Genetic diversity of *Oenococcus oeni* reveals the industrial implications of strains used in malolactic fermentation

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Background

Expanding the understanding of strain-dependent genetic variations in the genome of *O. oeni* is important for realising its full potential in industrial fermentation processes. Whole genome comparison was performed on 191 commercial and environmental isolates of *O. oeni* from Australia, Europe, North and South America and the Middle East. From this rich source of genetic information, statistical and computational approaches were employed to identify highly variable regions of its genome which confer substantial differences in amino acid biosynthesis, natural competence, sugar utilisation, diacetyl accumulation and tolerance to low pH and high ethanol stress conditions. Compilation of this vast amount of genomic information can be used to inform research by allowing the identification of strains with combinations of desirable genotypic, and therefore phenotypic, characteristics.

Methods used

- Genome sequencing and alignment
- Development of computational tools to align and rapidly compare genomic sequences across large numbers of bacterial strains
- Statistical methodologies to identify genetic markers associated with industrially relevant traits

![Diagram](image)

**A**: Genetic relatedness of 191 *O. oeni* strains isolated from various regions, dates and wine varietals. **B**: Phenotypic measurements of tolerance to high ethanol and low pH stress. The numbers represent the fold increase in time to complete MLF under stress. The most stress-tolerant strains are coloured in green, followed by yellow and then red represents the most sensitive of strains. **C**: Metabolic pathways and cellular processes which are affected by the presence/absence of genes in highly variable genomic regions. A coloured box represents the presence of a full-length gene or complete pathway of genes. **D**: Highly variable genomic regions in *O. oeni* strains, the presence of which are coloured in blue. Highly variable genomic regions are one of the defining characteristics of bacterial strains. Statistical and computational methods identified genes and genomic regions present in less than 75% of the population. Computational analysis revealed that these highly variable genomic regions contain genes that contribute to several important industrial traits, such as resistance to stress.

**Results**

- Computational and statistical methods identified many genomic regions which were highly variable within the strain population.
- These regions were found to confer important differences in amino acid utilisation, sugar utilisation, natural competence, stress tolerance and diacetyl accumulation.
- Genes and genomic regions identified as genetic markers were used to predict robust *O. oeni* strains for evaluation at lab-, pilot- and winery-scale MLF trials.
- A potential genetic determinant of high diacetyl concentration in wine was identified.

**Conclusions**

- *O. oeni* strains often have exacting nutritional and environmental requirements, elevating the risk of sluggish or stuck fermentations.
- Comprehensive compilation and characterisation of *O. oeni*'s genetics enables identification of strains containing the required combinations of genetic attributes for optimal MLF.

**Reference**