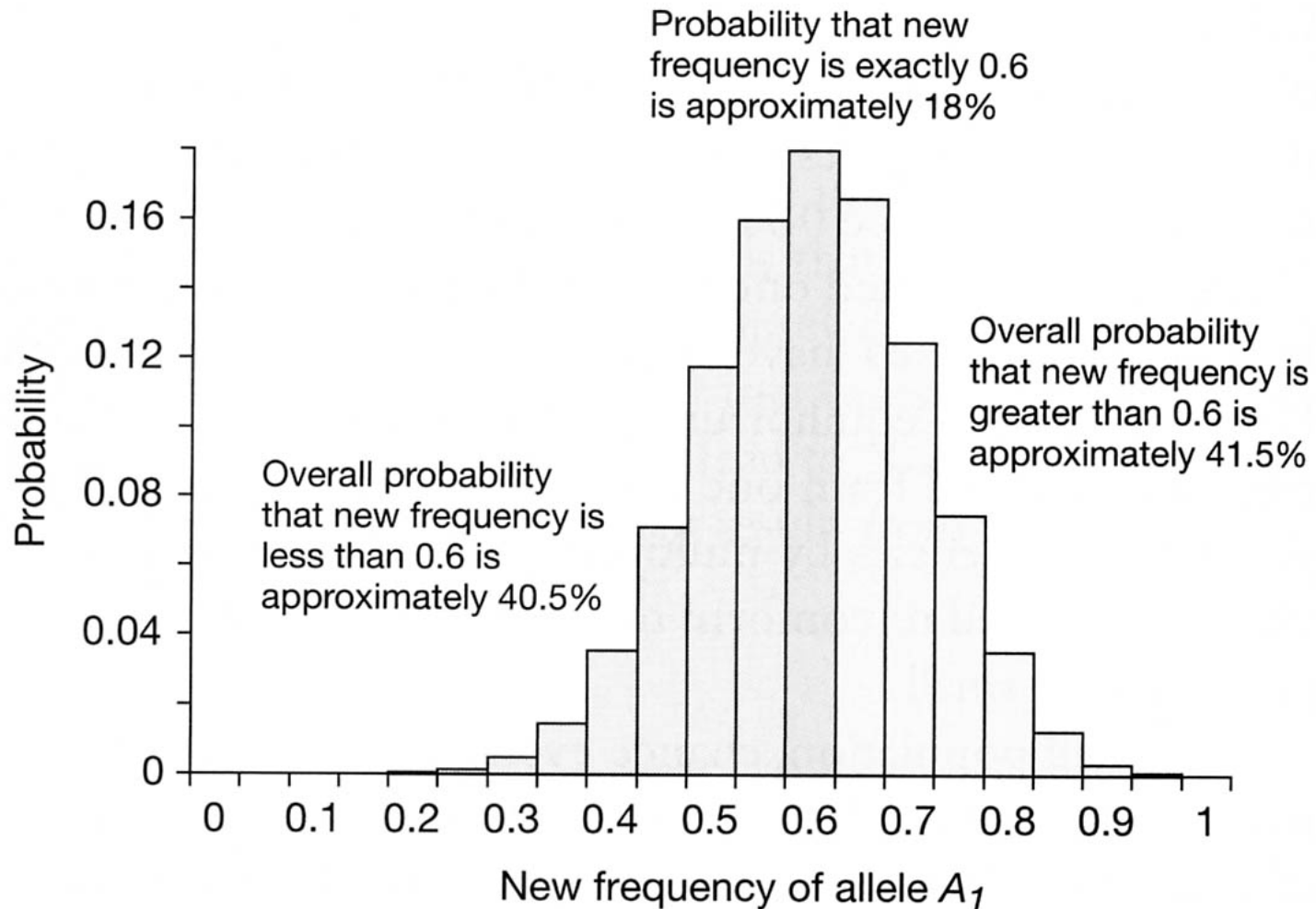
# Population size and genetic drift

- Flip a coin, odds are even (50:50) heads or tails
- If you flip the coin 10, 000, 000 times
  - You'd better get really close to 50:50
- If you flip the coin only 4 times, you have a good chance of getting either all heads or all tails
  - 12.5% chance, even if the coin is a fair coin

