

Team member: H. Quitmann, B. Landwehr, F. Winkler, S. M. Pötsch and L. Salinas Tejedor
Supervisor: Prof. Dr. An-Ping Zeng
Project term: 2006 – 2010
Financed by: Hamburg University of Technology



Description:

Rapid sampling and proper sample processing are critical steps for microbial metabolome study due to a low turnover time (as low as second) of the metabolites. The usually complicated procedures can cause large variations and errors. Achieving an efficient separation of the exo- and endometabolome is another challenge. In this project, we aim at developing new technologies and methods to address these problems, especially to minimize the absolute errors and to access the true intercellular metabolic dynamics.

Rapid Sampling Unit: A new fully automated rapid sampling unit is under development. The implementation satisfies the needs for flexibility and for accuracy without compromise. A special valve system assures defined sample volumes and efficient mixing of the sample with the quenching solution. The system is designed to handle five hundred samples with a frequency up to ten samples per second. All parts with contact to the fermentation broth are in situ sterilizable to allow working with pathogens. Thanks to the modular structure, different experimental setups can be easily realized. For example, different quenching methods can be tested automatically. A 3D model of the rapid sampling unit has been generated, which allows easy design of new components for new experiments.

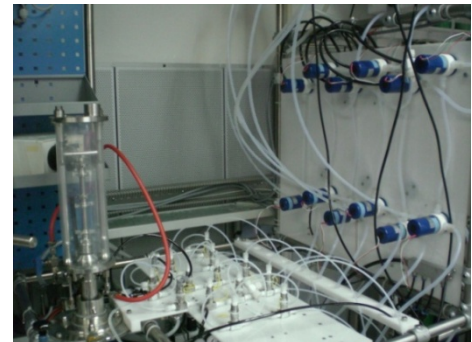


Fig.1. The protocol of the rapid Sampling Unit assembled with a 2L fermentor

Sample processing: To define the best quenching and extraction methods, we established a complete protocol to track and evaluate the solutions from each processing step. The protocol can accurately distinguish between the intra- and extracellular metabolites. In focus of our research are also different quenching and extraction methods to establish protocols with a high accuracy for the separation of intra- and extracellular metabolites in microorganisms such as *Escherichia coli* and *Bacillus megaterium*.

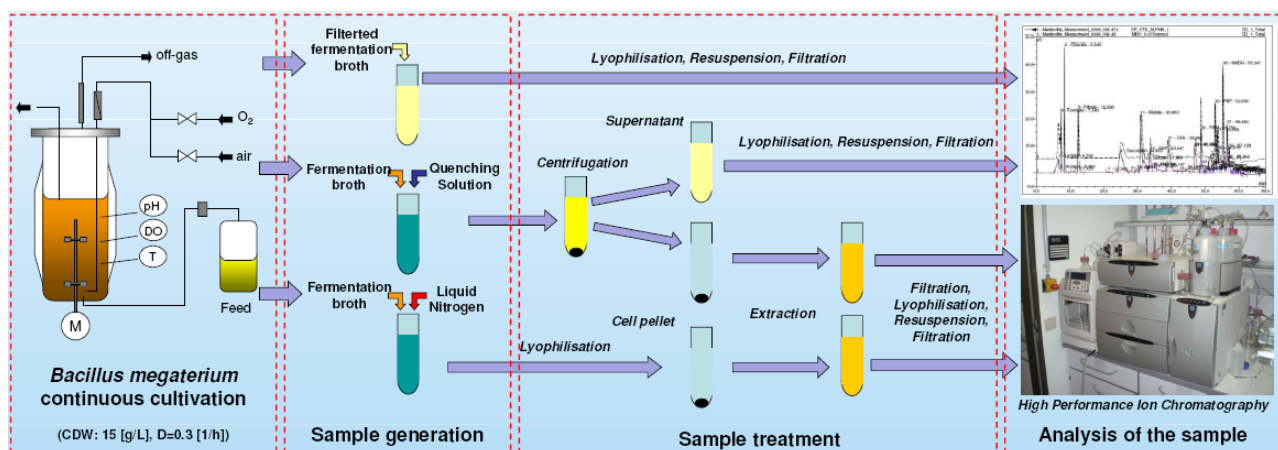


Fig.2. A scheme to evaluate different fast sampling and sample processing approaches

References:

- Landwehr, B. (2008) Diplomarbeit, Entwicklung eines Steuerungsprogramms für ein Abfüllsystem einer Bioreaktoranlage.
- Pötsch, S.M. (2008) Diplomarbeit, Entwicklung von analytischen Methoden zur Quantifizierung von Metaboliten bei Hochzellichtfermentationen von *Bacillus megaterium*.
- Landwehr, B. (2007) Studienarbeit, Aufbau, Modifikation, Einrichtung und Testen der Prototypen-Abfülllinie eines Schnellprobenentnahmesystems für einen Bioreaktor.
- Winkler, F. (2007) Diplomarbeit, Entwicklung analytischer Methoden zur Quantifizierung von intra- und extrazellulären Metaboliten bei *Escherichia coli*.

Contact: Prof. Dr. An-Ping Zeng

Institute of Bioprocess and Biosystems Engineering, Hamburg University of Technology.
 Denickestrasse 15, D-21073 Hamburg, Germany.
 Phone: +49-40-42878-4183 Email: aze@tuHH.de Web: www.tuHH.de/ibb