



## The wine microbial consortium: A real terroir characteristic

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In this paper the authors demonstrate significant microbial differences between 4 estates (or chateaux) in the Bordeaux area.

- The authors compare the microorganism population on the grapes at harvest of 4 estates, one in Graves (A), two in Libournais (B, C), and one in Medoc (D). Then, for important microbial genera (*Saccharomyces cerevisiae*, *Brettanomyces bruxellensis*, *Oenococcus oeni*), they go a step further and do the same comparisons at the strain level. Their goal is to determine whether the microbial “consortium” of a vineyard is unique enough to be considered a “terroir” characteristic. [In the original French article, the authors use the word “consortium” –maintained in the English translation- in the sense of “population”].
- To identify the different yeasts and bacteria, at both the genus and the strain level, the authors combined classical plating to enumerate microbes growing on specific selective media, with modern molecular tools, such as *PCR-RFLP* (multiplication through Polymerase Chain Reaction, followed by separation through Restriction Fragment Length Polymorphisms) and *PCR-DGGE* (Polymerase Chain Reaction, followed by Denaturing Gradient Gel Electrophoresis).
- **Effect of estate.** Geographical location was shown to be very important in determining the species of yeast and bacteria present. Regarding yeast, while 2 yeast species (*Rhodotorula graminis* and *Pichia anomala*) were present in the vineyards of all 4 estates, others (*Bulleromyces albus*, *Metschnikowia fructicola*, and *Candida cantarelli*) were present only in some estates. As for the bacteria, the same pattern was true. While two bacteria species considered crucial in the berry community (*Gluconobacter oxidans* and *Burkholderia vietnamiensis*) were present in all estates, a third species (*Pediococcus parvulus*) was present in only 2 of the 4 estates. The presence of specific berry flora able to persist in the wine (some do not persist; for instance, *Rhodotorula graminis* and *Bulleromyces albus* do not seem to survive in the wine), can have a significant effect at the beginning of the fermentation, and therefore on final wine quality.
- **Effect of vintage.** When the authors looked at 3 consecutive vintages, they also noticed significant differences in the total population size of yeast and bacteria. Chateau C (Libournais) always had the lowest yeast and bacteria populations, whereas Chateau D (Medoc) had the highest yeast populations all 3 years.
- **Effect of winemaking stage.** The authors evaluated the diversity at the strain level of 1) *Saccharomyces cerevisiae*, 2) *Brettanomyces bruxellensis* and 3) *Oenococcus oeni* in the different cellars at different stages in the winemaking process. The survival of *S. cerevisiae* and *O. oeni* in wine at different stages was clearly strain-specific.

- 1) Concerning the indigenous strains of *Saccharomyces* in the different cellars, there was no strain common to all of them, each owning its specific pool of *S. cerevisiae* able to perform the alcoholic fermentation. Even when yeast starters were used (as was the case for estates A, B, and D), the cellar environment still had a significant effect. In some cases, a specific yeast profile could be tracked all the way to the bottle. (The authors do not go into details about winemaking practices, such as filtration, at the different estates).

- 2) *Brettanomyces*. The strain discrimination of *Brettanomyces* is important because this is one of the most feared yeasts in wineries, responsible for the formation of volatile phenols (such as the infamous barnyard/band aid “Brett” aroma). The authors found that each estate had its specific *B. bruxellensis* strain, and this remained true in all 3 consecutive vintages. Since strains vary in the amount of volatile phenols they produce, this would mean that some cellars would be more prone than others to have a “Brett” problem in their wines.

- 3) *Oenococcus*. The authors focused on *Oenococcus* due to its important role in malolactic fermentation (MLF). They found that the main strain conducting the MLF was specific to each cellar. The levels of other lactic acid bacteria (LAB) populations were also specific to each cellar, and strongly dependent on the type of winemaking practices, particularly the levels of SO<sub>2</sub>, fining, and filtration.

So, in summary, the microbial population of a winery tends to be unique, and a result of the combination of the vineyard indigenous flora, and the winemaking practices in the cellar. In the case of important protagonists, such as *S. cerevisiae* and *O. oeni*, the main fermenting strains are specific, and a constant, in each cellar. As for *B. bruxellensis*, the levels of volatile phenols produced are also likely strain-dependent, with some cellars being more prone to an obvious “Brett” problem than others. To the authors, these indigenous populations play an important role in a wine’s “terroir” characteristics.

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