# Sampling error in small populations

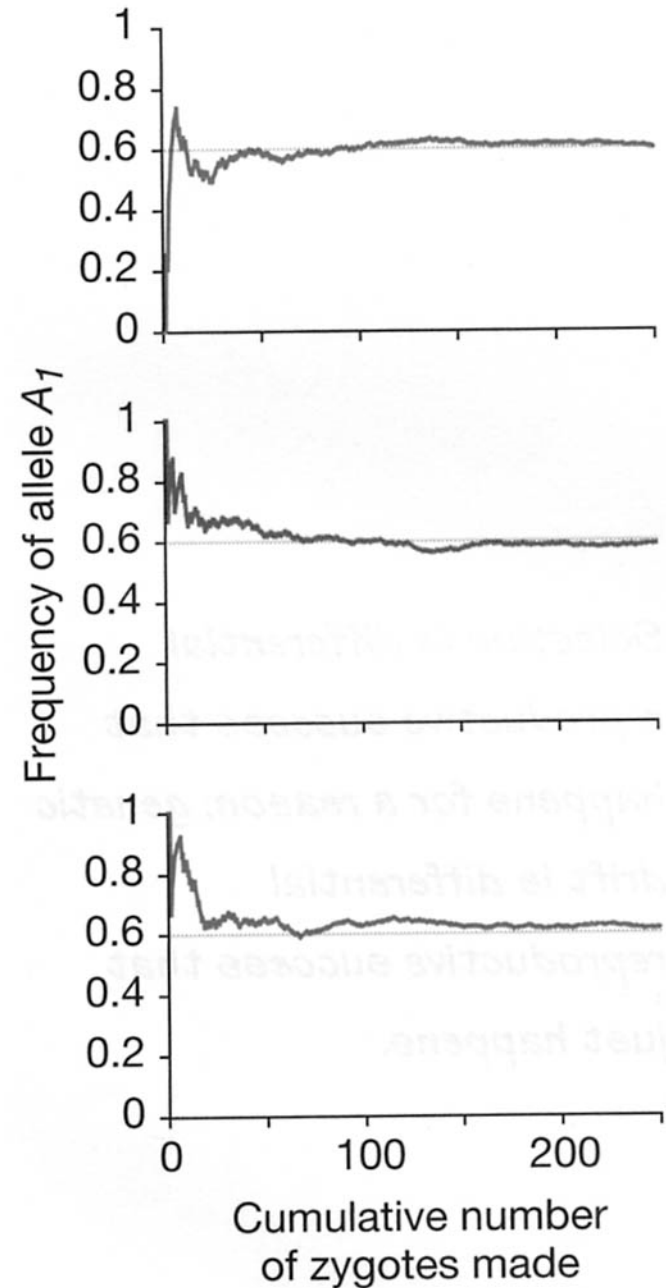


# Chance of random allele frequency change, $N = 10$ zygotes



# Drift versus sample size

- 3 runs of a simulation model
- True allele frequency 60:40





# Drift as an evolutionary force

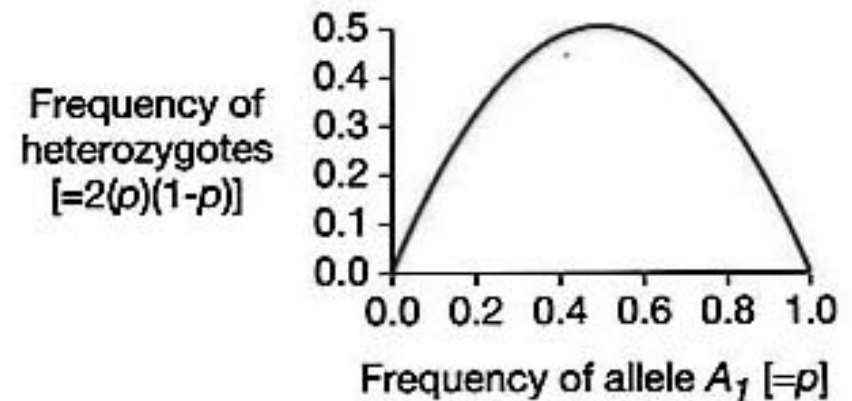
- Drift not an important evolutionary force in large populations
- Can be important in small populations
  - Founding of new populations
  - Fixation of alleles, loss of heterozygosity

# Founder effect

- High  $F_{st}$  in *Silene dioica* young populations
- In humans,
  - Ellis-van-Creveld syndrome
    - Rare form of Dwarfism
    - Allele frequency around 0.001 in most populations
    - But found at 0.07 in Pennsylvania Amish descended from 200 founding individuals

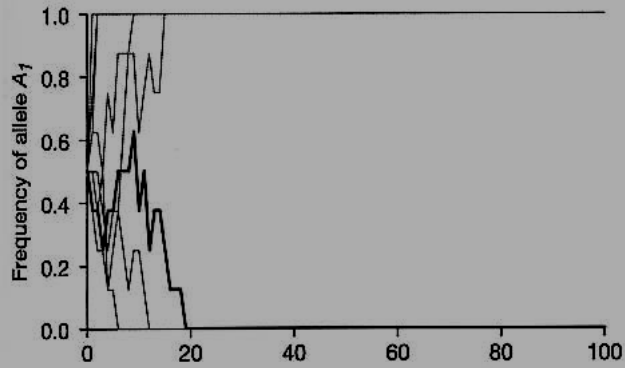
# Drift and allele frequency change

- small populations over many generations
- Fixation: an allele is *fixe* at a locus if it is at a frequency of 100%
- Heterozygosity decrease as alleles becomes rarer

