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Modelling microbial transport in simulated low-grade heap bioleaching systems: The biomass transport model

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ABSTRACT

A model was developed to describe microbial growth and transport in the flowing bulk solution and ore-associated phases within a mineral bioleaching heap. The retention of micro-organisms was assumed to be a function of microbial transport between the ore surface and the bulk solution, as well as growth in each of these phases. Transient variations in the corresponding microbial concentrations are presented together with predicted microbial growth, transport and oxidation kinetics within the agglomerate-scale, whole ore environment. The transport model presented in this paper was developed under the assumption that the microbial concentration gradient between the identified phases was the driving force for microbial transport. Further the population balance model was super-imposed to account for available reaction surface. The model was able to predict the change in microbial concentrations in both the bulk solution and ore-associated phase. The resulting microbial transport rates to and from the ore-associated phase were found to be significantly lower than the maximum specific microbial growth rates presented, suggesting that microbial transport is not governed by the microbial concentration difference. These findings confirm the value of the modelling approach in which the population balance model is included, while demonstrating that concentration gradient as the driving force is not the main contributor to microbial transport.

1. Introduction

The modelling of heap bioleaching processes for the purpose of predicting process outcomes is challenging as a result of numerous variables, each involved in interdependent sub-processes. The interactions within a cluster of agglomerated particles involve the reaction of chemical and/or biological species present in discrete zones associated with the mineral surface, in the flowing and stagnant solution and in the gaseous phase, as well as the transport of chemical species, gases and micro-organisms across the respective boundary layers. For the heap bioleaching of chalcopyrite, the most abundant and refractory copper-bearing mineral sulphide in the world, the mechanisms involved in mineral dissolution are poorly understood (Brierley, 2010; van Staden et al., 2008; Watling, 2006). In a recent study, Hiroyoshi et al. (2008) highlighted the effect of the ferric to ferrous iron ratio on chalcopyrite dissolution. In the model system addressed in this study, the dissolution of low-grade chalcopyrite ore was assumed to occur via ferric iron attack (Eq. (1)), with *Acidithiobacillus ferrooxidans* (*A. ferrooxidans*) oxidation of ferrous iron responsible for the regeneration of the mineral oxidising agent (Eq. (2)).

$$CuFeS_2 + 4Fe^{3+} \rightarrow Cu^{2+} + 5Fe^{2+} + 2S^0 \quad (1)$$

$$4Fe^{2+} + 4H^+ + O_2 \xrightarrow{A.\ ferrooxidans} 4Fe^{3+} + 2H_2O \quad (2)$$

With respect to the solid phase, mineralogical characteristics vary with particle size and mineral type. Mineral surface properties change with exposure to chemical and biological species. In the heterogeneous mineral bioheap environment, the mineral, solution and gaseous phases may coexist in isolated zones. However, there are also locations within the heap where the gaseous and solution phases, either flowing or stagnant, are not present. The ratio of actively flowing to stagnant solution volumes is dynamic with heap configuration and bulk density, solution flow characteristics, mineral surface properties and physicochemical conditions. Consequently, the concentration of chemical and biological species associated with the mineral and in the stagnant and flowing solution phases varies spatially and temporally.

In an earlier study of dump bioleaching systems, Murr and Brierley (1978) demonstrated the variation in temperature, oxygen concentration

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and microbial activity across the depth of a pilot scale reactor system. The authors found that the microbial abundance in solution was lower than that associated with the ore, with both varying along the depth of the ore bed; as suggested in the earlier study by Bhappu et al. (1969).

Solution flow dynamics through unsaturated, porous systems has been studied extensively in soils. For instance, studies have been aimed at the complete removal of pathogens from soil using hydrodynamic properties of flow-through experimental systems (Marshall, 1976; McCaulou et al., 1994; Tan et al., 1994). In general, microbial retention within these homogenous porous systems is modelled using a general advection–dispersion equation for one-dimensional microbial transport (Tufenkji, 2007). However, most models do not account for the presence of substrates or the association of micro-organisms with the solid phase. The contribution of microbial growth to retention rate is poorly understood and most often ignored.

In the modelling of mineral oxidation rates in unsaturated heap mineral bioleaching systems, previous studies have considered the following: the impact of irrigation rate as a function of heap configurations (Pantelis and Ritchie, 1991, 1992), mineral diffusion models (Bartlett, 1997), the presence of stagnant and flowing solution volumes (Bouffard and Dixon, 2001), the effect of bulk ore density (Bouffard and West-Sells, 2009) and transport properties at various scales (Yin et al., 2011). In most of these studies, microbial growth and activity were assumed to mimic those in submerged culture where substrate availability was not limited.

Common practice in laboratory and industrial scale heap bioleaching operations is to quantify microbial growth rates by monitoring the microbial cell concentration in the exiting liquid streams, commonly referred to as pregnant leach solution (PLS). In earlier studies of microbial kinetics in submerged culture systems, the presence and growth of the microbial community associated with the reactor wall in chemostat systems were acknowledged (Rossi, 1990) but few studies have accounted for the resultant exaggerated overall growth rate owing to ongoing inoculation of the liquid phase from the wall growth (Boon et al., 1999; MacDonald and Clark, 1970). In a recent study of microbial population dynamics in agglomerate scale heap bioleaching reactors, it was shown that the microbial concentration exiting the whole ore system in the flowing PLS was not representative of that associated with the low grade ore (Govender et al., 2013a). The microbial concentration associated with the agglomerated ore was some two to three orders of magnitude greater than that in the PLS on a basis of liquid volumes. Indeed, the growth of micro-organisms in the PLS was shown to be in the same order of magnitude as that for chemostat systems with wall growth, suggesting microbial transport from the ore-associated phase to the PLS.

