Activity - Continuous Genetic Variation

Throughout most A-level courses, you will be introduced to traits whose variation is apparently controlled by one or, just a small number of genes. For instance, when you learn about dominance, you will learn how we can predict the outcome of particular parental crosses using a Punnett square. Knowing how such inheritance works is important if we are to understand the role of evolution some of our genes. For instance, it helps us explain why deleterious recessive alleles are still found in human genomes, despite millions of years of evolution.

However, variation in most traits is more difficult to analyse because it is controlled by *multiple* genes (giving *polygenic* traits). This makes prediction of between-generation inheritance very difficult. Further, the environment can also alter the expression of traits; for instance, your height can clearly be affected by your diet! These two things lead to differences between individuals that are *quantitative.* Examples of quantitative differences occur in traits including weight, flowering time, and even genome size.

For polygenic traits it is impractical to consider the fate of individual variants of genes (alleles). However, we can consider how selection acts on the values of traits across populations as a whole. There can be stabilising selection (when both extreme values of a trait are selected against), directional selection (when trait values at one extreme have highest fitness) and disruptive selection (when intermediate values have both extremes are selectively favoured).

An American biologist, Sewall Wright (1889–1988), was an influential pioneer in identifying how multiple genes interact to produce specific phenotypes. Using a model system of guinea pigs, he realised that sometimes the combined effect of the alleles at two different loci was equal to the sum of these alleles' individual effects (the additive model). He was also struck by the many instances when the combined effect of the alleles at two different loci was either greater or less than the sum of the alleles' individual effects (known as epistasis).

Wright also developed a way of graphically representing a phenotype in relation to its fitness in the form of a *fitness landscape* or *adaptive topography*. You can investigate the concept of an adaptive topography at the following link:

http://www.blackwellpublishing.com/ridley/tutorials/Multi-locus_population_genetics25.asp

This concept has been used in many studies of evolution, but is particularly interesting when applied to an incredible long-term experiment on artificial evolution that is being conducted at Michigan University by Richard Lenski and colleagues. Have a browse around the website below and see if you can identify where adaptive topographies might be useful in understanding the process of evolution.

http://myxo.css.msu.edu/ecoli/index.html