SETGO
Science, Engineering & Technology Gateway Ohio

Art of Science Community…

When: February 18th, 5-7pm

Where: Perry Field House, BGSU

Who: Emily Sautter

NW Ohio Wind Energy Research

- **Qualify for Summer Research!**
- **Career and Networking Opportunities!**
- **Door Prizes!**

Contact **Liz Ross**, Program Manager, if you have any questions...

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304 Life Sciences, BGSU

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Population genetics I: Hardy-Weinberg

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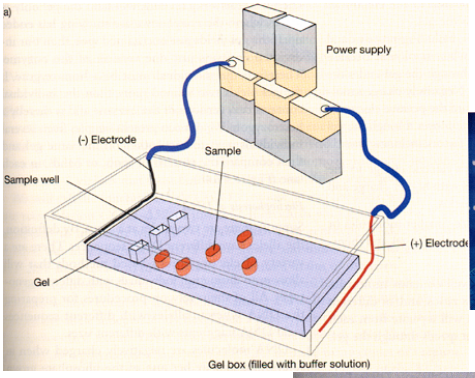

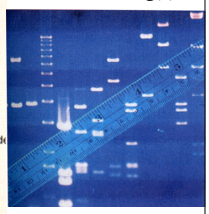

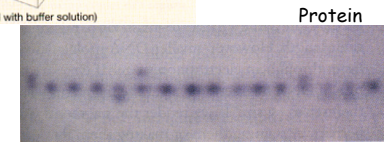

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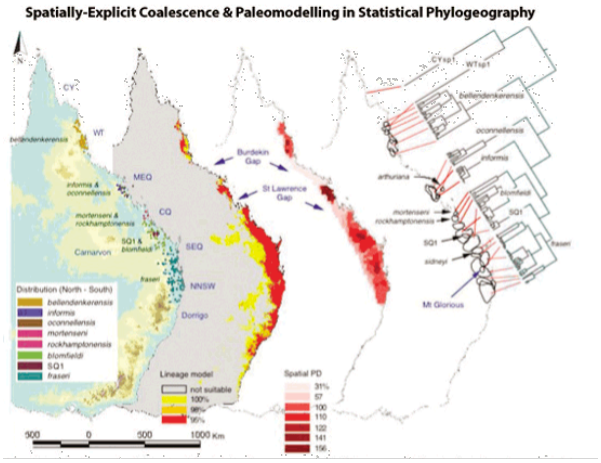

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"The science of population genetics is the automechanics of evolutionary biology."

Richard Lewontin, 2000

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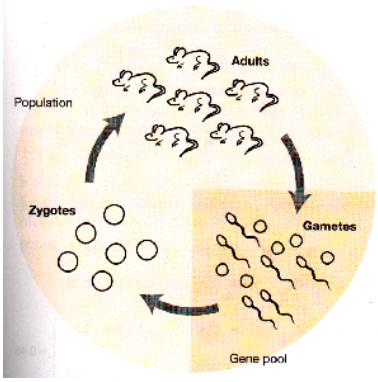
A model for gene frequencies in the absence of evolution……

Does the gene pool predict the distribution of genotypes within a population?



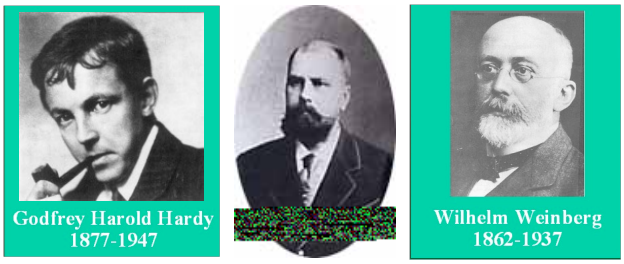
Allele Frequency: the proportion of all alleles of the gene that are of the prescribed type

Information needed to describe the genetic composition of a population?

- # alleles at the locus
- freq of alleles
- freq of genotypes

	A1A1	A1A2	A2A2
Population 1	50	0	50
Population 2	25	50	25

1908: Godfrey H. Hardy (mathematician)
Wilhem Weinberg (physician)
Sergei Chetverikov (geneticist)



Hardy-Weinberg (HWP) principle
expectation/equilibrium/equation

AA or Aa
aa -> multi

Assume a gene with 2 alleles……A & a

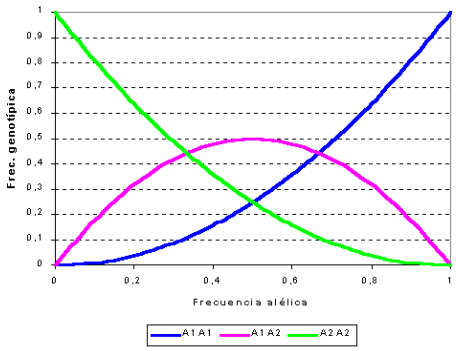
Allele Frequency:
Freq of A = p (range from 0-1)
Freq of a = q

Genotype frequency:
For random mating with 2 alleles at frequencies p & q

Egg \ Sperm	Allele Frequency	A p	a q
	A p	AA p^2	Aa pq
	a q	aA pq	aa q^2

Therefore the HW expectation is…..

$$P^2 + 2pq + q^2 = 1$$ (Binomial law)



Assumptions…..

