“Darwin’s Finches”
1976

Year One

Number of finches

Beak depth (mm)
The seeds of Caltrop, in the genus *Tribulus*.

- It takes a medium ground finch with a beak at least 11mm long to open one.
Figure 13.21 Heritability of beak depth in one of Darwin's finches, Geospiza fortis. The slope of the regression line is an estimate of heritability, which can range from 0 (no heritability) to 1 (perfect heritability). (Modified from Boag 1983.)
• What do you think will happen to the size of the finch population between Years 1 and 3?
Q: Which is the most appropriate description of evolution by natural selection?

A: Organisms can evolve to match their environment out of need.
B: A population can become more adapted to its environment via natural selection.
C: Individuals can evolve to perfectly match their environment.
D: Natural selection is a random process.
What is a population?
Population genetics – study of genetic structure of populations

- allele frequencies
- genotype frequencies
Population Genetics: Terms

• Gene pool:

• Allele frequencies:

• Genotype frequencies:
Allele and genotype frequencies

- 200 white (rr)
- 500 pink (Rr)
- 300 red (RR)

total = 1000 flowers
Allele and genotype frequencies

Genotype frequencies

\[
\begin{align*}
260 \quad &\frac{100}{400} = 0.25 \text{ GG} \\
&\frac{160}{400} = 0.40 \text{ Gg} \\
&\frac{140}{400} = 0.35 \text{ gg} \\
\end{align*}
\]

0.65

Phenotype frequencies

\[
\begin{align*}
260/400 = 0.65 \text{ green} \\
140/400 = 0.35 \text{ brown} \\
\end{align*}
\]

Allele frequencies

\[
\begin{align*}
360/800 = 0.45 \text{ G} \\
440/800 = 0.55 \text{ g} \\
\end{align*}
\]
What can cause changes in allele frequencies?

“null” model

*Populations at Equilibrium* - no change in allele frequencies between generations

Godfrey Hardy  
Wilhelm Weinberg
• **H-W principle**: Gene frequencies will remain constant in a *randomly breeding* population unless acted on by external forces
• Counting **Alleles**
  – assume 2 alleles = $A_1$, $A_2$
  – **Freq. of dominant allele** ($A_1$) = $p$
  – **Freq. of recessive allele** ($A_2$) = $q$
    • frequencies must add to 1 (100%), so:
      $$p + q = 1$$

---

**Hardy-Weinberg theorem**

**Sperm**
- $fr(A_1) = p$
- $fr(A_2) = q$

**Eggs**
- $fr(A_1) = p$
- $fr(A_2) = q$

**Zygotes**
- $fr(A_1A_1) = p^2$
- $fr(A_1A_2) = pq$
- $fr(A_2A_2) = q^2$

<table>
<thead>
<tr>
<th></th>
<th>$A_1A_1$</th>
<th>$A_1A_2$</th>
<th>$A_2A_2$</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$p^2$</td>
<td>$2pq$</td>
<td>$q^2$</td>
<td>$1.0$</td>
</tr>
</tbody>
</table>
Observed vs. Expected frequencies

- 100 cats: 36=AA, 48=Aa, 16=aa
- Allele freqs
  - $f(A) = p = \frac{2(36)+48}{200} = \frac{120}{200} = 0.6$
  - $f(a) = q = \frac{2(16)+48}{200} = \frac{80}{200} = 0.4$
- Expected genotype freqs under HWE:
  - $F(AA) = p^2 = (0.6)^2 = 0.36$
  - $F(Aa) = 2pq = 2(0.6)(0.4) = 0.48$
  - $F(aa) = q^2 = (0.4)^2 = 0.16$

<table>
<thead>
<tr>
<th></th>
<th>$F(AA)$</th>
<th>$F(Aa)$</th>
<th>$F(aa)$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Observed</td>
<td>0.36</td>
<td>0.48</td>
<td>0.16</td>
</tr>
<tr>
<td>Expected</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Example 2

