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A simplified steady-state model of a hybrid bioreactor composed of a bubble column bioreactor and biofilter compartments

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Abstract

In a previous study, a hybrid bioreactor comprised of a bubble column bioreactor section and a biofilter section was successfully applied to the treatment of benzene. In order to design and optimize the bioreactor system for actual use in the field, simple but effective mathematical models of the two-stage system were required. Since the liquid phase in the bubble column bioreactor section was well mixed, a CSTR (continuously stirred tank reactor) model was adopted for this section, with benzene removal by both air stripping and biodegradation being considered in the model equations. The gaseous benzene degradation in the biofilter section was described using a PFR (plug flow reactor) model. The combined model was validated through independent experiments, and the simulation results were in a good agreement with measured data.

Keywords: Hybrid bioreactor; Modeling; Bubble column bioreactor; Biofilter; CSTR; PFR

1. Introduction

It was shown that a hybrid bioreactor comprising of a bubble column bioreactor and a biofilter was a novel and excellent bioreactor system for the treatment of benzene, a volatile organic compound [1]. Recently, a Korean company tried to apply the hybrid bioreactor to actual wastewater treatment and needed simple but applicable mathematical models for the purpose of system design and optimization.

Many mathematical analysis have been done on bubble column bioreactors and biofilters separately. In general, it is known to be very difficult to analyze bubble column bioreactor because the fluid dynamics of air bubbles and liquid phase in the bioreactor is very complex [2,3]. Therefore, experimental equations representing gas hold-up, mass transfer, liquid mixing and gas mixing are frequently used to establish models of bubble column bioreactor with many assumptions [4]. Hecht et al. [5], for example, developed a model of bubble column bioreactor containing immobilized microorganisms with following assumptions: (1) gas phase in plug flow, (2) well-mixed liquid phase, (3) quasi steady-state conditions for mass transfer and reaction rates, (4) biomass concentration is an independent variable, (5) first order reaction with regard to biomass and substrate, zero order for oxygen, and (6) isobaric conditions. When the length of bubble column bioreactor is long enough compared with inner diameter of the column, a model equation representing pollutant concentration profile along the column is required to predict the pollutant degradation in a bubble column bioreactor [6,7]. However, if a pollutant concentration in effluent stream is the same as that in bubble column bioreactor (no concentration gradient along the column), complete mixing can be assumed, which makes mathematical model noticeably simple.

In contrast to model of bubble column bioreactor, scientists and engineers have been trying to develop theoretical models of biofilter. Pioneering research in this area was conducted by Ottengraf and Van Den Oever [8] who considered the problem as composed of two phase: a bulk gas and a wet stagnant biolayer on the surface of solid particles in which contaminants are free to transfer from one to another. Based on this conceptual framework, they introduced a model in which a pair of equations, for each phase, accounts for diffusion and reaction in the biolayer, and advection in the vapor phase with equilibrium constraints at the interface. The same model, but with Haldane kinetics [9], was then applied by Shareefdeen and Baltzis [10] to predict methanol degradation. Hodge and

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Devinny [11] made the following modifications to the original model: (1) added dispersion to the gas phase, (2) ignored diffusion in the biofilm, and (3) took into account the presence of carbon dioxide. Even with the added features, some discrepancy still exists between the model predictions and the measured ethanol concentration along the biofilter. Another modification to the model was made with the incorporation of substrate adsorption and a rate expression suitable for two-substrate systems [12,13].

As models become more refined, the more measurements which are necessary not only to validate the models but also to inspire modelling are required [2]. Although they have developed the models theoretically, many assumptions were still involved and many experimental data were required to get parameters. Shareefdeen and Baltzis [10] used 14 assumptions for the model development. Hodge and Devinny [11], Deshusses et al. [12], Zarook et al. [14] and Lu et al. [15] used 7, 10, 13 and 8 assumptions, respectively. Also, much time should be devoted to solve the partial differential equations suggested by them but the models did not show high accuracy in a wide experimental range. Therefore most of biofilter models were developed with the assumptions such as constant effective diffusivity, constant mass transfer rate, constant cell mass and thus quasi steady-state [11,16,17]. They supposed 1st-order degradation rate and the parameters contained in those models sometimes do not have clear physical or biological meanings. Although their simplified macro-kinetic models are very convenient to calculate removal efficiency at quasi steady state, they do not predict the behavior of pollutant precisely in the wide experimental range mainly because the rate of degradation is not necessarily 1st order [18].

In this study, the bubble column bioreactor and biofilter were mathematically described separately by adopting the simple concept of CSTR (continuously stirred tank reactor) and PFR (plug flow reactor), respectively. Each model required just 3–5 assumptions and 2–5 parameters to be determined. The models were validated through independent experiments and the simulation data were in a good agreement with measured ones.

