



Construction of a Wine Yeast Genome Deletion Library (WYGDL)

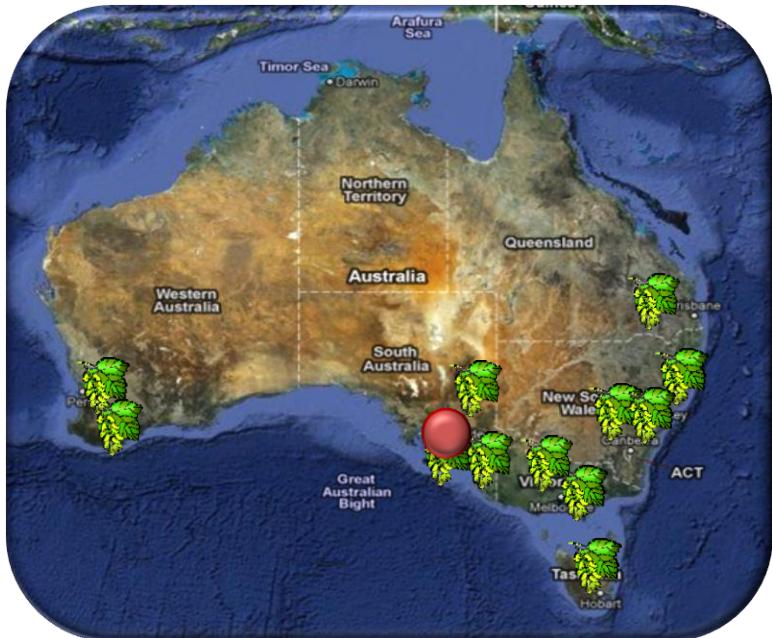
Tina Tran, Angus Forgan,
Eveline Bartowsky and Anthony Borneman



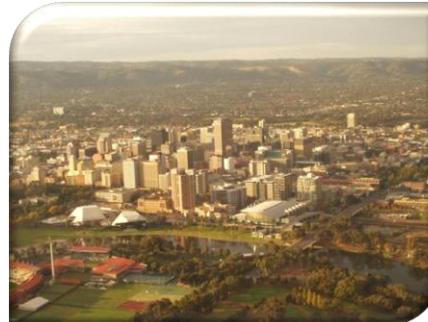
Australian Wine Industry



The Australian Wine Research Institute



- ❖ Australia has about 60 wine regions.
- ❖ 170,000 hectares under vine
- ❖ Australia was ranked 6th in the list of world wine producers in 2005 producing 1.4 billion L of wine
- ❖ Australia is the 4th largest exporter after France, Italy and Spain.
- ❖ Our wines are drunk in more than 100 countries



AWRI

Established
26th April 1955



Location
Adelaide,
Waite campus



Main funding
Australian
Grapegrowers +
Winemakers
& Australian Gov

Research
Microbiology
Chemistry
Sensory



What is a WYGDL?

- ❖ In winemaking *Saccharomyces cerevisiae* is the species of yeast most commonly used for fermentation.
- ❖ *S. cerevisiae* has about 5000 genes.
- ❖ We are creating a collection of strains derived from a single *S. cerevisiae* wine strain, in which each strain has a different, single gene deleted.
- ❖ Eventually we will have a collection of up to 5000 strains (1 per gene).
- ❖ In collaboration with Charlie Boone's lab (University of Toronto).



What is a deletion library good for?



The Australian Wine
Research Institute



AWRI

- ❖ At the AWRI we are interested in understanding the basis of wine characteristics (flavour, aroma etc) and fermentation processes (robust, predictable etc).

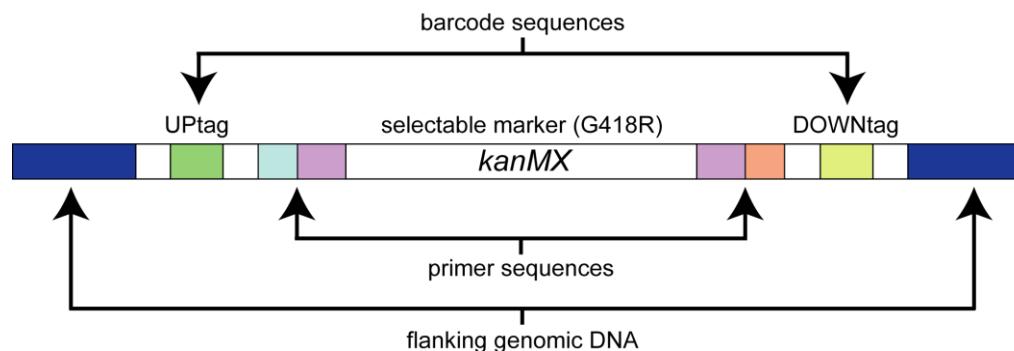
The Deletion Library

- ❖ Provides a collection of mutant yeast strains.
 - No need to do gene knockouts, simply go to the library
- ❖ Mutant screens.
 - No need to do mutagenesis, all the mutants are there with tags to aid in their identification
- ❖ Enables parallel screening using the barcode sequences.