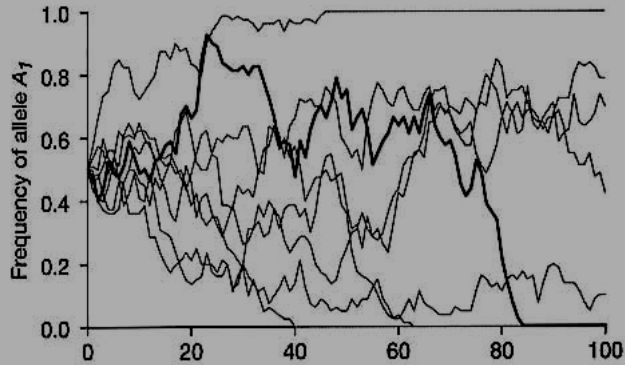


Note:  $2(p)*(1-p)$   
 $= 2pq$

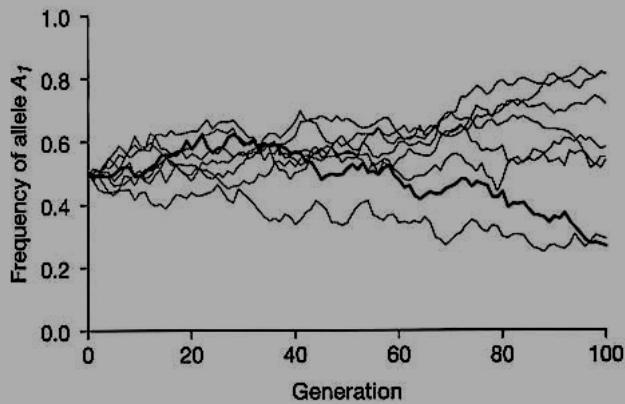
(a) Population size = 4



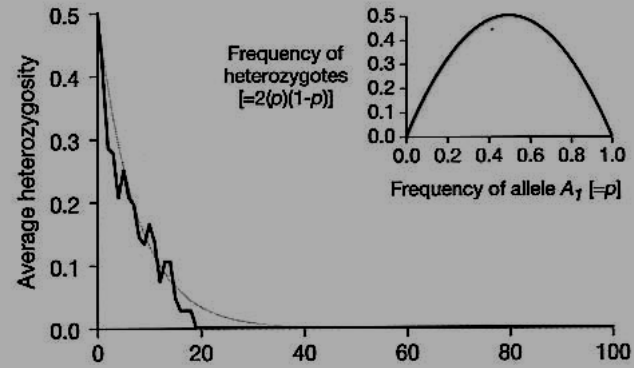
(b) Population size = 40



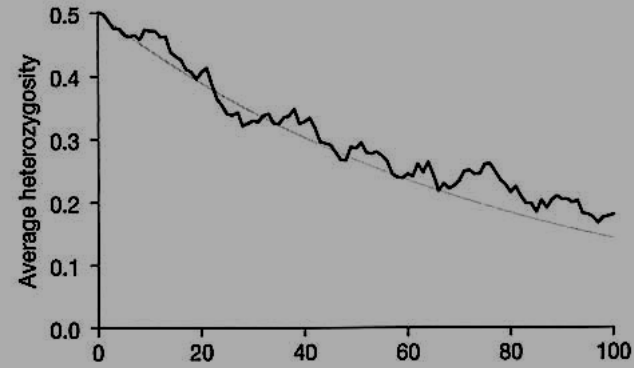
(c) Population size = 400



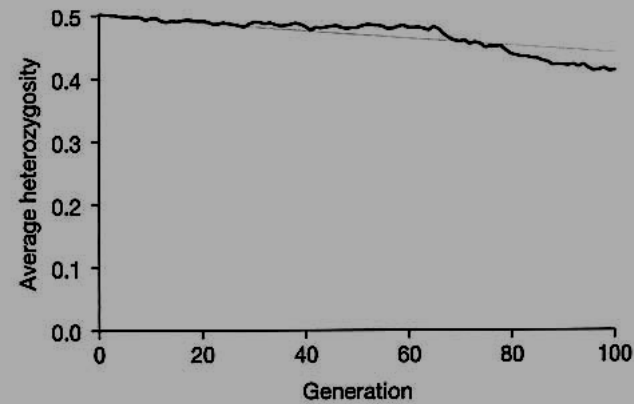
(d) Population size = 4



(e) Population size = 40



(f) Population size = 400

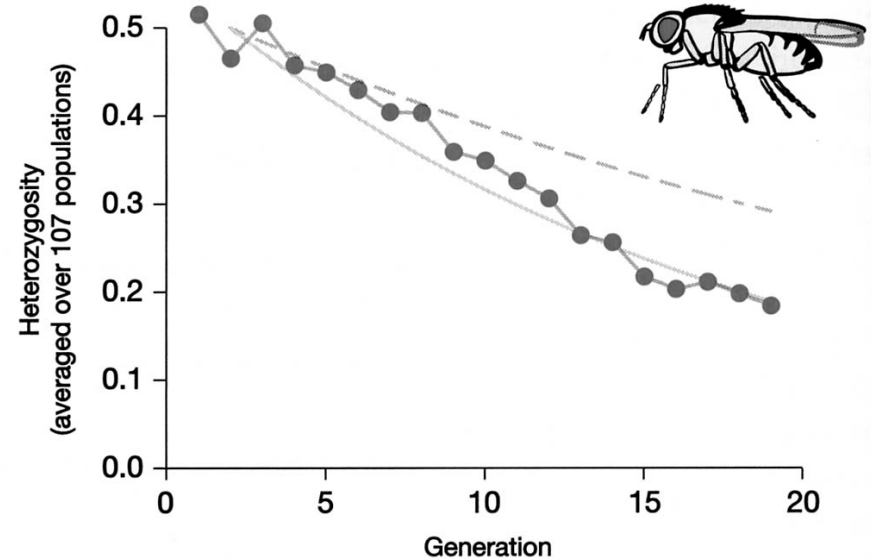


# Fixation of alleles

- If allele frequency goes to 1 it is fixed
- If it goes to 0 the allele is lost, and the alternative allele is fixed (if there are only two alleles)
- Probability that an allele goes to fixation equal to its initial frequency
  - With drift alone that is (no mutation, no selection, etc.)

