Bacterial induced transformation of iron oxides: Morphology and rate effects from natural and engineered living cells

 $\begin{array}{c} K.\,K.\,Sand^1, M.\,Teravest^3, C.\,M.\,Ajo\text{-}Franklin^2 \text{ and } \\ J.\,De\,\,Yoreo^1 \end{array}$

¹Physical Sciences Division, Pacific Northwest National Laboratories, Richland, USA.

²Molecular Foundry, Lawrence Berkeley National Laboratories, Berkeley, USA

³California Institute for Quantative Biosciences, University of California, USA

Microbes influence the nanoscale processes of formation and transformation of nanoparticulate iron oxy(hydr)oxides (hereafter "oxides"). It is known that the associated extracellular matrices (EM) from bacteria influence the mineralogy of iron oxides in the subsurface [1]. It has also been found that electron transport from bacterial metabolism can have a significant impact on the existing mineralogy [2]. The end-product from microbial induced transformations of existing nanoparticulate iron oxide minerals is hard to predict because of the influence from both EM and reduction rate.

Shewanella oneidensis is a naturally occurring biofilm producing metal-reducing bacterium. It transports electrons via the Mtr pathway which is a series of transmembrane intermolecular electron transfer events to extracellular solid minerals. In contrast the popular model microbe *Escherichia coli* lacks the Mtr pathway and is not able to reduce solid metals. In this study we use model systems and engineered bacteria expressing the Mtr pathway or to supress EM production. We explore the transformation rate and pathway of iron oxide reduction of 2-line ferrihydrite and lepidocrocite under anaerobic conditions.

Our result shows that bacterial reduction affects transformation rate, product and morphology. The rate of reduction by engineered Mtr is outcompeted by wild type *Shewanella*. This study show promise for using engineered electron transport and extracellular matrices as a tunable parameter for mineral transformation.

[1]. Konhauser, K. 2007, United Kingdom: Blackwell [2]. Zegeye, A., et al. *Geomicrobiology Journal*, 2007. **24**, 51-64.