Comparative proteome analysis of *Brettanomyces bruxellensis* under hydroxycinnamic acid growth

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**Abstract**

**Background**

*Brettanomyces* bruxellensis is an important spoilage yeast in the winemaking process. The capacity of this yeast to generate an undesired off-flavor constitutes a significant loss in the Chilean wine industry.

**Results**

The proteomic profile of *B. bruxellensis* in the presence of *p*-coumaric acid was determined by 2D gel electrophoresis, gel image analysis and differential spot selection. A set of 41 proteins showed a differential accumulation of ±2 and a *p*-value ≤ 0.0001. The homology sequence analysis was performed using the databases available. Differential proteins belonged to the categories of ‘energy production and conversion’ and ‘amino acid transport and metabolism’.

**Conclusions**

The proteomic profile of *B. bruxellensis* cultivated in the presence of *p*-coumaric acid in synthetic wine, agrees with the hypothesis of metabolic flux regulation, allowing a better conditioning to an adverse environment. This study involved the translational level of *B. bruxellensis* in the production of ethylphenols and corroborated that this yeast presented an advantage in these stress conditions. Thus, this work will allow an understanding of the regulation and processes involved in the production of ethyl-derivate compounds by *B. bruxellensis*. Furthermore, it allows the development of newer and better techniques for spoilage yeast control.