

Anthony Borneman
The Australian Wine Research Institute

Research Projects

Yeast comparative genomics

The yeast *Saccharomyces cerevisiae* is an important industrial microorganism with vital roles in the baking, brewing, biofuel, winemaking and pharmaceutical industries. The industrial scope of *S. cerevisiae* is directly attributable to its phenotypic plasticity, with each industry using distinct strains that have been selected for specific production requirements and limitations. As this phenotypic diversity is genetically determined, the comparative analysis of yeast genomes provides significant insight into how genomes evolve in response to specific selective pressures. This project will apply next-generation sequencing to obtain genome sequence information from industrial yeasts (both *S. cerevisiae* and other related species) that will be compared to obtain insight into the genetic characters that underlie the phenotypic differences that separate these strains.

Engineering flavour-active yeasts

While yeast is responsible for imparting many flavours and aromas during wine production, many compounds are derived from the grape, bacteria and oak that are used in the winemaking process. However, as the contribution of flavour compounds from these non-yeast sources can vary from season to season, we will engineer the complex biosynthetic pathways that allow for their formation into the yeast. This will enable wine yeast strains to produce these desirable compounds during the fermentation process and will allow for the precise control of wine flavour through the use of biologically-tailored yeast strains.

*Functional genomics of *Oenococcus oeni**

Oenococcus oeni is the bacterium responsible for the malolactic fermentation that occurs in some wines. This bacterium has several characteristics that make it particularly suitable for comparative genomics studies. Genome sequencing and comparative genomics performed by our lab and others around the world have shown that *O. oeni* has a small, but highly variable genome, with many strains carrying novel genomic cassettes which may impart desirable phenotypic characters to these strains. We will apply whole-genome functional genomic techniques to study the phenotypic and genotypic differences that are present in *O. oeni* to identify the genomic loci that are responsible for regulating key phenotypic characters.