## 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  $q^2$

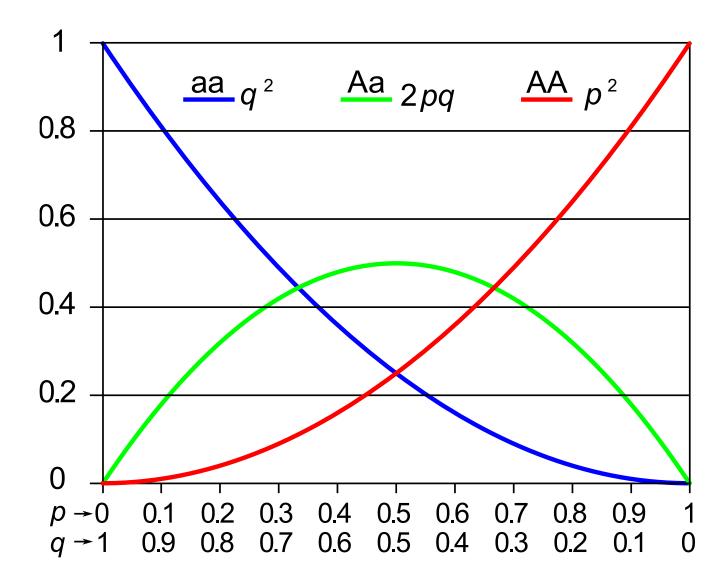
## **Common misperception**

- 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.
- \* <u>The frequency of a homozygous genotype</u> 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

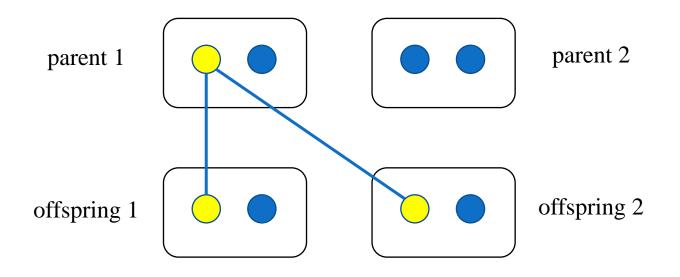
- Rare alleles can become common via drift.
- Deleterious homozygous genotypes become more likely.

• 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**:

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

#### 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

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

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-tolast 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  $\chi^2$  statistic is given. The null hypothesis tested is: "H<sub>0</sub>: 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.