1 INTRODUCTION

An adequate model of microalgal growth is of paramount importance both for the optimal photobioreactor (PBR) design and the optimal PBR control (i.e. to optimize operating conditions, see e.g., Papáček et al., 2008). Nevertheless, even having an adequate dynamic lumped parameter model (LPM) of microalgal growth, another serious difficulty resides in the description of microorganism growth in a PBR, i.e. in a distributed parameter system. Because the traditional scale-up methodology of PBR design fails, in the next section we explain how to ‘extend’ the LPM into 3D.

2 MODEL DEVELOPMENT

2.1 Governing equations of algal growth – LPM

The photosynthetic microorganisms growth is usually modeled as the steady-state light response curve (so-called P–I curve), which represents the microbial kinetics (either of Monod or Haldane type). However, in order to describe some dynamic phenomena, e.g. the flashing light environments (Davis, 1953), a dynamic model is needed. The problem is even more complicated due to the fact that the relevant transport and reaction phenomena operate in very different time-scales, for more detail see Papáček et al., 2007b. Nonetheless, the phenomenological three-state model of photosynthetic factory (PSF model) proposed by Eilers & Peeters (1993) and further developed by Papáček et al. (2007a), correctly describes the principal physiological mechanisms: photosynthetic light-dark reactions and photoinhibition, see Fig.3 below. For the PSF model parameter (α, β, γ, δ) estimation, see Rehák et al. (2008).

2.2 DPM of algal growth – Eulerian approach

The systems with distributed parameters are usually described by means of partial differential equations (PDE). The PBR as Convection-Reaction-Diffusion (Dispersion) System is thus represented by the following governing equations:

\[
\frac{\partial c_i}{\partial t} = \nabla \cdot (D_i \nabla c_i) - \nabla \cdot (V_i c_i) - k_i (c_i - c_{i,\text{ref}}),
\]

where \( c_i \) is cell-in-state-A(activated)-concentration (unit: cell m\(^{-3}\)), \( D_i \) represents the velocity field, \( D_i \) is the hydrodynamic dispersion coefficient and \( k_i \) (unit: s\(^{-1}\)) is the rate at which the concentration \( c_i \) is approaching to its steady-state value \( c_{i,\text{ref}} \). Similar equation could be written for the cell-in-state-R(resting)-concentration and for the cell-in-state-B(inhibited)-concentration, unless the method of order reduction is similar. The above PDE (1) can be solved simultaneously with the Navier-Stokes equation system, e.g. by a Finite Difference Method (FDM) or by a commercial CFD code, e.g. Fluent, see Fig.2.

2.3 Multicompartment/CFD approach - ODE based DPM of algal growth

A fresh approach, leading to the model of ‘well mixed’ interconnected vessels (compartments) with lumped parameters, see Fig.4, and ODE system (2), was studied in Bezzo et al. (2003). Usually the fluid dynamics operates on a much faster time-scale than the reaction, therefore it is not necessary to calculate the reaction term in each time step and every point as the CFD code does for the fluid flow. Moreover, the compartment volumes can be of several orders bigger than that for CFD simulation, the problem simplifies and it is possible to use ODE based DPM instead of CFD.

\[
\frac{dc_i}{dt} = \sum_{j=1}^{n} k_{ij} (c_j - c_i) + V_i c_i + \text{sources and sinks},
\]

While the problem of reaction term (matrix \( V_i \), and mass transfer coefficients \( k_{ij} \) determination was treated in Papáček et al. (2007b), the problem How to set-up the optimal compartment size? i.e. how to reconcile the discretisation based on the hydrodynamic conditions with the discretisation based on the irradiance profile? is still waiting for a convincing solution.

3 CONCLUSION

We presented some approaches for photosynthetic microorganisms growth modeling and simulation. The ‘classical’ approach is based on PDE (reaction-hydrodynamic dispersion system) and CFD. Some innovation is put into Multicompartiment/CFD approach. Lagrangian approach naturally allows us to involve the ‘cell memory’ into the growth model. For all three approaches, the complications residing in modeling of multi-scale transport and reaction phenomena were clarified. An innovative solution consisting on the phenomenological state description of microalgal culture (PSF model) rather than on real microalgal cell concentration, has been chosen. Our future goal is to evaluate the advantages and inconveniences of each approach performing the simulation of some benchmark case study.

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References