# Loss of heterozygosity

- Heterozygote frequency =  $2pq$ 
  - Alternatively  $2p(1-p)$
  - At a maximum when  $p = 0.5$
- Buri *Drosophila* experiment
- 107 lines of 8 females 8 males
- Start  $p = q = 0.5$
- Qualitative: heterozygosity decrease
- Quantitative: for population with size 16, heterozygosity should follow dashed line; instead followed solid gray line - the prediction for  $n = 9$



# Effective population size

- Buri's fly populations lost heterozygosity as predicted IF the population size was 9 not 16
- If some died, or failed to reproduce, then the **effective population size** can be smaller than the actual population size
- $N_e = (4 N_m N_f) / (N_m + N_f)$ 
  - Nm = number of sexually reproductive males
  - Nf = number of sexually reproducing females
- 5 males 5 females,  $N_e = 10$
- 1 male 9 females,  $N_e = 3.6$

# Drift and the neutral theory

- Alleles that have no fitness effect called neutral
- Allelic substitution can be by drift or selection
- If most mutations produce selectively neutral alleles, the fate of those alleles will be governed mostly by drift
  - Basis of idea behind molecular clock



# Genetic drift summary

- Random effects
- Importance highly dependent on population size
  - Effective population size even smaller
- Can allow a neutral allele to replace another simply by chance
- Decreases allelic diversity and heterozygosity

# Non-random mating

- Obviously individuals do not mate randomly
  - Really, would you want to mate randomly?
- We are talking about random mating *with respect to particular alleles*
- Not non-random mating with respect to money, sexiness, or ability to make your heart go pitter-patter
  - That is sexual selection, a form of natural selection

# Non-random mating with respect to alleles

- Positive assortative mating
  - Like mates with like
- Mating among genetic relatives called *Inbreeding*

# Inbreeding and heterozygosity

- Imagine extreme inbreeding
- Self fertilization
- Homozygotes produce all homozygotes
- Heterozygotes produce  $1/2$  homozygotes and  $1/2$  heterozygotes
- Proportion of heterozygotes decreases by  $1/2$  each generation

# Selfing and heterozygosity

**Table 6.1 Changes in genotype frequencies with successive generations of selfing**

The frequency of allele  $A_1$  is  $p$  and the frequency of allele  $A_2$  is  $q$ . Note that allele frequencies do not change from generation to generation—only the genotype frequencies. After Crow (1983).

<b>Generation</b>	<b><math>A_1A_1</math></b>	<b>Frequency of <math>A_1A_2</math></b>	<b><math>A_2A_2</math></b>
0	$p^2$	$2pq$	$q^2$
1	$p^2 + (pq/2)$	$pq$	$q^2 + (pq/2)$
2	$p^2 + (3 pq/4)$	$pq/2$	$q^2 + (3 pq/4)$
3	$p^2 + (7 pq/8)$	$pq/4$	$q^2 + (7 pq/8)$
4	$p^2 + (15 pq/16)$	$pq/8$	$q^2 + (15 pq/16)$

