14.5: Linked Genes

Mendel was lucky. He studied a variety of traits in pea plants and his data were consistent with his idea of traits being encoded by pairs of discrete heritable units. He did not call these “genes” and had no idea about their chromosomal origins or chemical makeup. It turns out that the genes he studied were either on different chromosomes and so assorted independently (Chapter 9), or so far apart on the same chromosome that linkage could not be detected (Chapter 10).

Symbols for a gene can be drawn on a page to communicate their position on a chromosome. To do this, we use a forward slash (/) to demonstrate what is on each chromosome. Figure A1.4 shows how we might conceptualize the position of a gene on two chromosomes by collapsing the chromosomes into a single line.

![Figure A1.4](https://bio.libretexts.org/Bookshelves/Genetics/Book%3A_Online_Open_Genetics_(Nickle_and_Barrette-Ng)/14%3A_Append…)

There’s no question about where the gene is located when only one trait is under investigation: it will be at the same position on each homolog. Two genes, however, can be one of three possibilities. Each possibility has implications for gene mapping and predicting ratios from a dihybrid cross. Figure A1.5 shows the positions of genes for an unlinked situation as well as linked genes in coupling and repulsion configurations. If genes are unlinked, put the allele symbols for one gene on either side of one slash followed by a semicolon (indicating that it’s unlinked) and the other gene with the alleles separated by a second slash (A/a; B/b). When genes are linked, only one slash is used: remember, the slash stands for a pair of homologous chromosomes. Genes in coupling would have the dominant genes together on one side of the slash and recessives on the other side (AB/ab). Repulsion would represent the other arrangement (Ab/aB).
Figure A1.5: Three gene arrangements for cells of genotype AaBb. Chromosomes are replicated (shown with sister chromatids). a) demonstrates unlinked genes: A/a; B/b. Linked genes are shown in b) repulsion Ab/aB and c) coupling AB/ab. *(Modified by T. Nickle from an original by J.Locke- CC BY-NC 3.0 from Chapter 18)*

Practice your skills with identifying linked and unlinked genes online in module 1.5. Some examples of different forms of gene symbols are shown in Table 2. Keep in mind that sometimes you have flexibility in which system of nomenclature you use, but sometimes it is dictated to you, for example in publications or other formal submissions. You are discouraged from inventing your own system or mixing up different systems because it will confuse your readers (or graders!).

<table>
<thead>
<tr>
<th>Examples</th>
<th>Interpretation</th>
</tr>
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<tbody>
<tr>
<td>A and a</td>
<td>Uppercase letters represent dominant alleles and lowercase letters indicate recessive alleles. Mendel invented this system but it is not commonly used in publications because not all alleles show complete dominance and many genes have more than two alleles. It’s quick and easy for you to use when working out genetics problems when you are sure each gene involves only two alleles.</td>
</tr>
<tr>
<td>$a^+$ and a</td>
<td>Superscripts are used to indicate alleles. For wild type alleles the symbol is a superscript +. The mutant allele of gene a would be recessive.</td>
</tr>
<tr>
<td>$\text{met}^+$ and $\text{met}^-$</td>
<td>This is typical of a prokaryote gene symbol. It could be referring to wild-type (functional) and mutant (nonfunctional) alleles of a gene that makes a protein in the methionine synthesis pathway.</td>
</tr>
<tr>
<td>AA or A/A</td>
<td>Sometimes a forward slash is used to indicate that the two symbols are alleles of the same gene, but on homologous chromosomes. Both representations in this row are identical: it represents a homozygous dominant.</td>
</tr>
<tr>
<td>Aa/Aa or Aa/aa</td>
<td>Note that this example shows two alleles of the gene Aa. We know that the gene symbol is two letters because the slash separates the allele found on each of the homologous chromosomes. We cannot tell if the mutant phenotype is recessive because there’s no indication which is wild type.</td>
</tr>
<tr>
<td>$\text{Gm}^+$ shr/ Gm shr</td>
<td>The three-letter system is used here. “Gm” might mean that the phenotype is “green”, but we can’t be sure. What we do know is that the mutant allele codes for a protein leading to a dominant phenotype. The wild-type allele must be recessive to the mutant allele. Maybe “shr” means “shrunken” or “short”, but we know that the mutant phenotype can only be seen in the homozygous recessive configuration. The phenotype for this organism is mutant for both Gm and shr traits. Final note: the genes are on the same chromosome based on the position of the slash.</td>
</tr>
<tr>
<td>$\text{bob}^+$/bob; mia/mia</td>
<td>This also uses the three-letter system. The organism is heterozygous for bob but shows the wild-type trait in its phenotype. It is homozygous recessive for mia and therefore shows that mutant phenotype. The genes are unlinked.</td>
</tr>
</tbody>
</table>

A more advanced system of nomenclature is outlined in Appendix 2. New rules are introduced to help you identify sex.
linked genes and predict phenotypes from gene symbols alone.