Small 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

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
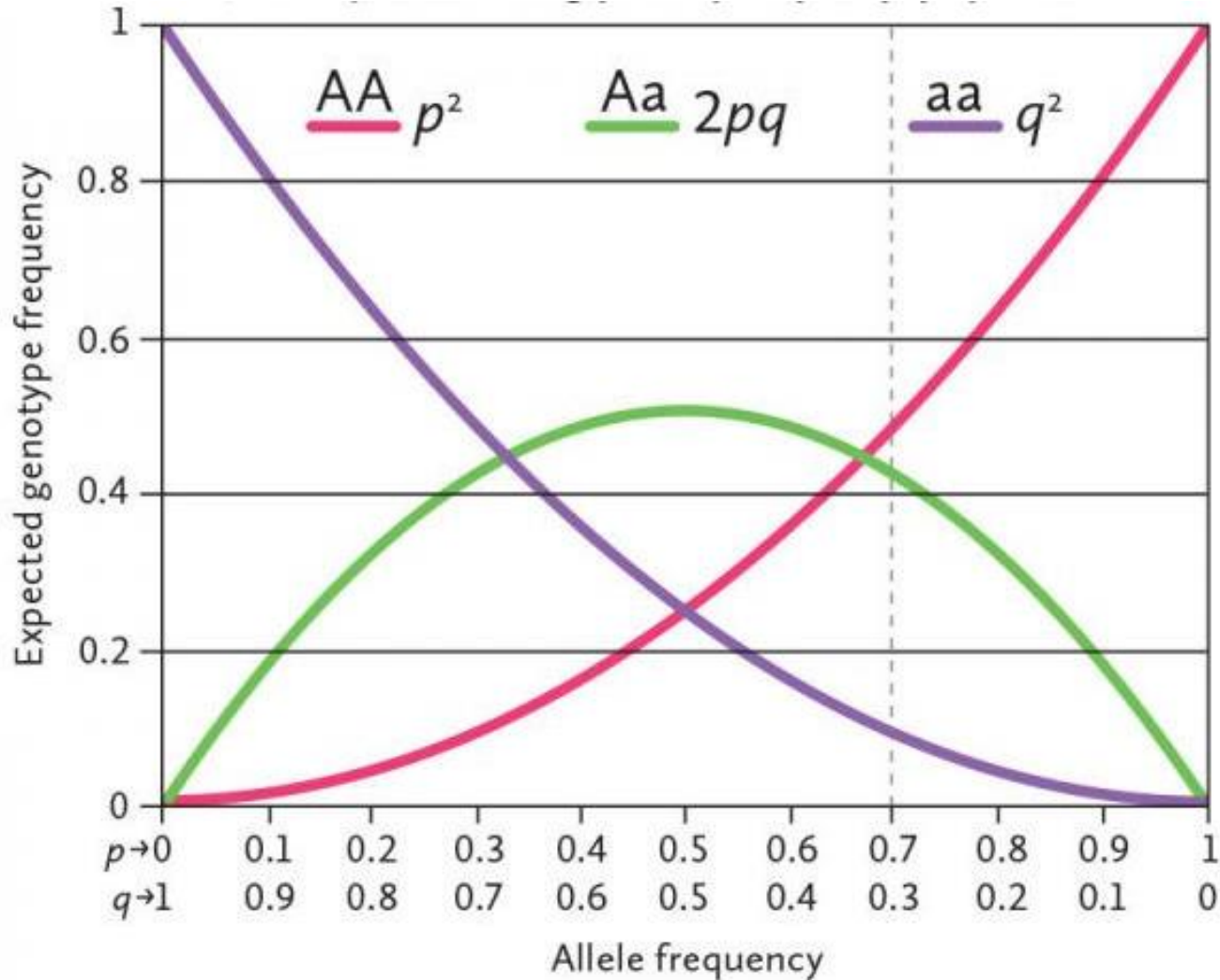
Small population sizes

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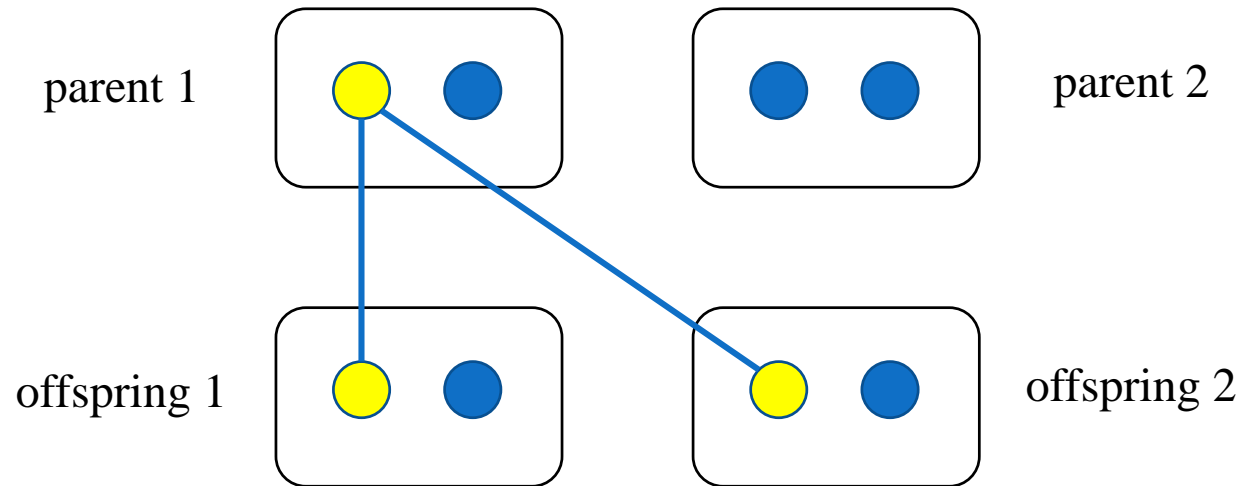
- Alleles that derive from a common ancestral allele are IBD.

Inbreeding Coefficient

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

  F_t = Pr (2 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

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

  N = population size
  (# individuals)

  new inbreeding   old inbreeding

- If $F_0 = 0$, then:

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

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 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.