Evolution 3

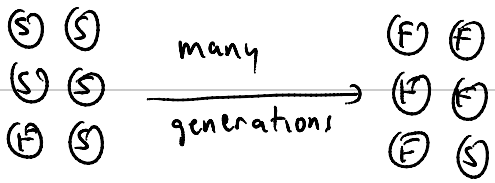
- Population Genetics I
  - intro
  - Mendelian Genetics
  - Hardy-Weinberg Population Genetics
- iClicker Question #0 - Register iClicker at Bio 111/112 Home page
- Labs start ~~THIS~~ Next week; meet at HMNH - free tickets after class
  - go to HMNH anytime it's open
  - no pre-lab this week
  - report due week of Feb 8 - just answers to questions

* don't forget the "Tree-Building Survey" - see link at lecture "Evolution 6
  - due Evolution 7

Population genetics

a population = a group of interacting & interbreeding organisms

ex. cheetahs in one area



how to study this?
- genetics individuals
∴ approximation - use population data

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genetics review ↷ very over-simplified

Gene - controls a character (ex speed of cheetah)

Allele - alternative form of gene (controls trait)

ex - the very fast allele of speed gene (R)

- slow allele " (r)

Genotype: the alleles an individual has (ex. RR, Rr, rr)

Phenotype - observable feature of organism (ex. speed)

* suppose we have 100 cheetahs in our population

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① I want to predict speeds in next generation

phenotype	#	genotype	frequency
v. fast	10	RR	0.10
fast*	20	Rr†	0.20
slow	70	rr	0.70
counted		inferred	

*incomplete dominance

sum of freqs always = 1

* to get next generation

② calculate allele frequencies = fraction of total alleles in population's "gene pool" [assume that each organism has 2 alleles to contribute to gene pool → this simulates each organism contributing equally to gene pool = same total # of egg or sperm from each]

from before

genotype	#	alleles contributed to gene pool: #R	#r
RR	10	20	0
Rr	20	20	20
rr	70	0	140
		40	160

totals: #R = 40, #r = 160 } gene pool

* frequency of R = $\frac{40}{200}$ = 0.2 (called "p")

200 ← 2 alleles from each of 100 cheetahs

* freq of r = $\frac{160}{200}$ = 0.8 (called "q")

p + q = 1 always

③ predicting next generation (make simplifying assumptions)

The Hardy-Weinberg model (simplification of real life)

* if all of the following hold true:

④ very large ~~poo~~ population size

(a) very large pop population size

(b) no migration out/in

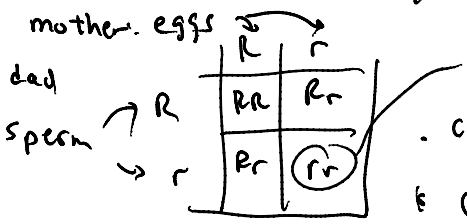
(c) no mutation

(d) random mating

(e) equal fitness (no natural selection)

* then can predict genotype freq's in next generation

If this were regular genetics, would use punnett square



chance is 1/4 because:

- chance of getting r egg from mom = 1/2
- & chance of getting r sperm from dad = 1/2

∴ chance of getting r from both
= 1/2 x 1/2 = 1/4

for <u>populations</u> = "mating is random" means egg & sperm drawn randomly from gene pool

∴ chance of R or r depends on <u>allele frequencies</u> (not necessarily 50/50)

∴ need modified punnett square

	R p=0.2	r q=0.8
R p=0.2	RR p^2 = 0.04	Rr pq=0.16
r q=0.8	Rr pq = 0.16	rr q^2 = 0.64

if all 5 conditions hold, in next generation:

freq of RR = p^2 = 0.04 — if 100 cheetahs 4 v-fast

- freq of Rr = $2pq$ = 0.32 — 32 fast
- freq of rr = q^2 = 0.64 — 64 slow

& also population is at Hardy-Weinberg Equilibrium (HWE)
⇒ no further change (no evolution)