**Hybridisation and Evolution**

For over a century, scientists have focused on natural selection as the driving force of evolution.  Darwin noted that just as important as selection is variation.  So where does all this variation come from?

Hybridization is the  interbreeding between animals or plants of different species that results in a novel offspring. Hybridization, though infrequent, is a powerful driver of evolution.With DNA sequencing technology, scientists are learning more and more about how variation comes about.  And one of the most important sources of variation is hybridization. Hybridization is the  interbreeding between animals or plants of different species that results in a novel offspring. Though infrequent, hybridization is a powerful driver of evolution. Famous hybrid animals include mules (horse/donkeys), zeedonks  (zebra/donkey), beefalo (bison/cow); liger (lion/tiger); killer bees (European bee and African bee.) **Hybrid plants include wheat (three wild grasses  ) and grapefruit (pomelo/orange).**

Hybridization may influence evolution in a variety of ways. If hybrids are less fit, the geographical range of ecologically divergent populations may be limited, and prezygotic reproductive isolation may be reinforced. If some hybrid genotypes are fitter than one or both parents, at least in some environments, then hybridization could make a positive contribution. Single alleles that are at an advantage in the alternative environment and genetic background will introgress readily, although such introgression may be hard to detect. 'Hybrid speciation', in which fit combinations of alleles are established, is more problematic; its likelihood depends on how divergent populations meet, and on the structure of epistasis. These issues are illustrated using Fisher's model of stabilizing selection on multiple traits, under which reproductive isolation evolves as a side-effect of adaptation in allopatry. This confirms a priori arguments that while recombinant hybrids are less fit on average, some gene combinations may be fitter than the parents, even in the parental environment. Fisher's model does predict heterosis in diploid F1s, asymmetric incompatibility in reciprocal backcrosses, and (when dominance is included) Haldane's Rule. However, heterosis arises only when traits are additive, whereas the latter two patterns require dominance. Moreover, because adaptation is via substitutions of small effect, Fisher's model does not generate the strong effects of single chromosome regions often observed in species crosses.