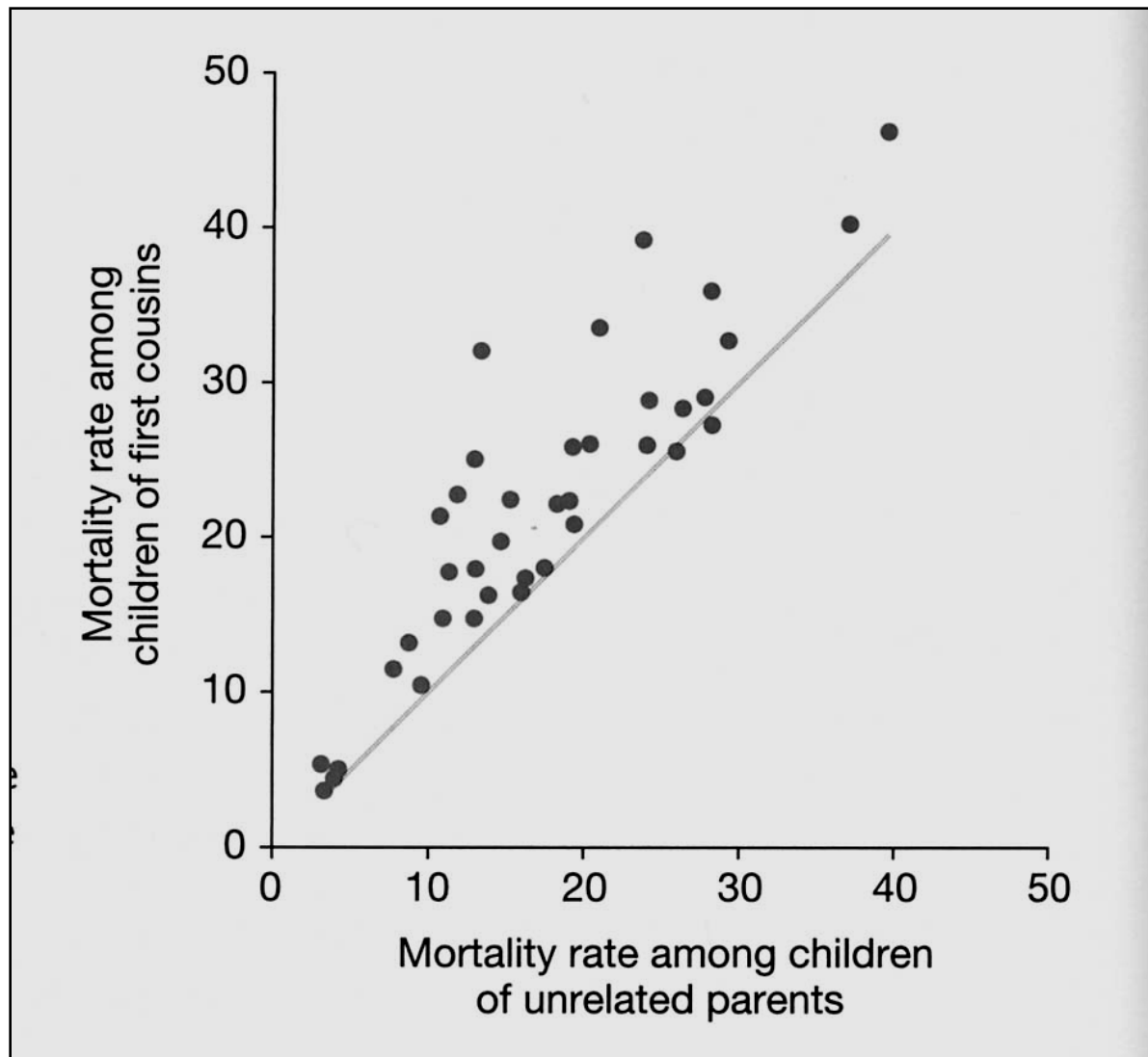
# Inbreeding produces excess homozygotes

- More homozygotes than predicted by Hardy-Weinberg suggests something, perhaps inbreeding is going on
- One generation of random mating re-establishes Hardy-Weinberg genotype frequencies

# Inbreeding depression

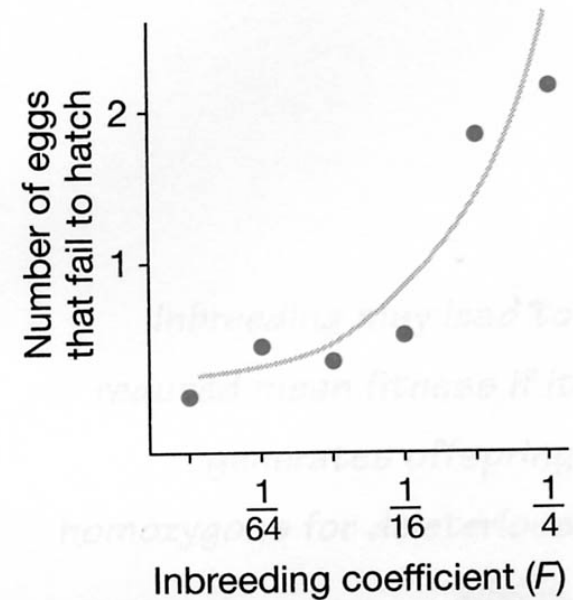