Laboratory Strain Deletion Library

- ❖ A Genome Deletion Library is already available in a laboratory strain of *S. cerevisiae*, S288c.
- ❖ It was created by a consortium of 13 labs over several years from 1997-2002.
- ❖ 96% of all ORFs >100 codons deleted
 - Replaced with kanMX marker gene
 - Two unique 20 bp “barcodes”



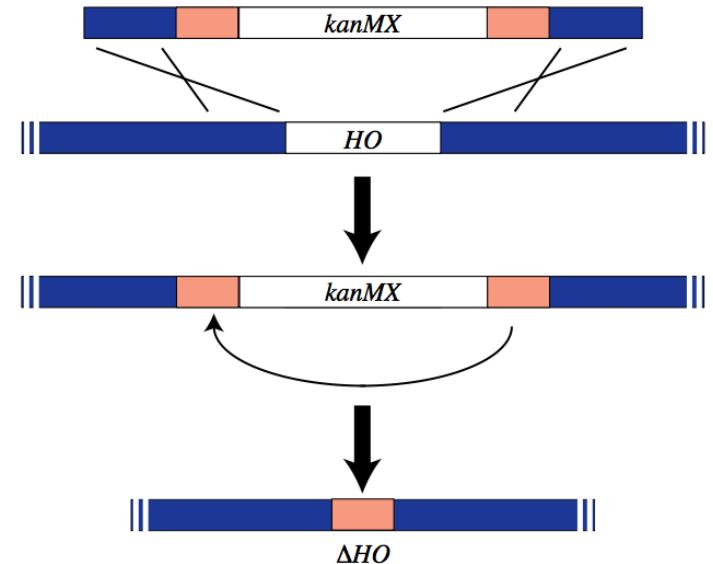


Why make a deletion library in a wine yeast?

- ❖ The lab strain yeast performs poorly under winemaking conditions.
- ❖ To more fully understand the contribution of yeast genetics to flavour, aroma and grape-juice fermentation characteristics we require a strain that is suitable for both molecular biology and winemaking.
 - Haploid, stable genome
 - Reliable fermentation performance without the production of off-flavours
- ❖ We selected a wine strain (N96) from our collection.
- ❖ N96 is a robust fermenter with neutral sensory characteristics.

Preparing the wine strain

- ❖ Most wine-yeast strains, including N96, are diploid.
- ❖ Haploid yeasts revert to a diploid state via mating type switching followed by mating between opposite mating types.
- ❖ *HO* gene is a key requirement for mating type switching
- ❖ *HO* was therefore deleted from the N96 diploid progeny using *HO::kanMX* from Walker et al., 2003





Sensory comparisons

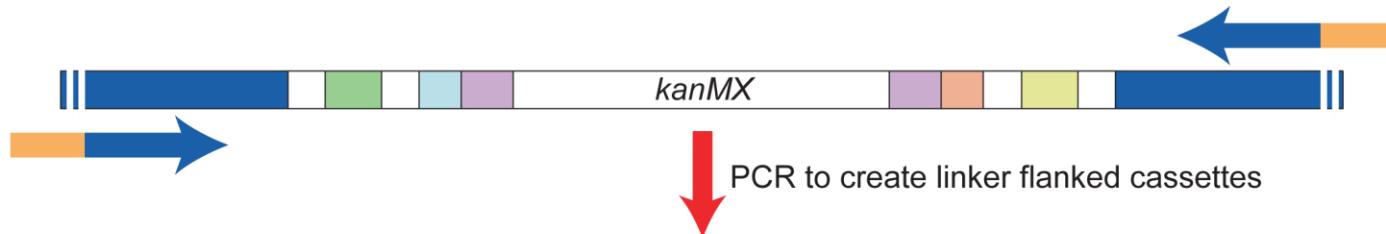
- ❖ We obtained several haploid progeny which displayed fermentation rates and metabolite profiles (glycerol, acetic acid, ethanol) which were comparable to the diploid parent.
- ❖ Sensory trials determined that the haploids produced wine with similar characteristics to the diploid parent.
- ❖ We selected one AWRI1631 to use as the deletion library strain.



