The Grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla - The French-Italian Public Consortium for Grapevine Genome Characterization

A first draft of the grapevine (*Vinus viterifa*) genome was completed in 2007 at a coverage of 8.4x. The genome was assembled using Arachne then a genetic map to determine linkage groups. The authors found large numbers of stilbene synthase, terpene synthase and monoterpene synthase genes within the grapevine genome. These genes encode products that are found in wine!

The authors searched for paralogous regions within the grapevine genome to determine whether paleopolyploidy may have occurred. They found groups of three paralogous regions - this suggested that an ancient hexaploidization event may have occurred. Next, the authors used the paralogous regions of chromosomes 6, 8 and 13 to search for similar regions in the published genomes of poplar, *Arabidopsis thaliana* and rice (*Oryza sativa*). They found that each segment of the grapevine used aligned with two within the popular genome, but the overall structure of each paralogous segment aligning to a separate mate was maintained. This suggested that poplar shared the same ancient hexaploidization event as grapevine, but additionally underwent a more recent whole genome duplication event. Next, the authors used the same protocol to align the regions of the grapevine genome to the *Arabidopsis* genome. Again, each region aligned to a separate mate, showing that the ancient hexaploidization event occurred before the lineages that gave rise to grapevine and thale cress diverged. Lastly, the authors compared the grapevine regions to the rice genome. They found that the paralogous regions mapped to one area, rather than finding separate mates. These findings suggest that an ancient hexaploidization occurred after Monocotyledons and Dicotyledons split, but before the lineages that gave rise to popular, thale cress and grapevine diverged.

Discussion Questions:

1. The authors compare the grapevine genome to the genomes of rice, poplar and *Arabidopsis*. Do you think making three comparisons is enough to come to this conclusion? Can the evidence be interpreted any other way?
2. The authors decided to sequence an individual from an inbred grapevine cultivar. Why did they do this?
3. After a polyploidy event, diploidization of the genome occurs. Genes are lost and chromosomal segments may be rearranged. Do you think that genome diploidization may obscure ancient polyploidy events?
4. Are there any other ways to look for ancient polyploidy events?

The population genomics of plant adaptation - Siol et al 2010

In this review, the authors describe current methods of analysis of the genomics of plant adaptation and investigate the potential pitfalls of these methods. They describe genome-wide methods that look for outlier loci that either show an excess or deficit in

variation compared to the rest of the genome. Another method of detecting selection relies on comparing synonymous mutations (proxy for neutral evolution) with non-synonymous mutations within the coding region of a gene. One assumption within this test is that the fraction of non-neutral non-synonymous mutations are highly deleterious. If they persist as a polymorphism, then this will be a source of error in the resulting estimate of selection. Bottlenecks or changes in population size can be common in plant species that are able to self or reproduce asexually. It is important to consider the many factors that influence effective population size because this influences genetic drift. Taking into account population size, structure and history is hugely important when attempting to detect signatures of selection to prevent false positives.

Discussion Questions:

1. The paper explains how important it is to think about population size, structure and history when designing an experiment to look for molecular evidence of selection. How do you think these factors would differ between plants and animals?
2. What do you think would be easier to detect, ancient or recent signatures of selection?
3. Do you think it would be more difficult to detect evidence of selection in a polyploid? Could you learn anything interesting by applying the MK test to paralogous genes within a polyploid?