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Kinetic model evaluation of ethanol fermentation from lactose

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Key words

ethanol fermentation of lactose, recombinant *Saccharomyces cerevisiae*, kinetic model,
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This work presents a multi-route, nonstructural kinetic model for characterization of ethanol fermentation of lactose using a recombinant flocculent *Saccharomyces cerevisiae* strain expressing both the *LAC4* (coding for β -galactosidase) and *LAC12* (coding for lactose permease) genes of *Kluyveromyces lactis*. In this model, the values of different metabolic pathways are calculated applying a modified Monod equation rate in which the growth rate is proportional to the concentration of a key enzyme controlling the single metabolic pathway. In this study, three main metabolic routes for *S. cerevisiae* are considered: oxidation of lactose, reduction of lactose (producing ethanol) and oxidation of ethanol.

The main bioprocess variables determined experimentally were lactose, ethanol, biomass and dissolved oxygen concentrations. Parameters of the proposed kinetic model were established by fitting the experimental data obtained in a small lab-scale fermentor with the initial lactose concentrations ranging from 5 g dm⁻³ to 50 g dm⁻³. A very good agreement between experimental data and simulated profiles of the main variables (lactose, ethanol, biomass and dissolved oxygen concentrations) was achieved.

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