LINKAGE: violates “independent assortment”

1/22/92, rvd 1/26/94, 1/19/96, 1/22/97, 1/3/98, 19 Jan 00, 19 Jan 01, 21 Jan 04, 19Jan05, 24Jan08, 21Jan09, 22Jan10, 21Jan11, 20Jan12, 23Jan12

Exceptions (violations) of Mendelian-predicted behavior can yield new insights

Bateson and Punnett studying sweet pea:

cross: PP:LL x pp:ll | phenotype  | expected | observed
| Purple/red, Long/round grains: |
| PPLL x ppll: PpLi F1 (p 142), then selfed |
| F2 (selfing), 6952 progeny did not produce 9:3:3:1 ratio: (note excess of parental types) |

postulated “coupling”

Total: 6952

Morgan found similar prob in Drosophila (purple eyes / vestigial wings x w.t.), introduced concept of test cross technique (dominant phenotype of unknown genotype) page 131: (Note alternate convention for wild type (+) vs mutant (letters))

pr/pr @ vg/ vg x +/+; +/+;
F1: pr/+ vg/+ (then crossed times pr/pr @ vg. vg = TEST CROSS)

TEST CROSS: (notation: + = wildtype) direct analysis, parental genotype (use doubly homozygous recessive, should get 1:1:1:1 if independent), got:

| (p. 142) phenotype | expected | observed |
| ++ | 710 | 1339 (excess of parental types) |
| pr vg | 710 | 1195 |
| + vg | 710 | 151 |
| pr + | 710 | 154 |

Total: 2839

Morgan postulated both genes on same chromosome (= “linkage”) segregate together (violated Mendel’s 2nd law)

If genes are located on same chromosome, how do they separate? (Rare)

RECOMBINATION: meiosis: 1N differs fr either parental 1N genotype.
Evidence: Can be seen as chiasmata: exchange between non-sister homologous chromosomes

Note difference between INTERchromosomal recombination: (independent assortment)
INTRachromosomal recombination: by recombination

VIDEO: http://www.youtube.com/watch?v=op7Z1PxaO4&feature=related

“Recombinant type” phenotype defined as one trait from one parent, one trait from other parent

Recombination frequency: (total recombinant events/total progeny) = distance between in %

INTERchromosomal freq = ~50% (25% of each recombinant type in test cross, i.e., Ab and aB)
INTRachromosomal freq = <50% 

LINKAGE MAPS: (p 129 and 139) AABB x aabb: F1 = AaBb
Sturtevant (undergrad student of Morgan) proposed: Aa:Bb:
linear relationship on chromosome:
greater distance loci, more prob of cross over:
genetic map unit = distance yields 1% recombinants.
**Linkage of genes on X chromosome** easier than autosomal:

- Male is hemizygous, his phenotype = genotype
  - \( y = \) yellow body \( (+ = \) brown \) / \( + = \) red eye \( w = \) white eye

**Experiment**:

\[ P: \ yw+/yw+ \text{ fem} \times y+w/Y \text{ male} \]

\[ zB: \text{ heterozygous female x male} \]

\[ \text{will produce sons reflecting females genotype:} \]

- \( yw: \)
- \( y^w \)
- \( yw^+ \)
- \( y^w^+ \)

**Drosophila**:

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Expected</th>
<th>Observed</th>
</tr>
</thead>
<tbody>
<tr>
<td>( yw )</td>
<td>1128</td>
<td>43</td>
</tr>
<tr>
<td>( y^w )</td>
<td>1128</td>
<td>2146</td>
</tr>
<tr>
<td>( yw^+ )</td>
<td>1128</td>
<td>2302</td>
</tr>
<tr>
<td>( y^w^+ )</td>
<td>1128</td>
<td>22</td>
</tr>
</tbody>
</table>

Count only males:

\[ F_1: \ yw^+/y^w \times yw^+/Y: \text{ rec freq:} \frac{43 + 22}{4513} = 1.4\% \]