

## Contribution of the interaction between environment and genotype to flavour and aroma in *Saccharomyces uvarum*

Angela Maria Coral Medina<sup>1,2</sup>, Carole Camarasa<sup>2</sup> & John Morrissey<sup>1</sup> <sup>1</sup>Microbiology Department, University College Cork, Ireland; <sup>2</sup>INRA, SupAgro, Universite de Montpellier, France



FIG 2 Maximum specific growth rates of S. uvarum MTF3098 and S. cerevisiae Cen.PK133-7D in five different nitrogen sources.

## Developing fermentation conditions for comparative transcriptome analysis



**FIG 5** Fermentation progress Vs time for fermentations done with *S. uvarum MTF3098* in MM during 48 hours. Mean values were calculated from duplicates.

RNASeq - Analysis of the expression of genes involved in:

Time required by the strain to reach 0.3 fermentation progress, where the cell physiology is the same in the four nitrogen sources. Cultures in the same stages of growth allow meaningful comparison between the nitrogen conditions.

y ch the sthe s. ame d d ons. + the Phenol Fermentations -Conclusions

> We determined the nitrogen preference of *S. uvarum* and compare it with *S. cerevisiae*. Moreover, we developed fermentation conditions for

**FIG 3** Growth and consumption of Nitrogen of *S. uvarum MTF3098* in Synthetic Must during 48 hours. Mean values were calculated from duplicates.

Nitrogen preference of *S. uvarum* in synthetic wine showed a similar pattern to minimal medium. Moreover, the highest biomass formation and the fastest nitrogen consumption was observed in MS200 medium, that mimics a typical grape juice (18 amino acids and ammonium chloride). Figure 4 shows the consumption of all the nitrogen compounds in MS200 over time, allowing to discriminate the amino acids according to their order of uptake.



**FIG 4** Consumption of ammonium and amino acids by *S. uvarum MTF3098* during 48 hours of fermentation in Synthetic Must (MS200).







• the Ehrlich pathway