- 100 cats: 20=AA, 70=Aa, 10=aa
- Allele freqs
  - f(A) = p = (2(20)+70)/200 = 110/200 = 0.55
  - f(a) = q = (2(10)+70)/200 = 90/200 = 0.45
- Expected genotype freqs under HWE:
  - F(AA) = p^2 = (0.55)^2 = 0.3
  - F(Aa) = 2pq = 2(0.55)(0.45) = 0.5
  - F(aa) = q^2 = (0.45)^2 = 0.2

<table>
<thead>
<tr>
<th></th>
<th>F(AA)</th>
<th>F(Aa)</th>
<th>F(aa)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Observed</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Expected</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
More HW calculations

<table>
<thead>
<tr>
<th>1/100 AA, 18/100 Aa, 81/100 aa</th>
<th>10/100 AA, 80/100 Aa, 10/100 aa</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Observed</td>
</tr>
<tr>
<td></td>
<td>F(AA)</td>
</tr>
<tr>
<td>Observed</td>
<td>0.01</td>
</tr>
<tr>
<td>Expected</td>
<td>0.01</td>
</tr>
</tbody>
</table>

\[ p + q = 1 \]
\[ p = \frac{(2(1)+18)}{200} = \frac{20}{200} = 0.1 \]
\[ q = \frac{(2(81)+18)}{200} = \frac{180}{200} = 0.9 \]

\[ p^2 + 2pq + q^2 = 1 \]
\[ p^2 = 0.01 \]
\[ 2pq = 0.18 \]
\[ q^2 = 0.81 \]

\[ p + q = 1 \]
\[ p = \frac{(2(10)+80)}{200} = \frac{100}{200} = 0.5 \]
\[ q = \frac{(2(10)+80)}{200} = \frac{100}{200} = 0.5 \]

\[ p^2 + 2pq + q^2 = 1 \]
\[ p^2 = 0.25 \]
\[ 2pq = 0.50 \]
\[ q^2 = 0.25 \]
**TABLE 25.1 The MN Blood Group of Humans: Observed and Expected Genotype Frequencies**

The expected genotype frequencies are calculated from the observed allele frequencies, using the Hardy-Weinberg principle.

<table>
<thead>
<tr>
<th>Population and Location</th>
<th>Genotype Frequencies</th>
<th>Allele Frequencies</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>MM</td>
<td>MN</td>
</tr>
<tr>
<td>Inuit (Greenland)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Observed</td>
<td>0.835</td>
<td>0.156</td>
</tr>
<tr>
<td>Expected</td>
<td>0.834</td>
<td>0.159</td>
</tr>
<tr>
<td>Native Americans (U.S.)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Observed</td>
<td>0.600</td>
<td>0.351</td>
</tr>
<tr>
<td>Expected</td>
<td>0.602</td>
<td>0.348</td>
</tr>
<tr>
<td>Caucasians (U.S.)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Observed</td>
<td>0.292</td>
<td>0.494</td>
</tr>
<tr>
<td>Expected</td>
<td>0.290</td>
<td>0.497</td>
</tr>
<tr>
<td>Aborigines (Australia)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Observed</td>
<td>0.025</td>
<td>0.304</td>
</tr>
<tr>
<td>Expected</td>
<td>0.031</td>
<td>0.290</td>
</tr>
<tr>
<td>Ainu (Japan)</td>
<td>Observed</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.179</td>
<td>0.502</td>
</tr>
<tr>
<td></td>
<td>Expected</td>
<td></td>
</tr>
</tbody>
</table>

**EXERCISE** Fill in the values for allele frequencies and expected genotype frequencies for the Ainu people of Japan.

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A population is in Hardy-Weinberg Equilibrium for the H locus with alleles H and h. The frequency of the hh genotype is 0.36. What is the frequency of the H allele?

What is the frequency of heterozygotes in this population?
Conditions for Hardy-Weinberg Equilibrium

1. Random mating
2. No natural selection
3. No net mutation
4. No gene flow
5. Large population size