- No selection
- No mutation
- No migration
- No random events
- Pop. infinitely large, stable, equal sex ratio
- Mating within population at random (panmixia)

i.e. No evolution!

……an ideal population

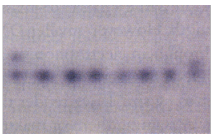
Significance of HW….

$$p^2 + 2pq + q^2 = 1$$

- Allele frequencies predict genotype frequencies
- At equilibrium, allele & genotype frequencies do not change from generation to generation
- If population displaced from equilibrium, return to equilibrium occurs in one generation

A numerical example…..

Sample a squirrel population (N= 73)
MDH locus >> 2 alleles, Medium & Fast



3 genotypes possible
MM 20
MF & FM 36
FF 17
Total N = 73 animals

3 genotypes possible

MM	20
MF & FM	36
FF	17
Total	N = 73 animals

Calculate allele frequencies…….

M = 76 $P_m = 76/146 = 0.5205$

F = 70 $P_f = 70/146 = 1\text{-}P_m = 0.4795$

Total alleles 2N = 146

Do these data conform to HW expectations?

	MM	MF	FF
Expected proportions	0.5205^2 = .2709	2(0.5205x0.4795) .4992	0.4795^2 .2299 = 1
Expected number	.2709x73 =19.776	.4992x73 =36.4426	.2299x73 =16.783
Observed number	20	36	17

Do these data conform to HW expectations? (Chi-squareTest)

H_o: No deviation from expected proportions

$$X^2 = \sum \frac{(Obs - Exp)^2}{Exp}$$

$$= \frac{(20 - 19.776)^2}{19.776} + \frac{(36 - 36.442)^2}{36.442} + \frac{(17 - 16.773)^2}{16.773}$$

$$= 0.00251 + 0.005427 + 0.00277$$

$$X^2 = 0.011$$

To check significance…….
df = # of classes -1- # parameters calculated from data
= 3-1-1=1

Critical X^2 at α 0.05 = 3.1415
Since $X^2 < X^2_{.05} = 3.1415$ we fail to reject the H_o
i.e. the data conform to HW

If $X^2 > X^2_{.05}$…….
then we reject H_o, conclusion is that the population is not in HW and (at least) one of the assumptions of HW is invalid

2 additional wrinkles in practice….
For loci with more than 2 alleles:
Expand the binomial e.g. for 3 alleles

$$p + q + r = 1$$

$$p^2 + q^2 + r^2 + 2pq + 2pr + 2qr = 1$$

For many loci:
If assume all loci are independent of one another then you can repeat this procedure for each one, add all the df & X^2 values, and check significance over all loci

Ideal populations are entirely predictable:

No…
- selection
- mutation
- migration
- random events
- infinitely large, stable, equal sex ratio
- random mating (panmixia)

freq.(A1A1 in zygotes) = p^2 (1)
freq.(A1A2 in zygotes) = 2pq (2)
freq.(A2A2 in zygotes) = q^2 (3)

- If all assumptions are true, then equations 1–3 must be true.
- If genotypes are in HW proportions, one (or more) of assumptions may still be violated.
- If genotypes are not in Hardy-Weinberg proportions, one or more of assumptions must be false.

If population is not in HW => some assumption has been violated…….

- Random chance/error
e.g. inappropriate selection of field site, sample not large enough
- Wahlund effect
  - Sample equally across populations in HW
  e.g. in aquatic thermocline, or behavioral subdivision
  - decrease hets & increase homozygotes
- Selection
- Inbreeding - Breed with others genotypically more like themselves
e.g. positive assortative mating, small population sizes
  - decreases hets & increases homozygotes
  - greater likelihood of shared deleterious alleles

Problems

1. In humans, the COL1A1 locus codes for certain collagen protein found in bone. The normal allele at this locus is denoted with S. A recessive allele s is associated with reduced bone mineral density and increased fractures in both Ss and ss women. A recent study of 1,778 women showed that 1,194 were SS, 526 were Ss, and 58 were ss (Uitterlinden et al 1998).

(a) Are these two alleles in Hardy-Weinberg equilibrium in this population?
(b) How do you know?
(c) What information would you need to determine whether the alleles will be in Hardy-Weinberg equilibrium in the next generation?

2. In the peppered moth (Biston betularia), black individuals may be either homozygous (A_1A_1) or heterozygous (A_1A_2), whereas pale gray moths are homozygous (A_2A_2). Suppose that in a sample of 250 moths from one locality, 108 are black and 142 are gray.

(a) Which allele is dominant?
(b) Assuming that the locus is in Hardy-Weinberg equilibrium, what are the allele frequencies?
(c) Under this assumption, what proportion of the sample is heterozygous?
(d) What is the number of heterozygotes?
(e) Under the same assumption what proportion of black moths is heterozygous?
(f) Why is it necessary to assume Hardy-Weinberg genotype frequencies in order to answer parts b-d?