**From pangenomes to traits – linking genome variation with phenotype variation**

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The ability to assemble genomes at low cost is revolutionising our understanding of biology. Sequencing multiple individuals has identified significant structural genomic variation within a species, with as many as 40% of genes being absent in some individuals. These differences limit the application of single genome references as they may not contain the genes associated with observed heritable traits. This has led to the growth of pangenomics, with pangenomes representing the genomic diversity of a species or higher taxonomic group rather than a single individual. It has been demonstrated that pangenomes capture more heritability for traits than single reference genomes.

Pangenomics is still in its infancy, new approaches for pangenome construction and analysis are being developed as long read DNA sequencing improves. Costs continue to reduce, permitting population level analysis. The analysis of pangenomes within and between species is providing a greater understanding of species diversity, evolution, adaption and supporting the acceleration of crop improvement.

Here I will present our findings from constructing and analysing pangenomes for several species and demonstrate how they can be applied to identify haplotypes in populations that confer favourable traits.