Introducing barcoded deletions into *S. cerevisiae*



The Australian Wine
Research Institute





The Australian Wine
Research Institute

Transformation and confirmation

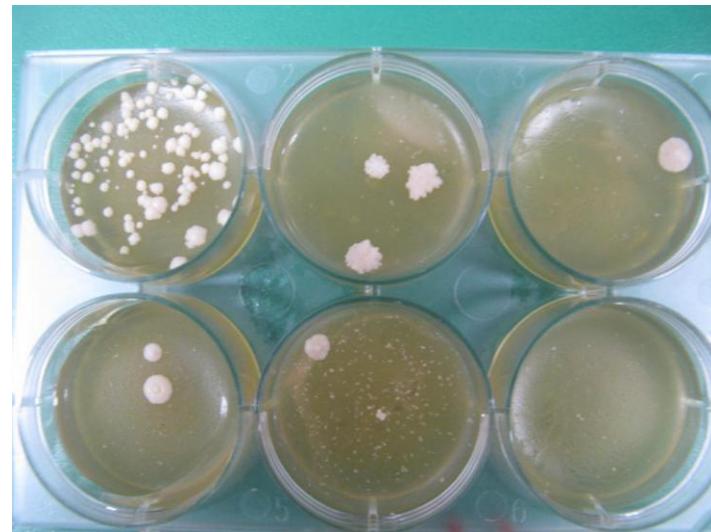
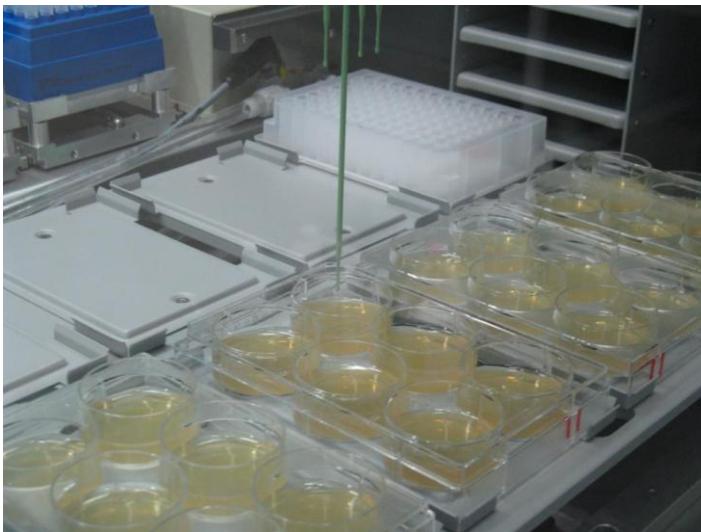
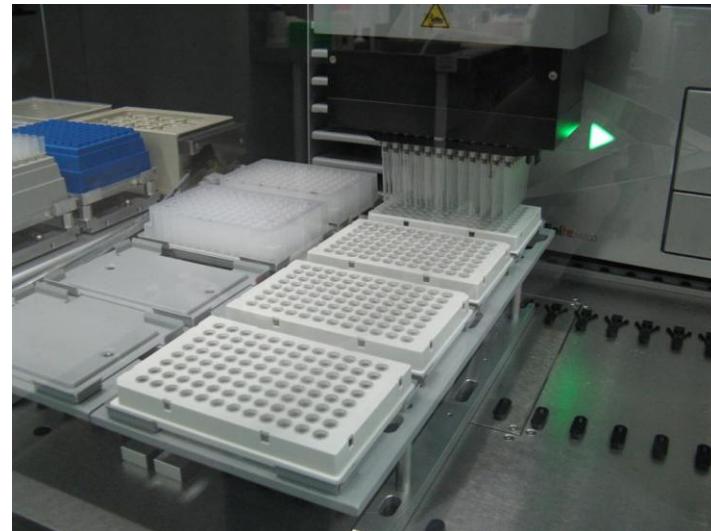
- ❖ Transformations are underway using a standard heat shock transformation protocol.
- ❖ Strains are selected on YPG agar + G418