2. Materials and methods

2.1. Microorganism

Alcaligenes xylosoxidans Y234 isolated from crude oil-contaminated soil was used in this study. It can degrade benzene, toluene *m*-xylene and phenol [1]. *A. xylosoxidans* Y234 was precultured at 30 °C in a 500 mL flask containing 200 mL of medium (10 g/L glucose, 5 g/L yeast extract, 5 g/L $(NH_4)_2SO_4$, 5 g/L KH_2PO_4 and 1 g/L $MgSO{\cdot}7H_2O$).

2.2. Immobilization

Sodium alginate was dissolved in hot distilled water to produce 5% solution. The microorganisms harvested from precultured solution by centrifugation (Hitachi, SCR 18B) were resuspended in distilled water and mixed with the same volume of sodium alginate solution to produce 5 g/L of cell mass. This mixture was extruded through a thin needle attached to a peristaltic pump into a 1% $CaCl_2$ solution thus forming beads with a diameter of about 3 mm. After hardening for 1 h in this solution, the beads were washed several times with distilled water.

2.3. Reactor design and operation conditions

The hybrid bioreactor composed of a biofilter section and a bubble column bioreactor section was shown in Fig. 1. The diameter of a hybrid bioreactor was 6.0 cm. The working volume of bubble column bioreactor containing 100 mL of immobilized cells (beads) was 500 mL and that of the biofilter 760 cm^3 (height, 27 cm). Four and one sampling ports were attached to the biofilter and bubble column bioreactor section, respectively. The hybrid bioreactor was installed in an exhaust hood and operated at 30 °C. To maintain the beads wet and to provide nutrient medium to microorganisms in the biofilter, 100 mL of medium was added from the top of the hybrid bioreactor every 10 h. The medium contained 2 g/L $(NH_4)_2SO_4$, 0.3 g/L $MgSO_4{\cdot}7H_2O$, 0.1 g/L K_2HPO_4, 0.1 g/L $CaCl_2$ and 200 μL/L trace element. The trace element consisted of 16.2 g/L $FeCl_3{\cdot}6H_2O$, 10.2 g/L $CaCl_2{\cdot}2H_2O$, 0.22 g/L $CoCl_2{\cdot}6H_2O$, 0.15 g/L $CuSO_4{\cdot}5H_2O$, 0.13 g/L $CrCl_3{\cdot}6H_2O$, 0.09 g/L $NiCl_3{\cdot}6H_2O$ and 40.0 g/L citric acid. The residence time was changed by manipulating the pumping rate of influent benzene solution. Air flow rate was changed by manipulating the air flow regulator attached to an air compressor.

2.4. Adaptation

In order to eliminate adaptation time which alters the start point of degradation, microorganisms were fully adapted to benzene as follows. A 100 mL of beads were placed in a 500 mL flask containing 200 mL medium and cultured for 20 h at 30 °C. The medium also contained 120 mg/L of benzene and inorganic nutrients of which composition was described above.

2.5. Assays

The liquid benzene concentrations were analyzed by directly injecting 2 μL of the liquid sample into a gas chromatograph (HP 5890 II). To measure gas phase benzene, 1000 μL gas was directly withdrawn from off-gas port of biofilter section and injected into the GC. The detection limit of the GC was 0.05 mg/L. Cell mass in a bead was determined as follows. One hundred beads were dissolved in 7 mL of 65 mM phosphate buffer and sonicated. Cell free extract and alginate solution were separated by centrifugation. The total protein concentration in cell free extract was determined according to Bradford method [19] using a Bio-Rad protein assay kit with bovine albumin as a standard. The experiment showed that 1 g/L of cell mass corresponded to 0.47 g/L of protein.

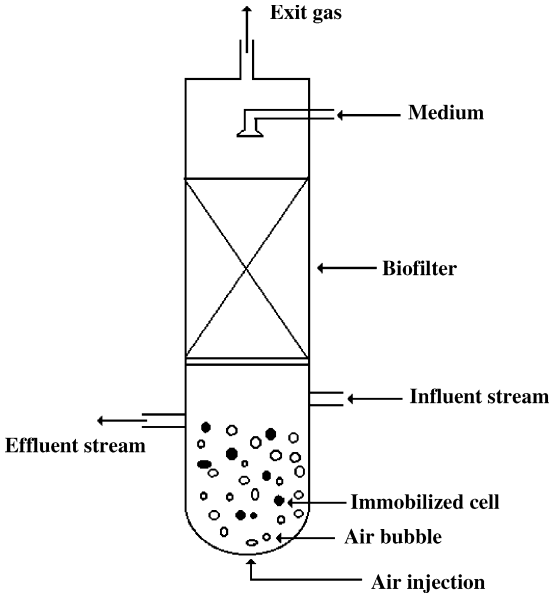

Fig. 1. Schematic diagram of the hybrid bioreactor.