

Presentation title: Systems Biology: a new paradigm for wine yeast strain development

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Abstract

Microbial strain development for industrial applications has benefited enormously from technological advances. For example, genetic engineering techniques and the ability to transform organisms with extraneous DNA paved the way for great advances in metabolic engineering of yeast and bacteria for pharmaceutical production. The next wave of new technologies, so-called 'omics' approaches, combined with the capacity to store and interrogate massive data sets, is poised to drive the next major shift in microbial strain development, particularly if integrated into a Systems Biology framework.

One approach to Systems Biology is to integrate datasets from different levels of 'omics' investigations to construct predictive models of complex biological systems. This can be achieved using informatics and mathematical tools to interrogate and iteratively refine accumulating knowledge bases for model organisms. Over recent years laboratory strains of the baking, brewing and winemaking yeast *Saccharomyces cerevisiae* have, for many scientists, been the organisms of choice to establish methodologies for Systems Biology. Thus, substantial groundwork is in place and can be built upon for research on industrial yeast and development of novel strains with improved, industrially relevant, phenotypes.

While most industrial yeasts are the same species as the laboratory strains used in pioneering Systems Biology work, they are unique in many features, including robustness and 'productivity'; traits that are critical for industrial applications. There are also differences in the production of secondary metabolites, which are essential for the sensory properties of wines and beers; in fact laboratory strains cannot make wine or beer. Consistent with this variation in phenotypes recent comparative genomics studies (Borneman *et al.*, 2008; *FEMS Yeast Research* 8:1185-1195; Borneman *et al.*, 2011; *PLoS Genetics* 7:pp.e1001287) performed at The Australian Wine Research Institute (AWRI) found that there is considerable intraspecific genetic variation between laboratory and industrial strains, and between strains used in different industries. From a wine R&D perspective, therefore, it is important to develop research models that use industrially relevant strains.

With this in mind, the AWRI in collaboration with Genomics Australia, Proteomics Australia, Metabolomics Australia, and Bioinformatics Australia, has embarked on a Systems Biology project that focuses on wine yeast fermentation. The aim of this project is to harness the expertise, infrastructure and technologies available across 'omics' platforms in Australia to develop systems-based mathematical models of yeast metabolism. These models will, in turn, be used to develop predictive models to inform design of new strains with improved, wine relevant, traits.