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A comprehensive mechanistic model for simulating algal-bacterial growth dynamics in photobioreactors

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ABSTRACT

A comprehensive mechanistic model with state of the art understanding and assumptions is presented to simulate major processes in a photobioreactor for describing the algal-bacterial growth dynamics. The model includes a total of 37 state variables that broadly cover all the essential physiological and physico-chemical processes in such a system. Model parameters are first calibrated with batch experimental data, and thereafter, extensive validation of the model is carried with long term independent experimental data in diverse conditions. The developed model is able to capture the complex system behavior with reasonable accuracy. Also, the comprehensive mathematical formulation with realistic assumptions make this model a valuable tool for gaining better insights into the complex system behavior.

1. Introduction

Wide applicability of algal-bacterial consortia in various fields such as wastewater treatment (Zhu et al., 2013), vitamin B12 production (Croft et al., 2005), high biomass productivity (Fuentes et al., 2016), bio-hydrogen and biogas generation (Lakatos et al., 2014; Wirth et al., 2015) requires a better understanding of the complex behavior of such species under diverse environmental conditions. The interactions between algae and bacteria are however quite complex in nature. At times, they show synergistic or antagonistic behavior varying from process to process. The dissolved organic carbon (DOC) released by live or dead algae cells serve as a primary carbon source for heterotrophic bacteria (Cole et al., 1982). In addition, oxygen produced as a result of algal photosynthesis is useful for bacterial respiration (Tison and Lingg, 1979). Bacteria also produce vitamins and essential nutrients for algal growth (Croft et al., 2005). Carbon dioxide released by bacterial and algal respiration is used for algal photosynthesis (Munoz and Guieysse, 2006). Apart from synergistic behaviors as described above, they show antagonistic behavior while competing for nutrients such as N and P in algal-bacterial systems (Cotner and Wetzel, 1992). Further, axenic algal culture conditions are rarely maintained in most of the natural systems (viz. oxidation ponds, algal ponds), and heterotrophic aerobic bacteria are always present even in predominantly algal systems (Fuentes et al., 2016; Ramanan et al., 2016). The bacteria in these systems even grow in close proximity with algae when limited sources of labile DOC are present.

Increasing evidences of algal-bacterial interactions in diverse fields argue for a combined mechanistic model for algae and associated symbiotic bacteria, which could serve as an important tool to study the interaction between these microorganisms. Modeling the consortia of algae and bacteria is more complex than algal culture alone as they behave differently in terms of mode of nutrition (autotrophic for algae and heterotrophic for bacteria), uptake rates (consumption of nutrients per unit biomass growth), nitrogen, phosphorous, oxygen, and carbon cycle (in terms of cell release, cell storage and luxury uptakes) (Thingstad et al., 1993). Consequently, much research has been done on algal model development in the past (Shriwastav et al., 2017). Most of the algal-bacterial models that have been developed incorporate plenty of simplified assumptions, viz. simple Monod kinetics for biomass production and multiplicative rules for multiple nutrient limitation, that restrict their applicability in natural scenarios (Zambrano et al., 2016; Solimeno et al., 2017). Other models are restricted only to few nutrients (such as phosphate) which again limit the model applicability (Zambrano et al., 2016). Development of mechanistic models illus-

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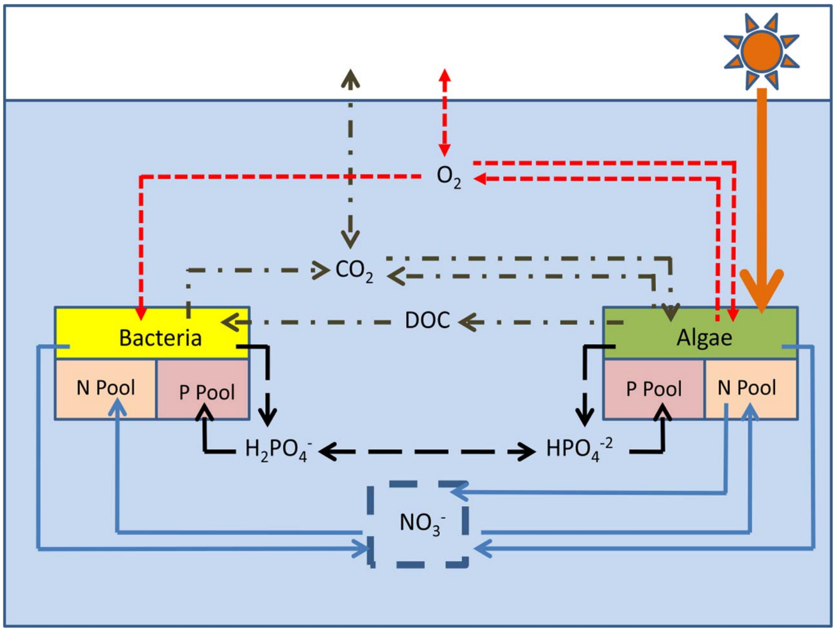

Fig. 1. Overview of processes in algal-bacterial system.

Table 1
Algal-bacterial growth dynamics model.