In this paper, the microbial transport model was developed to describe microbial growth in the ore bed. The model assumes that the microbial abundance in the PLS and ore-associated phase is a function of microbial growth in each phase and microbial transport between the phases; with microbial activity dependent on ferrous iron substrate utilisation kinetics. The experimental conditions presented previously (Govender et al., 2013a) were duplicated and the resulting microbial concentration profiles for the PLS and ore-associated (interstitial, weakly attached and strongly attached) phases were used to fit and verify the proposed model. Experimentally determined microbial growth and utilisation kinetic parameters are compared to the corresponding model parameters for further verification. This study is limited to a dual set of experimental data collected under replicate conditions. Varied physicochemical conditions are not considered.

2. Methodology

An experimental system was designed to simulate heap bioleaching of a low-grade chalcopyrite ore, using multiple, agglomerate-scale mini-column reactors (Govender et al., under review). Each column was assembled to be a representative grab sample of a larger heap; with identical ore sample size, particle size distribution and fluid flow regimes. A brief experimental methodology is presented in this paper, with a more detailed description in Govender et al. (2013a). A test consisted of one abiotic and seven biotic mini-column reactors. Each biotic mini-column in a test was inoculated from a single sample of a stock culture of *A. ferrooxidans* (DSM 14882), used as model micro-organism and grown on sterile autotrophic basal salt (ABS) medium containing trace elements (Johnson et al., 2008), 0.5 g L^{-1} Fe^{2+} ($FeSO_4 \cdot 7H_2O$) and 1% (w/v) γ-irradiated pyrite concentrate (<75 μm). Two sets of tests, A and B, were inoculated with approximately 10^{10} cells per ton dry ore (Tupikina et al., 2014) and run under identical conditions. Sterile feed solution containing 0.2 g L^{-1} Fe^{3+} ($Fe_2(SO_4)_3 \cdot xH_2O$), ABS and trace elements at pH 1.7 (96% H_2SO_4) was irrigated over the columns at 10 mL h^{-1}. For test B, shorter time intervals between column sampling were chosen. For the sampling of the ore-associated microbial population, a mini-column reactor from a test was sacrificed and a representative sample of the packed ore bed was processed using a standardised detachment protocol (Govender et al., 2013a). This method has been shown to release the majority of the ore-associated microbial community. The microbial concentrations in the effluent solution and associated with the ore were determined at regular intervals using the Miles–Misra serial dilution plating protocol (Miles et al., 1938) for the enumeration of viable colony forming units (cfu) on iron overlay plates containing approximately 1.5 g L^{-1} Fe^{2+} ($FeSO_4 \cdot 7H_2O$) (Johnson, 1995). Variance in quantification of viable cell numbers using the Miles–Misra plating technique was determined by analysing the PLS from multiple columns in an experiment at a single time point and by repeating analysis of cells recovered from a single ore-washed sample. The relative error associated with cell enumeration in columns in the same test was found to be less than 13% (data not shown). A residence time distribution study was used to determine the mean residence time, τ, to be 1.45 h. This study, together with compartment models, allowed for an estimation of the volumes of bulk flowing and stagnant solution within the packed bed reactor to be ca. 11.7 and 2.3 mL, respectively (Govender et al., under review).

3. Experimental growth and substrate kinetics of *A. ferrooxidans* on whole ore

The microbial concentrations in the PLS and ore-associated phases were converted from cfu per millilitre [cfu mL^{-1}] and cfu per gramme dry ore [cfu g DO^{-1}] to mol carbon per litre [mol C L^{-1}] using the known reactor working volume and the mass of dry ore loaded into each column. The number of moles of carbon in each cell was assumed to be 4.8×10^{-15} [mol C $cell^{-1}$] as per the study by Moon (1995). This simple conversion assumes uniform microbial dimensions and composition irrespective of environment conditions. It is recognised that some variation in carbon content can be expected with growth conditions (Bryan et al., 2012) but there are no data as to relative scale of these effects at present.

In Fig. 1, the change in microbial concentrations in the PLS and ore-associated phases for the duration of tests A and B, run over 690 and 334 h, respectively, is presented on the volumetric mol C basis. In the case of test A, this is a re-analysis of the data presented in Govender et al. (2013a) which investigated the location of microbial populations in the whole ore bioheap system. The data sets are presented in semi-log plot to display the different phases of microbial growth. Owing to detection limits, the first column to be sacrificed for sampling was at 48 h to allow time for attachment, growth and transport within the various phases. As a result of this sampling delay, insufficient data were available to indicate the duration of the lag phase as shown in Fig. 1. A good comparison of the microbial concentration profiles was observed between the repeated tests; particularly over the exponential phase of growth, showing that the data were reproducible.

The conventional approach used to quantify microbial growth kinetics in bioleaching systems, involves sampling the PLS exiting