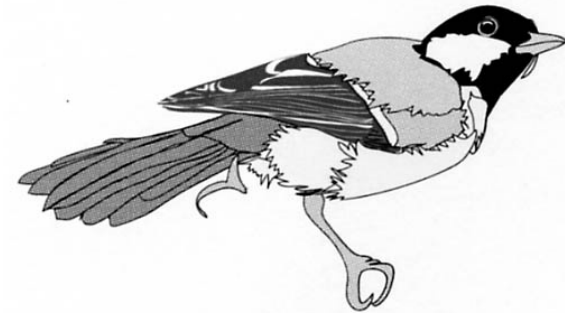
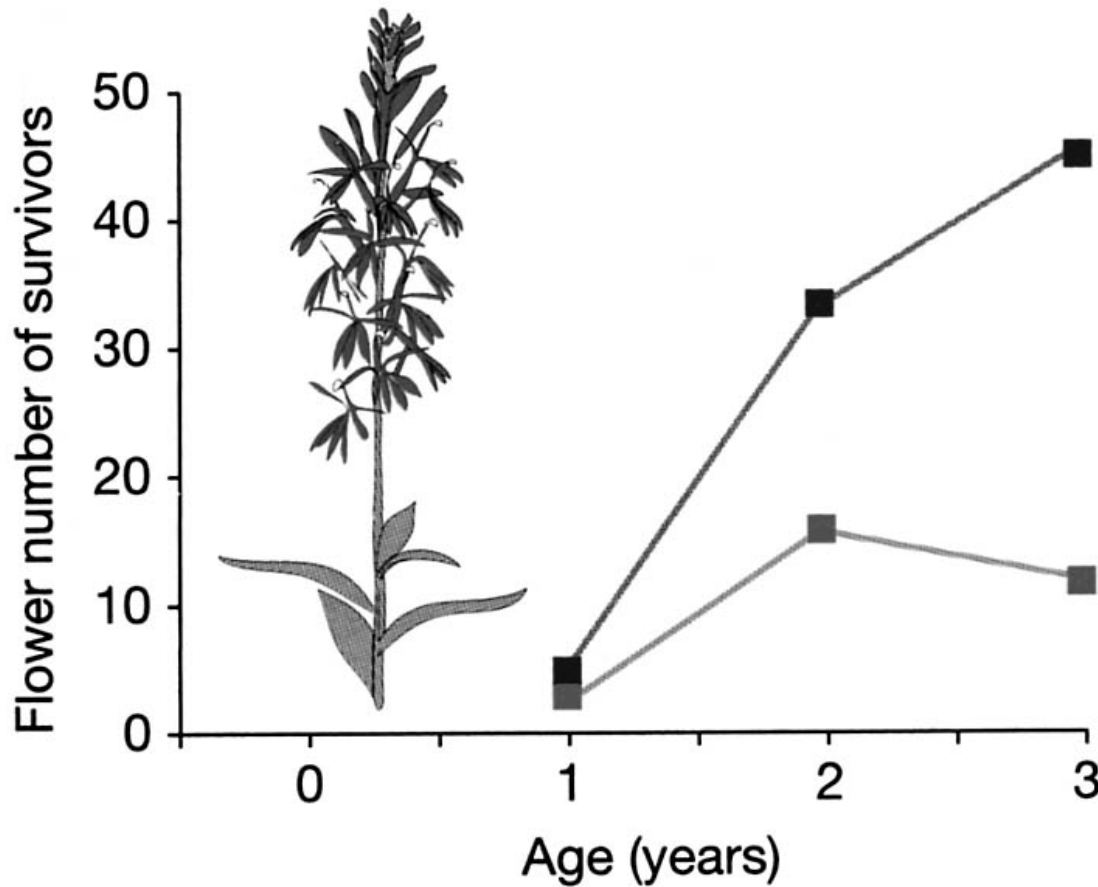
- Does not mean you are sad you kissed your cousin
- Inbreeding produces a deficit of heterozygotes and a surplus of homozygotes
- What if those homozygotes are of deleterious recessive alleles?

