

Finite Populations: Inbreeding

Inbreeding

- Mating between related individuals
 - Individual instances
 - generally outbreeding population; one-off matings of related individuals
 - Regular systems of inbreeding
 - e.g. creating recombinant inbred lines
 - Local breeding structures
 - e.g. based on proximity; assortative mating
 - Overall relatedness within small populations

Question ...

- In a small, randomly mating population, do you expect to see departures from Hardy-Weinberg frequencies?
 - AA p^2
 - Aa $2pq$
 - aa q^2

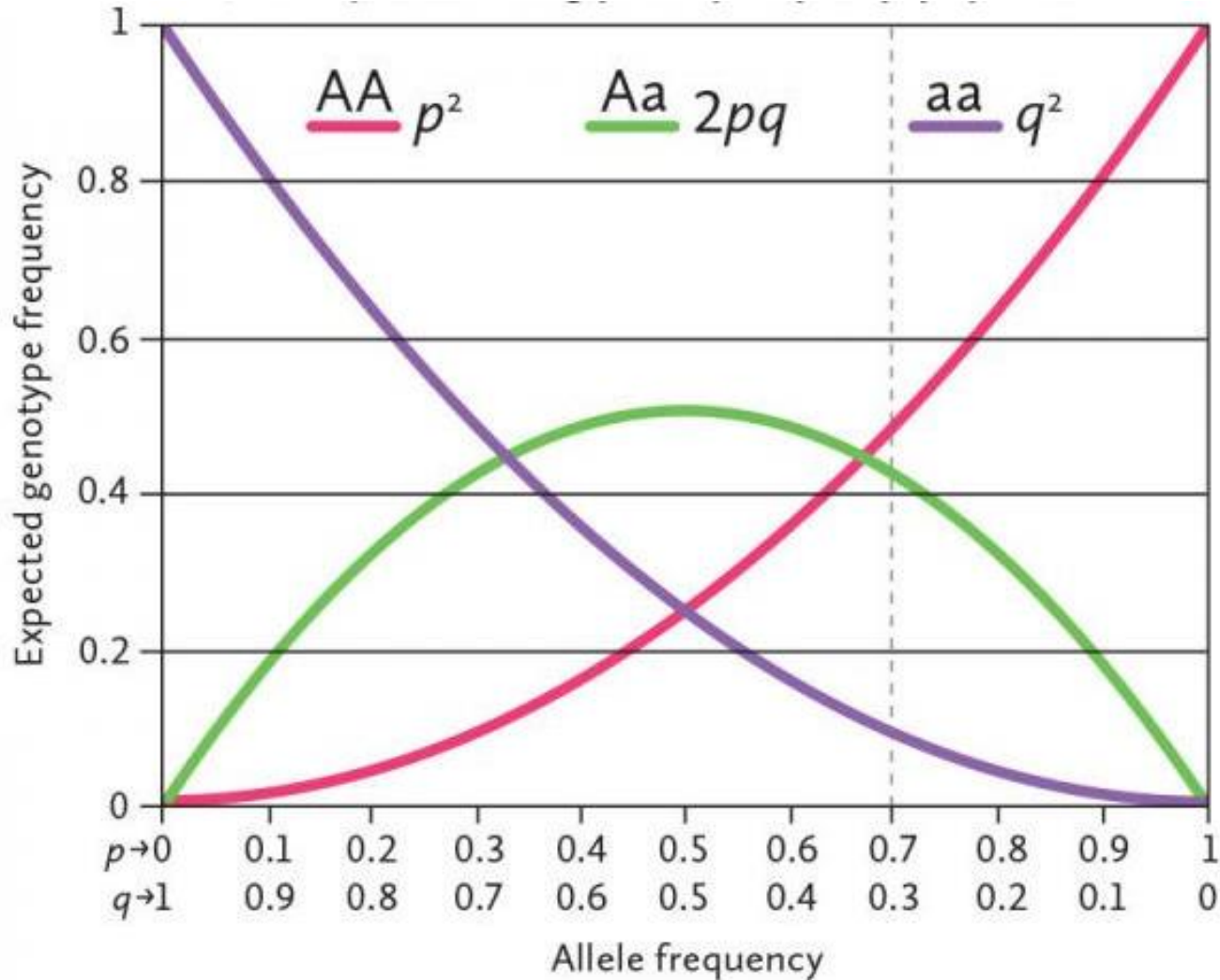
Common misperception

- Inbreeding leads to departures from Hardy-Weinberg equilibrium genotype frequencies.
 - Not necessarily true.
- (And: departures from H-W genotype frequencies lead to an excess of homozygotes, uncovering rare recessive alleles. This can be true, but not necessarily a function of inbreeding *per se*).

