Modelling the production of VFA from proteins by mixed culture fermentations

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Abstract: Mixed-culture fermentations (MCF) are recognised as a valid process to yield added-value products from organic wastes in the form of volatile fatty acids (VFA). The use of mixed cultures is attractive due to their economical and operational advantages (e.g. no sterilisation is needed). However, they also pose a fundamental challenge: they are complex and their regulation mechanisms remain still unclear. One of the main limitations of the process is its low product selectivity: the productivity of the different VFA is highly dependant on operational conditions (e.g. pH, retention time or feeding characteristics). In consequence, developing bioprocesses based on this technology remains a challenging task. In this context, we aim at establishing a model-based methodology for developing novel bioprocess using MCF. The emphasis is placed on two aspects: to reach a high productivity and a high selectivity on the desired VFA(s). The improvement of selectivity is carried out by means of a metabolic energy-based model while the productivity is maximised using a general kinetic-based model.

Metabolic energy-based models assume that in energy-constrained environments, such as anaerobic fermentations, microorganisms produce those products associated with a higher ATP yield. This kind of models has been proven to predict the VFA conversion stoichiometry of carbohydrate MCF and mechanistically explain the effect of pH on the product spectrum (González-Cabaleiro et al., 2015). However, protein MCF has not been tackled yet from a modelling point of view, which impedes the design of processes using interesting protein-rich agro-industrial wastes (e.g. cheese way or canning industry wastewater). in this work we develop a metabolic model for the production of VFA from proteins in MCF following the methodology of González-Cabaleiro et al. (2015).

The conversion of 17 amino acids is simulated at different pH and retention time values. The model is capable of reproducing satisfactorily the product spectrum of gelatine MCF experimental data as well as the changes on the VFA yields with pH. The model offers for the first time mechanistic insight on the interactions among the different amino acids and on the pH effect on the product spectrum. This information can be exploited as we can now foresee how the pH value or the protein composition on amino acids affects the product spectrum and therefore direct the process towards one of more VFAs. This model will be the core of a tool for the early stage design of protein MCF ensuring a high selectivity on the desired VFA(s) (Fig. 1).

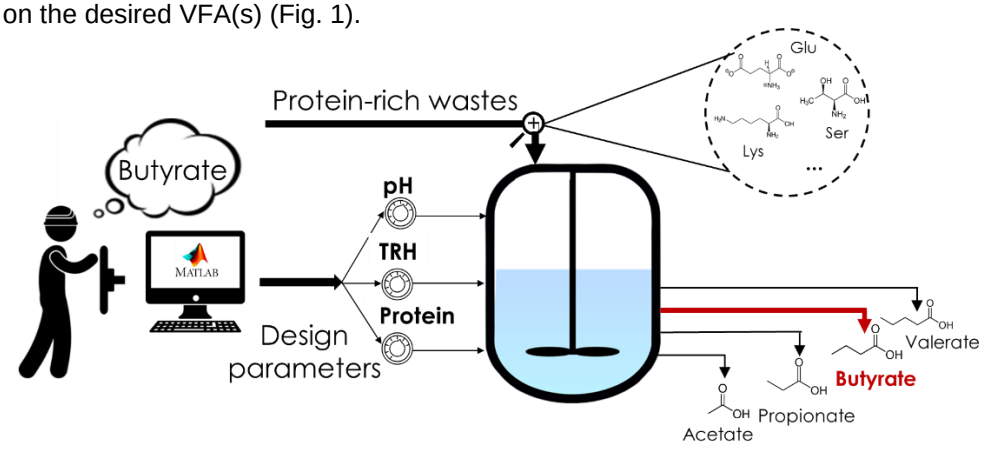

Fig. 1. Design parameters are selected with the metabolic model to maximise the targeted VFA production

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References

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