

# Wild Yeasts in Winemaking: Exploitation for potential new products

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This study aims to explore the indigenous microbiota driving wild wine fermentation in Catas Altas, Brazil, and assess its potential in co-culture with Palermo isolates for wine production. The scarcity of information regarding the microbiota of wild wines in Catas Altas offers a unique opportunity to delve into an unexplored microbial microcosm influenced by diverse climatic and geographical conditions. In a competitive landscape within the wine industry, consumers continuously seek authentic and innovative experiences. Our research into the co-culture of indigenous yeasts from various origins promises to impart wines with truly distinct and innovative aromatic profiles and flavors. We isolated unique yeast colonies from five samples of wild wine in Catas Altas, identified as G-01 LU1, G-01 LU2, G-02 MU1, G-02 MU2, H-03 AU1, and H-03 AU2. Strains LU1 and LU2 exhibit elliptical morphologies with budding, resembling the *Saccharomyces* spp. genus. On the other hand, strains MU1, MU2, and AU1 display rod-shaped cells with limited budding, while strain AU2 is smaller and features cyclic-shaped cells. Stress tolerance tests revealed distinct responses among the strains. In the osmotolerance test, concentrations of 30%, 35%, 40%, and 50% (w/v) glucose were used. In the ethanol tolerance test, concentrations of 8%, 12%, 14%, 16%, and 18% (v/v) ethanol were employed. In the sulfite tolerance test, concentrations of 100 mg/L, 150 mg/L, and 200 mg/L sodium metabisulfite were utilized. Most samples displayed satisfactory growth rates with glucose concentrations ranging from 30% to 50%. Samples H-03 AU1 and H-03 AU2 exhibited unique behavior, indicating greater resistance to lower glucose levels. In the ethanol tolerance test, strains LU1 and LU2 showed linear growth at concentrations of 8% and 18% ethanol, while strains H-03 AU1 and H-03 AU2 demonstrated low ethanol tolerance. In the sulfite tolerance test, all samples exhibited a reduction in cell density with increasing concentrations of sodium metabisulfite, except for strains JP14 and AU1, which displayed atypical behaviors. In summary, based on the results obtained from the microbial stress tests, using JP14 as a reference commercial yeast, we can infer that strains LU1, LU2, and AU1 likely belong to the *Saccharomyces* spp. genus. Conversely, the yeasts associated with codes MU1, MU2, and AU2 are related to unconventional yeasts, and future phylogenetic analyses will be conducted to deepen our understanding of their characteristics.

**Keywords:** Vinicultural Microbiome, Terroir-Driven Fermentation, Microbial Biodiversity in Winemaking.

## Please provide the Portuguese version of the title (mini-versão em Português)

Esta pesquisa investiga a microbiota endógena envolvida na fermentação de vinhos selvagens em Catas Altas, Brasil, avaliando seu potencial em co-cultura com isolados de Palermo, Itália, para a produção de vinho. Observamos diferenças morfológicas entre as colônias isoladas a partir de cinco vinhos selvagens. Essas cepas serão identificadas e testadas quanto à sua resistência a estresses e potencial fermentativo, para então serem usadas em co-cultura com isolados de vinhos selvagens de Palermo. Buscamos desvendar o potencial dos microrganismos endógenos, promovendo avanços na produção de vinho regional e internacional

**Palavras-chave:** Microbiota Vitivinícola, Fermentação Terroir, Biodiversidade Microbiana; Produção de Vinhos selvagens

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