The actual problem

- In smaller populations, drift is a stronger force than selection – deleterious alleles can increase in frequency.
- * The frequency of a homozygous genotype increases as the allele frequency increases.
 - Recessive deleterious alleles are uncovered.
- Also ... allele frequencies depend on population sizes.
 - If a population contains 20 diploid individuals, the rarest allele has a frequency of $1/40$.

H-W genotype frequencies



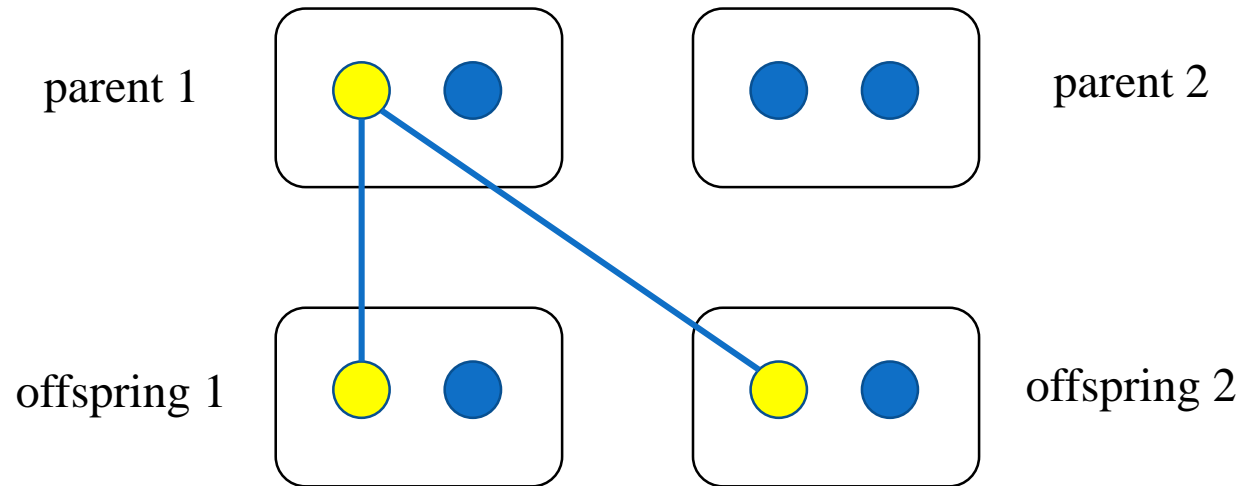
Small population sizes

- Rare alleles can become common via drift.
- Deleterious homozygous genotypes become more likely.
- Increase in relatedness between individuals is also a consequence of small population sizes.

Inbreeding

- Individuals in the population tend to carry more and more alleles that are **identical by descent (IBD)**.

Identity by Descent (IBD)



- Alleles that derive from a common ancestral allele are IBD.

Inbreeding Coefficient

- Measure inbreeding via the **Inbreeding Coefficient**:

$F_t = \text{Pr} (2 \text{ alleles w/in an individual at a locus are IBD})$

Inbreeding coefficient in gen $t+1$

- Generating inbreeding: F_{t+1}

Sample the first allele, then ...

- this allele is sampled again (new inbreeding in gen $t+1$)

or

- a second allele is sampled, but it was already IBD with the first allele at gen t (old inbreeding)

Inbreeding coefficient in gen t+1

- $F_{t+1} = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right)F_t$

N = population size
(# individuals)

new
inbreeding

old
inbreeding

- If $F_0 = 0$, then:

$$F_t = 1 - \left(1 - \frac{1}{2N}\right)^t$$

Inbreeding Coefficient

- Increases over time as alleles in a population are lost to drift.
- Eventually, one allele will become fixed in a population ...
- $F_t = \Pr (2 \text{ alleles w/in an individual at a locus are IBD}) \Rightarrow 1.$

Inbreeding exercise

- statgen.ncsu.edu/dahlia/inbreeding
 - [click on 'go']
- Simulates a small population over time.
- First value in each row is the generation number, starting at zero.
- Next are the genotypes of the thirteen individuals in the population.
 - [how many alleles are there at this locus?]

- Successive generations are simulated until only two alleles are left in the pop.
 - How many generations did this take?
 - Will this be the same every time the simulation is run? Why or why not?
- What are your expectations for the inbreeding coefficient of this population at this point?
- What are your expectations for genotype frequencies at this point?
 - Do you expect H-W genotype frequencies in this population?

- What information does the second-to-last column (next to the genos) provide?
 - Can this number increase between generations? Why or why not?
- What information does the final column provide?
 - Does this value always decrease over time? Why or why not?
- At the bottom of the page, a χ^2 statistic is given. The null hypothesis tested is: “ H_0 : genotype frequencies follow H-W expectations.” What results do you get?

Some take-home messages

- Small populations are affected strongly by drift.
- Alleles will be lost over time.
 - Which alleles are lost is random.
- The inbreeding coefficient increases over time as alleles are lost.
- We still may expect to find H-W genotype frequencies in the population.
- * Genetic variation is reduced over time.