4.5: Some mutations may not have detectable phenotypes

Silent Changes

After mutagen treatment, the vast majority of base pair changes (especially substitutions) have no effect on the phenotype. Often, this is because the change occurs in the DNA sequence of a non-coding region of the DNA, such as in **inter-genic regions** (between genes) or within an intron region. Also, even if the change occurs in a base within a codon, it may not change the amino acid that it encodes (recall that the genetic code is degenerate; for example, GCT, GCC, GCA, and GCG all encode alanine) and is referred to as a **silent** mutation. Additionally, the base substitution may change an amino acid, but this doesn’t alter the function of the product, so no phenotypic change would occur.

Environment and Genetic Redundancy

There are also situations where a mutation can cause a complete loss-of-function of a gene, yet not produce a change in the phenotype, even when the mutant allele is homozygous. The lack of a phenotypic change can be due to environmental effects: the loss of that gene product may not be apparent in that environment, but might in another. Alternatively, the lack of a phenotype might be attributed to genetic **redundancy**, i.e. the encoding of similarly functioning genes at more than one locus in the genome. Thus the loss of one gene is compensated by another. This important limitation of mutational analysis should be remembered: genes with redundant functions cannot be easily identified by mutant screening.

Essential Genes and Lethal Alleles

Some phenotypes require individuals to reach a particular developmental stage before they can be scored. For example,
flower color can only be scored in plants that are mature enough to make flowers, and eye color can only be scored in flies that have developed eyes. However, some alleles may not develop sufficiently to be included among the progeny that are scored for a particular phenotype. Mutations in essential genes create recessive lethal alleles that arrest the development of an individual at an embryonic stage. This type of mutation may therefore go unnoticed in a typical mutant screen because they are absent from the progeny being screened. Furthermore, the progeny of a monohybrid cross involving an embryonic lethal recessive allele may therefore all be of a single phenotypic class, giving a phenotypic ratio of 1:0 (which is the same as 3:0). In this case the mutation may not be detected.

Naming Genes

Many genes have been first identified in mutant screens, and so they tend to be named after their mutant phenotypes, not the normal function or phenotype. This can cause some confusion for students of genetics. For example, we have already encountered an X-linked gene named white in fruit flies. Null mutants of the white gene have white eyes, but the normal white+ allele has red eyes. This tells us that the wild type (normal) function of this gene is actually to help make red eyes. Its product is a protein that imports a pigment precursor into developing cells of the eye. Why don't we call it the "red" gene, since that is what its product does? Because there are more than one-dozen genes that when mutant alter the eye colour; e.g. violet, cinnabar, brown, scarlet, etc. For all these genes their function is also needed to make the eye wild type red and not the mutant colour. If we used the name "red" for all these genes it would be confusing, so we use the distinctive mutant phenotype as the gene name. However, this can be problematic, as with the "lethal" mutations described above. This problem is usually handled by giving numbers or locations to the gene name, or making up names that describe how they die (e.g. even-skipped, hunchback, hairy, runt, etc.).