# Inbreeding reduces fitness: humans





# Also, plants, non-human animals



Blue outcrossed controls; red selfed

# Conservation Genetics: the case of the greater prairie chicken in Illinois

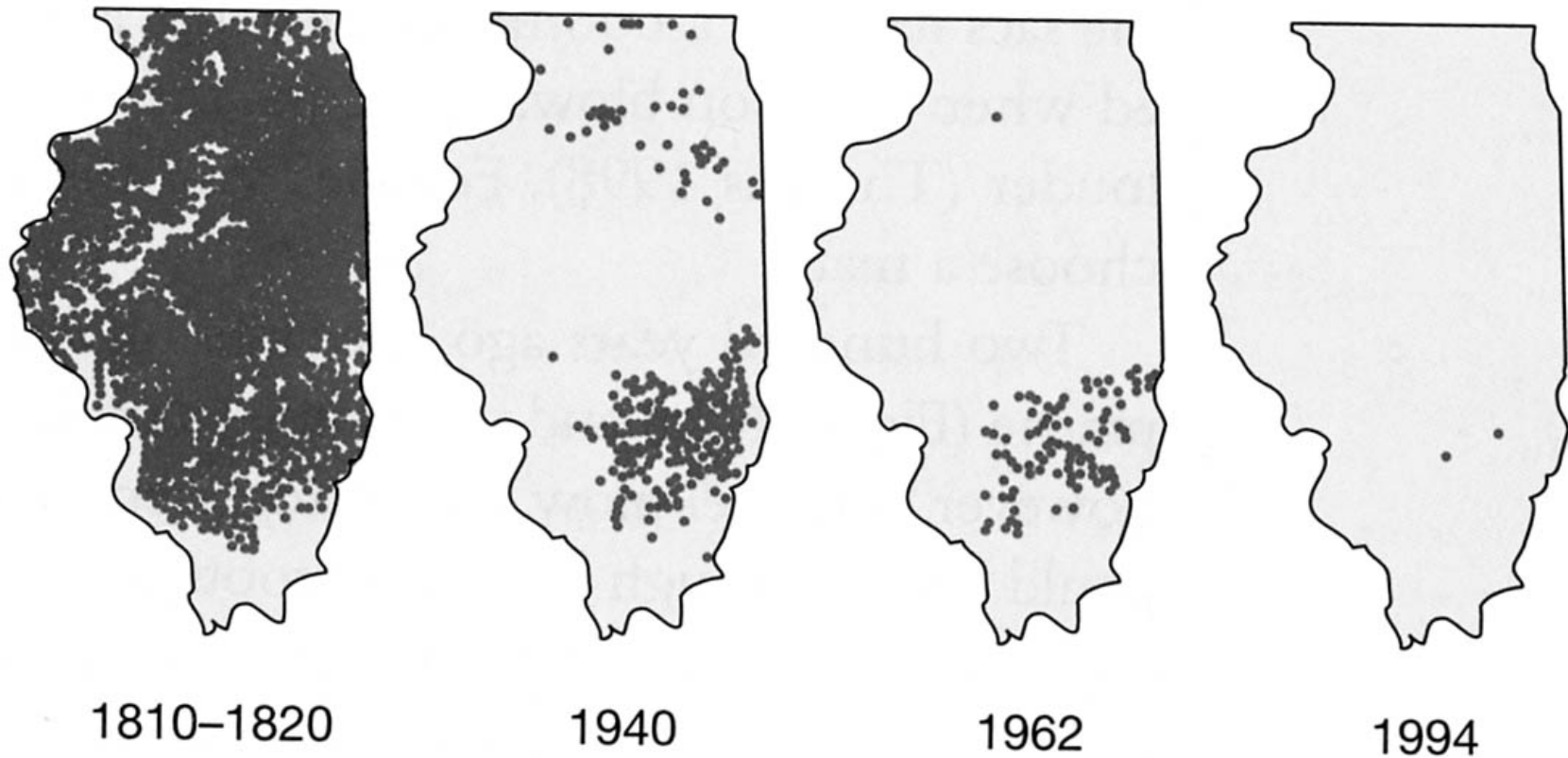


Movie time

# Decline

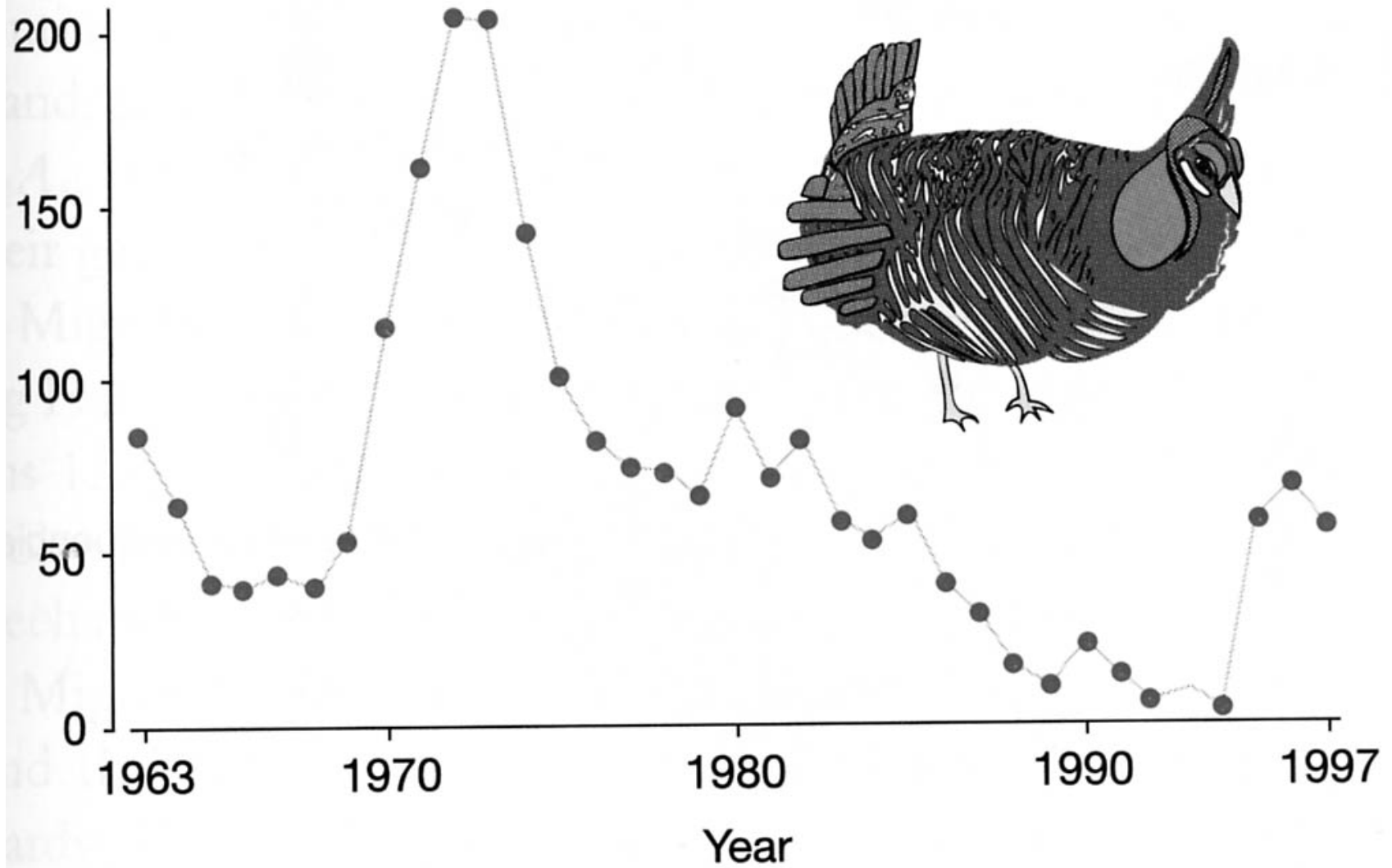
- Millions pre-1837 steel plow
- 25000 in 1933
- 2000 in 1962
- 500 in 1972
- 76 in 1990
- 50 or less 1994

