Influence of Oenococcus oeni and Brettanomyces bruxellensis on Wine Microbial Taxonomic and Functional Potential Profiles

The interactions between lactic acid bacteria, yeast, and other wine microbiota impact on wine quality. Some strains of lactic acid bacteria Oenococcus oeni possess cinnamoyl esterase activity that releases hydroxycinnamic acids (HCAs) that can subsequently be processed by some strains of the spoilage yeast Brettanomyces bruxellensis and lead to off-flavor compounds. Using metagenomic analyses, this study investigated the influence of O. oeni and B. bruxellensis on the taxonomic and functional potential profiles of the microbial community of Cabernet Sauvignon wine, particularly regarding flavor formation. Metagenomic datasets were generated from inoculations of three strains of B. bruxellensis, in combination with two O. oeni strains, with and without cinnamoyl esterase activity. Effect on the microbial profiles was found to depend on the O. oeni and B. bruxellensis strains being combined and on the abundance that the inoculants reach in the final wine, which depends on unidentified conditions (e.g., derived from microbial interactions). This study confirmed that the potential of B. bruxellensis to produce off-flavor compounds from HCAs is strain dependent. Interestingly, the samples without microbial inoculants also had this potential, suggesting that microbiota from the native grape could also influence the levels of HCAs. The metagenomic analyses complemented by experimental validation also found that the presence of B. bruxellensis did not interfere with the microbial functional potential to transform L-malic acid into L-lactic acid, which typically leads to a less acidic flavor. We show that metagenomic approaches can help uncover the complex wine microbial community traits, such as flavor, impacted by the simultaneous presence of O. oeni and B. bruxellensis.

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