ODE No.	Equation[a,b]	Unit
Algal Growth Dynamics		
1	$\frac{dA}{dt} = [(\mu_m)_a^{20}.\ Min[\phi_n,\phi_p,\phi_c,\phi_i] - (k_r)_a^{20}.\ \phi_r].\ \theta^{(T-20)}.\ A$	mg L^{-1} day^{-1}
Bacterial Growth Dynamics		
2	$\frac{dB}{dt} = [(q_m)_b^{20}.\ Y_b.\ Min[\psi_n,\psi_p,\psi_s,\psi_o] - (k_d)_b^{20}].\ \theta^{(T-20)}.\ B$	mg L^{-1} day^{-1}
Nitrogen Dynamics		
3	$\frac{d[AN]}{dt} = \left\{(\rho_{an})_{max}^{20}.\ \phi_{an}.\ \phi_{bn}.\ \left[\frac{A}{14000}\right] - (k_r)_a^{20}.\ \phi_r.\ [AON]\right\}.\ \theta^{(T-20)}$	moles L^{-1} day^{-1}
4	$\frac{d[AON]}{dt} = \frac{(q_{a0})n}{14000}.\ \frac{dA}{dt}$	moles L^{-1} day^{-1}
5	$\frac{d[AIN]}{dt} = \frac{d[AN]}{dt} - \frac{d[AON]}{dt}$	moles L^{-1} day^{-1}
6	$\frac{d[BN]}{dt} = \left\{(\rho_{bn})_{max}^{20}.\ \psi_{an}.\ \psi_{bn}.\ \left[\frac{B}{14000}\right] - (k_d)_b^{20}.\ [BON]\right\}.\ \theta^{(T-20)}$	moles L^{-1} day^{-1} [c]
7	$\frac{d[BON]}{dt} = \frac{(q_{b0})n}{14000}.\ \frac{dB}{dt}$	moles L^{-1} day^{-1}
8	$\frac{d[BIN]}{dt} = \frac{d[BN]}{dt} - \frac{d[BON]}{dt}$	moles L^{-1} day^{-1}
9	$\frac{d[DIN]}{dt} = -\frac{d[AN]}{dt} - \frac{d[BN]}{dt}$	moles L^{-1} day^{-1}
10	$\frac{d[DNO3]}{dt} = \frac{d[DIN]}{dt}$	moles L^{-1} day^{-1}
11	$\frac{d[TN]}{dt} = \frac{d[AN]}{dt} + \frac{d[BN]}{dt} + \frac{d[DIN]}{dt}$	moles L^{-1} day^{-1}
Phosphorus Dynamics		
12	$\frac{d[AP]}{dt} = \left\{(\rho_{ap})_{max}^{20}.\ \phi_{ap}.\ \phi_{bp}\left[\frac{A}{31000}\right] - (k_r)_a^{20}.\ \phi_r.\ [AOP]\right\}.\ \theta^{(T-20)}$	moles L^{-1} day^{-1}
13	$\frac{d[AOP]}{dt} = \frac{(q_{a0})p}{31000}\frac{dA}{dt}$	moles L^{-1} day^{-1}
14	$\frac{d[AIP]}{dt} = \frac{d[AP]}{dt} - \frac{d[AOP]}{dt}$	moles L^{-1} day^{-1}
15	$\frac{d[BP]}{dt} = \left\{(\rho_{bp})_{max}^{20}.\ \psi_{ap}.\ \psi_{bp}.\ \left[\frac{B}{31000}\right] - (k_d)_b^{20}.\ [BOP]\right\}.\ \theta^{(T-20)}$	moles L^{-1} day^{-1}
16	$\frac{d[BOP]}{dt} = \frac{(q_{b0})p}{31000}.\ \frac{dB}{dt}$	moles L^{-1} day^{-1}
17	$\frac{d[BIP]}{dt} = \frac{d[BP]}{dt} - \frac{d[BOP]}{dt}$	moles L^{-1} day^{-1}
18	$\frac{d[H_3PO_4]}{dt} = k_{pb1}[H^+][H_2PO_4^-] - k_{pf1}[H_3PO_4]$	moles L^{-1} day^{-1}
19	$\frac{d[H_2PO_4^-]}{dt} = k_{pf1}[H_3PO_4] + k_{pb2}[H^+][HPO_4^{2-}] - k_{pb1}[H^+][H_2PO_4^-] - k_{pf2}[H_2PO_4^-] - \frac{d[BP]}{dt}$	moles L^{-1} day^{-1}
20	$\frac{d[HPO_4^{2-}]}{dt} = k_{pf2}[H_2PO_4^-] + k_{pb3}[H^+][PO_4^{3-}] - k_{pb2}[H^+][HPO_4^{2-}] - k_{pf3}[HPO_4^{2-}] - \frac{d[AP]}{dt}$	moles L^{-1} day^{-1}
21	$\frac{d[PO_4^{3-}]}{dt} = k_{pf3}[HPO_4^{2-}] - k_{pb3}[H^+][PO_4^{3-}]$	moles L^{-1} day^{-1}
22	$\frac{d[DIP]}{dt} = \frac{d[H_3PO_4]}{dt} + \frac{d[H_2PO_4^-]}{dt} + \frac{d[HPO_4^{2-}]}{dt} + \frac{d[PO_4^{3-}]}{dt}$	moles L^{-1} day^{-1}

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