Genomics Perspectives on Metabolism, Survival Strategies, and Biotechnological Applications of Brettanomyces bruxellensis LAMAP2480

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Abstract

Wine production is an important commercial issue for the liquor industry. The global production was estimated at 275.7 million hectoliters in 2015. The loss of wine production due to Brettanomyces bruxellensis contamination is currently a problem. This yeast causes a "horse sweat" flavor in wine, which is an undesired organoleptic attribute. To date, 6 B. bruxellensis annotated genome sequences are available (LAMAP2480, AWRI1499, AWRI1608, AWRI1613, ST05.12/22, and CBS2499), and whole genome comparisons between strains are limited. In this article, we reassembled and reannotated the genome of B. bruxellensis LAMAP2480, obtaining a 27-Mb assembly with 5.5 kb of N50. In addition, the genome of B. bruxellensis LAMAP2480 was analyzed in the context of spoilage yeast and potential as a biotechnological tool. In addition, we carried out an exploratory transcriptomic analysis of this strain grown in synthetic wine. Several genes related to stress tolerance, micronutrient acquisition, ethanol production, and lignocellulose assimilation were found. In conclusion, the analysis of the genome of B. bruxellensis LAMAP2480 reaffirms the biotechnological potential of this strain. This research represents an interesting platform for the study of the spoilage yeast B. bruxellensis.