Abstract

Evaluating cell wall properties and mannoprotein content in laboratory and industrial wine yeast strains using mid- and near-infrared spectroscopies

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Introduction

Wine yeast, in addition to being responsible for primary alcoholic fermentation, is also able to impart other characteristics to wine (i.e. aroma and mouthfeel). Several yeast phenotypes that are relevant for fermentation, wine processing and wine quality (i.e. yeast adhesion phenotypes) have been correlated with altered cell wall properties (i.e. mannoprotein content and release). We wished to develop a rapid method for assessing cell wall and mannoprotein content of different yeast species and strains, as this would facilitate (1) the effective screening of new yeast strains for potential use by the wine industry and (2) the investigation of molecular mechanisms.

Materials and Methods

A total of 36 yeast strains were used, including non-*Saccaromyces* species (e.g. *Dekkera* sp., *Schizosaccharomyces* sp.), laboratory strains (e.g. W303), industrial strains (e.g. VIN13 and BM45) and genetically-modified strains (e.g. *gas1* mutant). Wet biomass and alcohol insoluble residues were prepared for analysis. Samples were scanned using a Nexus 670 Fourier Transform mid-infrared (FT-MIR) instrument. The spectral region (600–4000 cm^{-1}) was subdivided into six windows to facilitate data analysis. In addition, near infrared (NIR) spectra were acquired on a Bruker multi-purpose NIR analyser between 830 and 2500 nm. The first and second derivatives were extracted after smoothing with a 5 point Savitzky-Golay filter. PCA analysis of the data was performed using The Unscrambler (version 9.2; Camo Ltd., Trondheim, Norway) using cross-validation.

Results and Discussion

PCA analysis of FT-MIR data from the 36 yeast strains revealed distinct groupings: non-*Saccharomyces* strains were clearly separated from *Saccharomyces* species. Further inspection of the *Saccharomyces* groupings showed that some of the genetically-modified strains (specifically altered for cell wall composition) were distinct from the main group of industrial and laboratory species. It was determined that two spectral regions were responsible for the bulk of the separation using PCA. Spectral windows 2 (1768–1478 cm^{-1}) and 5 (1185–937 cm^{-1}) corresponding to amide bands (and some mannans) and β-glucans were driving the separation. FT-NIR data of the 36 strains revealed a similar separation using PCA but these data were not as easily correlated with specific cell wall polymers as FT-MIR data.

Conclusion

Both FT-MIR and FT-NIR spectroscopy in combination with multivariate analysis are potentially useful methods for rapidly assessing cell wall and mannoprotein content of yeast species and strains.

Reference paper as:
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