# Habitat loss: steel plow 1837



Two remaining habitats protected in 1962 and 1967

# Protection and population decline



# Why the post mid 1970's decline?

- Migration
- Drift
- Inbreeding

# Allelic diversity

**Table 6.4** Number of alleles per locus found in each of the current populations of Illinois, Kansas, Minnesota, and Nebraska and estimated for the Illinois prebottleneck population

Locus	Illinois	Kansas	Minnesota	Nebraska	Illinois prebottleneck*
ADL42	3	4	4	4	3
ADL23	4	5	4	5	5
ADL44	4	7	8	8	4
ADL146	3	5	4	4	4
ADL162	2	5	4	4	6
ADL230	6	9	8	10	9
Mean	3.67	5.83	5.33	5.83	5.12
SE	0.56	0.75	0.84	1.05	0.87
Sample size	32	37	38	20	15

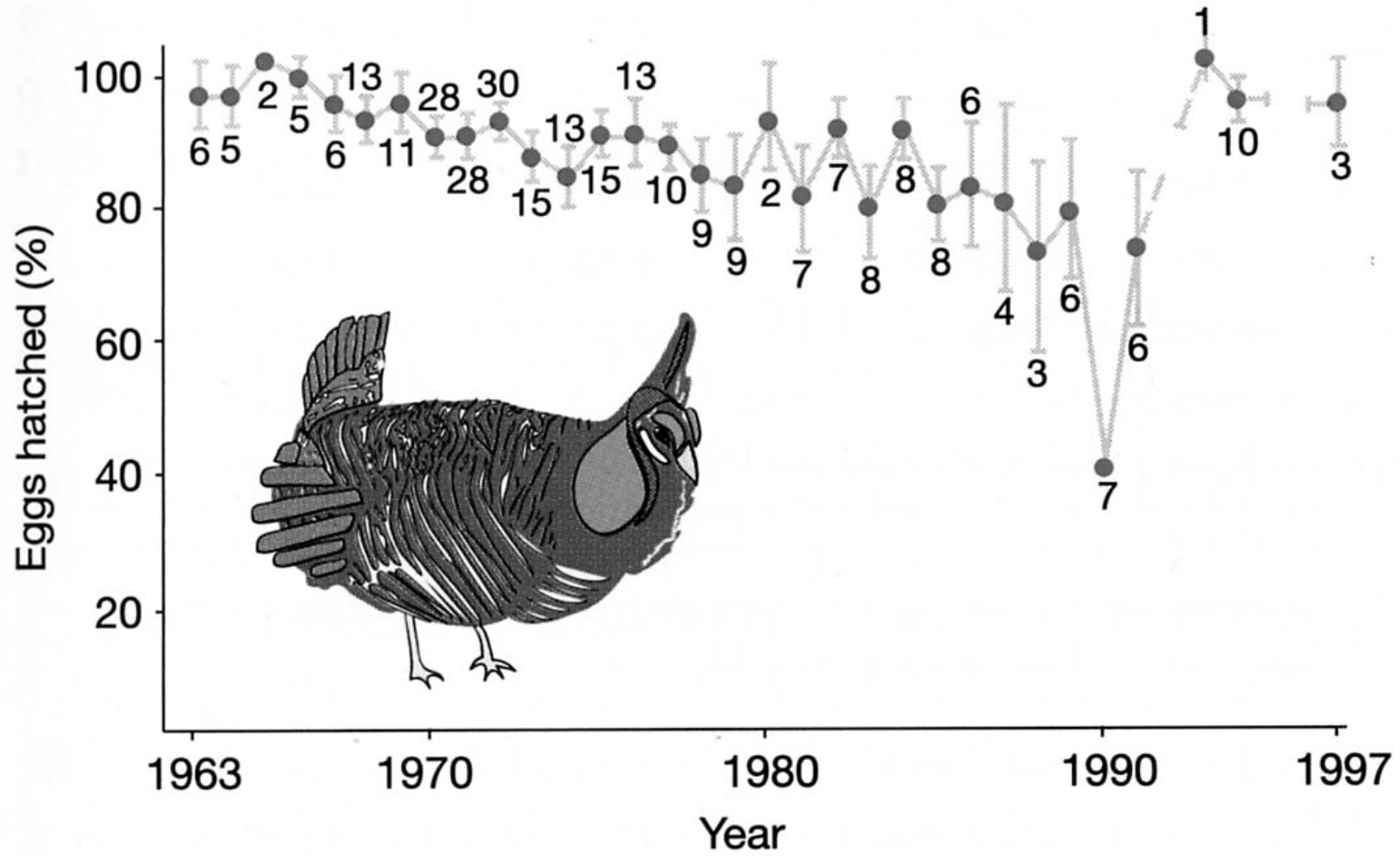
*Note:* SE indicates standard error of mean number of alleles per locus. The Illinois population in column 1 shows significantly less allelic diversity than the rest of the populations ( $P < 0.05$ ).

\*Number of alleles in the Illinois prebottleneck population include both extant alleles that are shared with the other populations and alleles detected in the museum collection.

*Source:* From Bouzat et al. (1998).



# Egg viability



# Evolutionary forces

- Drift
  - Small population
  - Even smaller effective population size
    - Lek mating system
- Low allelic diversity, low heterozygosity
- Migration reintroduces new alleles
  - Gene flow