1. Genotype and gene frequencies

For an autosomal locus, A, with two alleles, A1 and A2, there are three possible genotypes A1A1, A1A2, and A2A2. Then let

\[ n_1 = \text{number of } A_1A_1 \text{ genotypes in the population} \]
\[ n_2 = \text{number of } A_1A_2 \text{ genotypes in the population} \]
\[ n_3 = \text{number of } A_2A_2 \text{ genotypes in the population} \]

If N is the total number of organisms in the population, the frequencies of the three genotypes are

\[ x = \frac{n_1}{N} \quad \text{(frequency of } A_1A_1) \]
\[ y = \frac{n_2}{N} \quad \text{(frequency of } A_1A_2) \]
\[ z = \frac{n_3}{N} \quad \text{(frequency of } A_2A_2) \]

In a diploid population of size N, there are 2N gametes. The number of A1 allele gametes is 2n1 + n2 and the number of A2 allele gametes is n2 + 2n3. Therefore, the frequencies of the two alleles are

\[ p = \frac{2n_1 + n_2}{2N} \quad \text{or } x + \frac{1}{2}y \quad \text{(frequency of } A_1 \text{ allele}) \]
\[ q = \frac{n_2 + 2n_3}{2N} \quad \text{or } \frac{1}{2}y + z \quad \text{(frequency of } A_2 \text{ allele}) \]

2. Hardy-Weinberg equilibrium

Where there is random mating, the mating type frequencies are

<table>
<thead>
<tr>
<th>Males</th>
<th>A1A1 ( (x) )</th>
<th>A1A2 ( (y) )</th>
<th>A2A2 ( (z) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1A1 (x)</td>
<td>( x^2 )</td>
<td>xy</td>
<td>xz</td>
</tr>
<tr>
<td>A1A2 (y)</td>
<td>xy</td>
<td>( y^2 )</td>
<td>yz</td>
</tr>
<tr>
<td>A2A2 (z)</td>
<td>xz</td>
<td>yz</td>
<td>( z^2 )</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Females</th>
<th>A1A1 ( (x) )</th>
<th>A1A2 ( (y) )</th>
<th>A2A2 ( (z) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1A1 ( x )</td>
<td>xy</td>
<td>( y^2 )</td>
<td>yz</td>
</tr>
<tr>
<td>A1A2 ( y )</td>
<td>xz</td>
<td>yz</td>
<td>( z^2 )</td>
</tr>
</tbody>
</table>
In each cell are the frequencies of the specific mating types, i.e. frequency of $A_2A_2 \times A_2A_2$ is $z^2$. If reciprocal mating types are treated equally, $A_1A_1 \times A_1A_2 \, ♂ \times A_1A_1 \, ♀$ is the same as $A_1A_2 \, ♂ \times A_1A_1 \, ♀$, then the following mating type frequencies are obtained.

<table>
<thead>
<tr>
<th>Types of Mating</th>
<th>Frequency of Mating type</th>
<th>Frequencies of offspring</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A_1A_1 \times A_1A_1$</td>
<td>$x^2$</td>
<td>$x^2$</td>
</tr>
<tr>
<td>$A_1A_1 \times A_1A_2$</td>
<td>$2xy$</td>
<td>$xy$</td>
</tr>
<tr>
<td>$A_1A_1 \times A_2A_2$</td>
<td>$2xz$</td>
<td>-</td>
</tr>
<tr>
<td>$A_1A_2 \times A_2A_2$</td>
<td>$y^2$</td>
<td>$\frac{1}{2}y^2$</td>
</tr>
<tr>
<td>$A_1A_2 \times A_2A_2$</td>
<td>$2yz$</td>
<td>-</td>
</tr>
<tr>
<td>$A_2A_2 \times A_2A_2$</td>
<td>$z^2$</td>
<td>-</td>
</tr>
</tbody>
</table>

Total: $1 = (x + \frac{1}{2}y)^2 = p^2 \quad \downarrow \quad (\frac{1}{2}y + z)^2 = q^2$

$2(x + \frac{1}{2}y)(\frac{1}{2}y + z) = 2pq$

$p^2 : 2pq : q^2$

Remembering that $p = x + \frac{1}{2}y$ and $q = \frac{1}{2}y + z$ and substituting these values in the frequencies of the various types of offspring, it is found that the genotype frequencies are a function of the gene frequency $(p^2 : 2pq : q^2)$ after one generation of random mating. These genotypes frequencies are known as the Hardy-Weinberg equilibrium frequencies.

3. Mutation

$p = \text{frequency of allele } A_1$
$q = \text{frequency of allele } A_2$
$u = \text{probability of mutation } A_1 \text{ to } A_2$
$v = \text{probability of mutation } A_2 \text{ to } A_1$

The change in the gene frequency of allele $A_2$ is

$\Delta q = (\text{frequency of } A_1) (\text{probability of mutation } A_1 \text{ to } A_2) - (\text{frequency of } A_2) (\text{probability of mutation } A_2 \text{ to } A_1)$

$\Delta q = pu - qv$

If $pu = qv$, $\Delta q = 0$ This is an equilibrium.

The frequency of $A_2$ at equilibrium can be calculated

\begin{align*}
0 &= pu - qv \\
0 &= (1 - q)u - qv \\
0 &= u - qu - qv \\
q(u + v) &= u
\end{align*}
4. **Genetic Drift**

The mean change over a number of populations in gene frequency when only genetic drift is acting is zero. \( \bar{\delta q} = \overline{q_1} - q_0 = 0 \) As a result, its effect is best evaluated by looking at its variance \( \sigma_{\delta q}^2 \) which is

\[
\sigma_{\delta q}^2 = \frac{p_0q_0}{2N}
\]

One can see that this is a function of gene frequency and of the number of gametes in the population.

5. **Inbreeding**

Offspring which are the products of inbreeding may carry two genes at a locus which are identical because they are replicates of a single gene of an ancestor. These genes are said to be **identical by descent**. The probability of genes being identical by descent is called Wright’s coefficient of inbreeding, \( F \). \( F \) may also be looked at as a measure of the proportion by which heterozygosity is reduced in the population. Thus,

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Frequency before inbreeding</th>
<th>Frequency after inbreeding</th>
</tr>
</thead>
<tbody>
<tr>
<td>( A_1A_1 )</td>
<td>( p^2 )</td>
<td>( p^2 + Fpq )</td>
</tr>
<tr>
<td>( A_1A_2 )</td>
<td>( 2pq )</td>
<td>( 2pq - 2Fpq )</td>
</tr>
<tr>
<td>( A_2A_2 )</td>
<td>( q^2 )</td>
<td>( q^2 + Fpq )</td>
</tr>
</tbody>
</table>

Note that genotype frequencies change but gene frequencies stay the same.

In natural populations with random mating the probability of 2 gametes uniting which are identical by descent is \( \frac{1}{2N} \). Thus,

\[
\Delta F = \frac{1}{2N}
\]

Therefore, it appears that in small populations (\( N = 20 \) or less), a significant amount of inbreeding can develop in spite of random mating.

6. **Migration**

\( M \) = proportion of migrants

\( 1-M \) = proportion of non-migrants

\( Q \) = gene frequency of \( A_2 \) of migrants

\( q \) = gene frequency of \( A_2 \) of non-migrants

The gene frequency in the next generation is

\[
q_1 = (\text{proportion of non-migrants}) (\text{gene frequency of non-migrants}) + (\text{proportion of migrants}) (\text{gene frequency of migrants})
\]

\[
q_1 = (1 - M) q + MQ
\]