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Application of Metabolic Flux Analysis for Optimizing Specific Growth Rate of *Aspergillus niger* **R. Gheshlaghi** <*rgheshla@engmail.uwaterloo.ca*>, **J.M. Scharer** <*jscharer@engmail.uwaterloo.ca*>, **M. Moo-Young** <*mooyoung@cape.uwaterloo.ca*> and **P.L. Douglas** <*pdouglas@cape.uwaterloo.ca*>, Department of Chemical Engineering, University of Waterloo, Waterloo ON N2L 3G1.

Stoichiometric mass balances were used to determine flux distributions in a metabolic network and to identify the essential biochemical reactions under a variety of culture conditions of recombinant *Aspergillus niger*. The model includes 128 metabolites and 281 reactions, of which 211 represent biochemical conversions and 70 represent transport processes between different intracellular compartments and between the cell and the extracellular medium. The metabolic reactions were used in combination with biosynthetic requirements for specifying growth and for quantification of metabolic fluxes assuming pseudo-steady state for intracellular metabolites. Growth was simulated by optimization of the flux to biomass for a specified uptake rate of a selected carbon source. Metabolic flux distributions in the cells throughout the fermentation were determined using the model in combination with laboratory analysis of the extracellular metabolites. Two types of specific growth rates, stoichiometric and theoretical, were defined, maximized, and compared with observations.

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