Transformation using the Robot

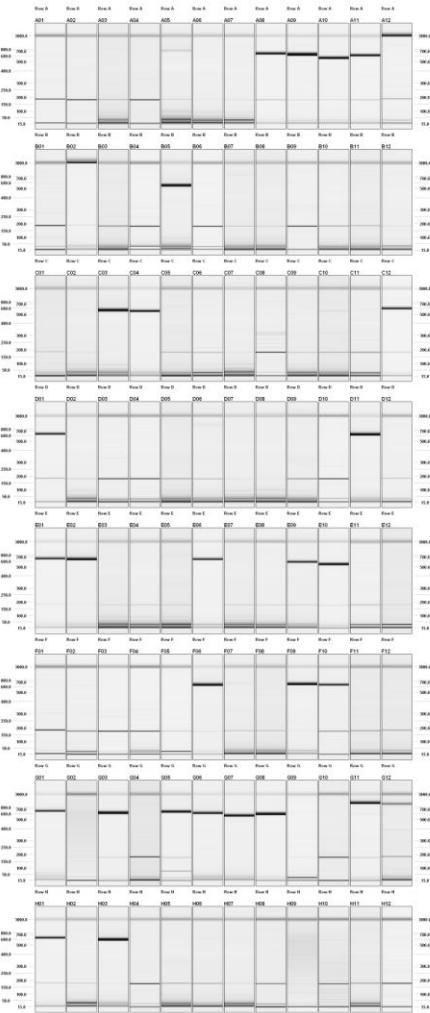
- ❖ We are now using a robotic liquid handling system to assist with transformations and for high throughput screening





Confirmation of deletion constructs

- ❖ Insertion of the deletion cassette at the correct location is confirmed by PCR.
- ❖ We have >2000 confirmed deletion strains.



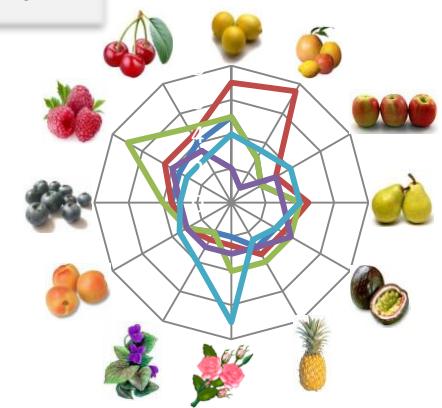
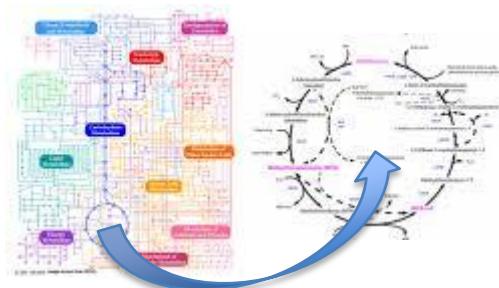
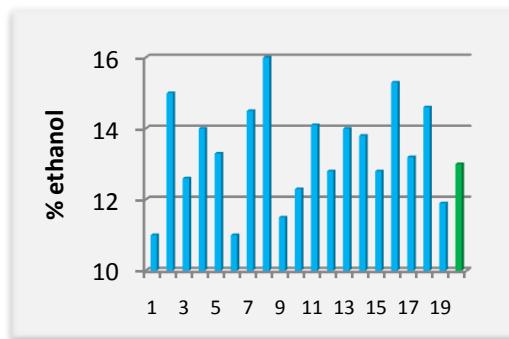
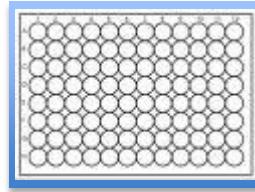
What are we doing with the deletion strains?

Understanding the *S. cerevisiae* genome

- ❖ 96 well master plates for screening
 - ‘live’ cultures
 - DNA

- ❖ *Saccharomyces cerevisiae*
 - Grape fermentation parameters
 - Alcohol %
 - Rate of fermentation
 - Aroma & flavour profiles

 - Genetics
 - Function of gene(s)





In conclusion ...

- ❖ Constructed a deletion library in a winemaking *S. cerevisiae* strain
 - AWRI1631 (haploid)



- ❖ > 2000 single gene deletion strains



- ❖ Robotic high throughput screening developed



- ❖ Next ...

- Screening for fermentation ↑ & ↓
- Aroma & flavour characteristics
- Specific gene function





The Australian Wine
Research Institute

Acknowledgements



Tina Tran



Angus Forgan



Anthony Borneman

This project is supported by Australia's Grapegrowers and winemakers through their investment agency the Grape and Wine Research and Development Corporation, with matching funds from the Australian Government.