**Pan-genomes and graphs: new ways to explore genetic variability within Lens spp.**

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Advances in sequencing technology have made it more affordable than ever to assemble high-quality genomes, and we have assembled at least one of every wild species within the genus Lens. However, even before the pan-genomics age, it was clear than a single reference genome was insufficient to represent an entire species, and that the new approaches and software currently being developed are required to fully examine the breadth of variation and make it accessible to geneticists and breeders. To avoid issues in computational time and complexity, we have applied different pan-genomic analyses to solve different problems within the breeding program. These include a gene-based graph to examine synteny, unique genes within each genome and duplications, as well as a full, de novo assembly-derived structural and SNP-level variation graph of two different species: *L. culinaris* and *L. orientalis*. This graph is being used to map reads in an interspecific MAGIC population as a means to reduce ascertainment bias caused by using a single reference. Finding that most graph viewing software has difficulties handling larger graphs, we have developed software to better understand some of the more complex regions of the graph and visualize them in detail. We have also examined 10x coverage PacBio HiFi of diverse lentil lines and compared de novo assembly and mapping approaches for making maximal use of high-quality, long read data.