**Quantitative complementation (deficiency mapping)**

- \( P_1 \) Height
- \( P_2 \) Stem

- \( x \) Deficiency
- \( y \) Balanced

A test for difference in phenotype between the two

Reciprocal hemizygosity

- **Reciprocal hemizygosity**

  - **a**
    - **Hybrid**
    - **Phenoptical
      - **Hybrid**
      - **Phenotypic
        - **Hybrid**
        - **Phenotypic**

  - **b**
    - **YFG1-25B9a**
    - **YFG1-154A**

Bristle Number in Fruit flies: A model for quantitative traits

- **ST** = sternopleural bristles
- **SC** = scutellar bristles
- **AB** = abdominal bristles

(apparent) Stabilizing selection on bristle number

**Deficiency mapping**

- **Deficiency mapping**

  - **Figure 1**: Deficiency mapping of second chromosome (2L). Affected areas (red dot) of 2L in yellow strain were cross-hybridized with radiolabeled probes of 2L. The DNA was then used to screen for deficiencies. The black dots indicate the presence of deficiencies. The red dots indicate the absence of deficiencies. The yellow area indicates the region of interest. The blue area indicates the region of non-interest. The green area indicates the region of overlap. The orange area indicates the region of non-overlap. The pink area indicates the region of overlap with the region of interest. The purple area indicates the region of non-overlap with the region of interest. The brown area indicates the region of non-overlap with the region of non-interest. The gray area indicates the region of overlap with the region of non-interest. The black area indicates the region of non-overlap with the region of non-interest. The white area indicates the region of non-overlap with the region of non-interest.
Linkage versus linkage disequilibrium

In a single generation (meiosis-family):
- Probability of no recombination = (1-\(d\))^n
  In two generations:
- Probability of no recombination = (1-\(d\))^{2n}
  In t generations:
- Probability of no recombination = (1-\(d\))^t

\[
\begin{align*}
A_1A_1 & \quad | \quad A_1B_1 & \quad | \quad A_1B_2 \\
A_2B_1 & \quad | \quad A_2B_2
\end{align*}
\]

Haplotype Frequency  Allele Frequency
\[
\begin{align*}
X_1B_1 & \quad x_{11} & \quad A_1 & \quad p_1 = x_{11} + x_{12} \\
X_1B_2 & \quad x_{12} & \quad A_2 & \quad p_2 = x_{12} + x_{22} \\
X_2B_1 & \quad x_{21} & \quad B_1 & \quad q_1 = x_{11} + x_{21} \\
X_2B_2 & \quad x_{22} & \quad B_2 & \quad q_2 = x_{12} + x_{22}
\end{align*}
\]

\[
D = x_{11} \cdot p_1 q_1
\]

correlation coefficient \( r = \frac{D}{\sqrt{(p_1-p_2)(q_1-q_2)}} \)

Decay of linkage disequilibrium

\[
\begin{align*}
D(t) &= D(0) e^{-2\theta t} \\
\theta &= \frac{4N_e}{\chi^2}
\end{align*}
\]

\[\chi^2 = \sum (O-E)^2 / E \]

\[N_e = \frac{\chi^2}{4} \]

\[\theta = \frac{4N_e}{\chi^2} \]

\[D(t) = D(0) e^{-2\theta t} \]

\[
\begin{align*}
D(t) &= D(0) e^{-2\theta t} \\
\theta &= \frac{4N_e}{\chi^2}
\end{align*}
\]
Molecular Quantitative Genetics: Sporulation in Yeast

Deutschbauer and Davis (2005)

RME1 – 1bp insertion in a repeat, noncoding
TACO – missense
MKT1 – missense
90% of variation explained


RAS2 – 1bp insertion in a repeat, noncoding
PMS1
SWI2
FKH2
60 kb region on Chr14


RME1 – 1bp insertion in a repeat, noncoding
TACO – missense and noncoding
RFS1 – missense
80-90% variation explained

RME1 – Regulator of meiosis, TF, represses IME1
IME1 – Inducer of meiosis, TF.
RFS1 – Respiration factor, mediates transition to respiratory growth.
TACO – Transcriptional activator, involved in polarized morphogenesis.
MKT1 – Maintenance of K2 killer toxin.
RAS2 – GTP binding protein that regulates nitrogen starvation response, sporulation, filamentous growth.
PMS1 – ATP binding protein required for mismatch repair.
SWI2 – Mitochondrial ribosomal protein of the small subunit.
FKH2 – Forkhead TF, regulates G2/M phase genes, silencing and transcriptional elongation.

Linkage versus association

<table>
<thead>
<tr>
<th>Method</th>
<th>Frequency</th>
<th>Effect size</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linkage</td>
<td>rare</td>
<td>large</td>
</tr>
<tr>
<td>Association</td>
<td>common</td>
<td>small</td>
</tr>
</tbody>
</table>