



Genome and fermentation analyses of *Enterococcus faecalis* DB-5 isolated from Japanese Mandarin orange: An assessment of potential application in lactic acid production

Daisuke Fukuda ¹✉, Yuji Aso ²✉, Cirilo Nolasco-Hipólito ³ ✉

Show more

Share Cite

<https://doi.org/10.1016/j.jbiosc.2023.04.003>

[Get rights and content](#)

Enterococcus faecalis strain DB-5 is a lactic acid bacterium newly isolated from the Japanese mandarin orange (mikan). The DB-5 strain produces organic acid from various carbohydrate sources including glycerol and starch. To gain deeper insights into its potential application in lactic acid fermentation (LAF), the genome and fermentation analyses of *E. faecalis* DB-5 were performed. Whole genome sequencing was carried out using the DNBSEQ platform. After trimming and assembly, the total size of the assembled genome was revealed to be 3,048,630 bp, distributed into 63 contigs with an N_{50} value of 203,673. The genome has 37.2% GC content, 2928 coding DNA sequences, and 54 putative RNA genes. The DB-5 strain harbored two L-lactate dehydrogenases (L-LDHs), both of which conserved the catalytic domain sequences. The optical purity measurement showed that strain DB-5 is homofermentative and produced only L-lactic acid (LA), which correlated with genome-based pathway analysis. To confirm its LA productivity at high temperatures, open repeated batch fermentation was performed at 45 °C using sucrose as a carbon source. The volumetric LA productivity of DB-5 was averaged at 3.66 gL⁻¹ h⁻¹ for 24h during the 3rd to 11th fermentation cycles. *E. faecalis* DB-5 could efficiently convert around 94% of sucrose to LA throughout the fermentation cycles at 45 °C. These genomic characteristics and fermentation properties of *E. faecalis* DB-5 provide beneficial information for a deeper understanding of the functional properties of future high-temperature LAFs from biomass resources.
