Final Report

Genome-Based Models to Optimize In Situ Bioremediation of Uranium and Harvesting Electrical Energy from Waste Organic Matter

DE-FC02-02ER63446

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The goal of this research was to provide computational tools to predictively model the behavior of two microbial communities of direct relevance to Department of Energy interests: 1) the microbial community responsible for *in situ* bioremediation of uranium in contaminated subsurface environments; and 2) the microbial community capable of harvesting electricity from waste organic matter and renewable biomass. During this project the concept of microbial electrosynthesis, a novel form of artificial photosynthesis for the direct production of fuels and other organic commodities from carbon dioxide and water was also developed and research was expanded into this area as well.

The major research goal was met with the clear demonstration that natural microbial communities could be evaluated and predictively modeled with a systems biology approach. For example, the growth of subsurface microorganisms was predictively modeled *in silico* with genome-scale metabolic models of key components of the microbial community coupled to hydrological and geochemical models to predict the outcome of subsurface uranium bioremediation. This approach was developed to such a degree that other DOE researchers were able to adopt our models and approaches for their own independent research. Furthermore, as highlighted below, this project established several new paradigms extracellular electron transfer and interspecies interactions.

At the end of our project the major findings of the project were summarized in several extensive peer-reviewed review articles including:

- Lovley, D. R., T. Ueki, T. Zhang, N. S. Malvankar, P. M. Shrestha, K. Flanagan, M. Aklujkar, J. E. Butler, L. Giloteaux, A.-E. Rotaru, D. E. Holmes, A. E. Franks, R. Orellana, C. Risso, and K. P. Nevin. 2011. Geobacter: the microbe electric's physiology, ecology, and practical applications. Adv. Microb. Physiol. 59:1-100.
- Mahadevan, R., B. O. Palsson, and D. R. Lovley. 2011. *In situ* to *in silico* and back: elucidating Geobacter physiology and ecology with genome-scale modeling. Nature Rev. Microbiol. 9:39-50.
- Lovley, D. R. 2011. Live wires: direct extracellular electron exchange for bioenergy and the bioremediation of energy-related contamination. Energy & Environmental Science 4:4896-4906.

Malvankar, N. S., and D. R. Lovley. 2012. Microbial nanowires: a new paradigm for biological electron transfer and bioelectronics. ChemSusChem 5:1039–1046.
Lovley, D. R. 2012. Electromicrobiology. Ann. Rev. Microbol. 66:391-409.

Detailed accounts of research progress can also be found in the annual progress reports. Research highlights are listed below.

Environmental Genome-Scale Metabolic Modeling

We developed an a novel approach for predicting the activity of environmentally relevant microorganisms under a diversity of environmental conditions which we have designated bottom-up genome-scale modeling, abbreviated BUGS modeling. In this approach appropriate conditons are designed for the isolation of the most important microorganisms in the environment of interest. Genome-scale metabolic models of these organisms are developed and then the models are coupled to the appropriate hydrological and geochemical models. The utility of BUGS modeling was demonstrated for predicting the outcome of stimulating subsurface microbial metabolism with the addition of acetate to promote *in situ* uranium bioremediation and for predicting the distribution of different species of iron reducers and sulfate reducers in the subsurface. The BUGS modeling approach is scalable to complex microbial activities in natural environments based on first principles of genome-encoded metabolic properties and without empirically derived performance parameters. At the end of this project we used the BUGS modeling approach to design optimized *in situ* uranium bioremediation strategies predicted to lead to long-term solutions to groundwater uranium contamination.

Extracellular Electron Transfer

When the project was initiated it was understood that *Geobacter* species needed to be in contact with iron oxides in order to reduce them, but the mechanisms for this extracellular electron transfer were not known. A completely unexpected mechanism for extracellular electron transfer was elucidated. We discovered that the pili of *Geobacter sulfurreducens* are electrically conductive along their length. The pili have metallic-like conductivity. This is surprising because it had been concluded that metallic-like conductivity would not be feasible in biological protiens. Reduction of iron oxides requires not only the conductive pili, but also the multi-heme *c*-type cytochrome, OmcS. The model for long-range electron transfer from the pili to the iron oxides. This model is based on multiple lines of evidence including mutational studies, adaptive evolution studies, and novel biophysical approaches.

Microbe-Electrode Interactions

A systems biology approach to the study of biofilms transferring electrons to graphite electrodes elucidated the biological properties that contribute to the production of high current densities in microbial fuel cells. Whole-genome analysis of gene expression patterns identified genes specifically expressed at high levels when the biofilm was producing current and gene deletion studies identified which of these genes were essential for current production. Purification, characterization and localization of key proteins required for current production, coupled with biophysical studies, suggested a model in which conductive pili are responsible for long-range electron transport through the biofilms, which have conducitivies rivaling those of synthetic

conducting polymers. The multi-heme c-type cytochrome, OmcZ, is required for high current densities and specifically accumulates at the biofilm-electrode interface. The proposed role of OmcZ is to facilitate electron transfer from the biofilm to the electrode. Gene reporter systems that could be monitored in real-time during biofilm growth on electrodes further confirmed this model for electrode biofilm function.

Direct Interspecies Electron Transfer

A study on the adaptive evolution of interspecies electron transfer in *Geobacter* species lead to the surprising discovery that different *Geobacter* species could directly exchange electrons to support syntrophic growth under conditions in which neither of the two strains could grow indpendently. Genome resequencing and gene deletion studies demonstrated a role for conductive pili and OmcS in the electron transfer. This discovery led to a new Genomic Sciences project which has determined that direct interspecies electron transfer is an important phenomenon in some methanogenic communities, including those converting organic wastes to methane.

Detailed Understanding of Geobacter Physiology and Physiological Status in the Subsurface

When this project began almost nothing was known about the physiology of *Geobacter* species. Genome-sequencing of multiple *Geobacter* species followed by detailed manual genome annotation, functional genomics, and protein isolation and characterization, coupled with genome-scale metabolic modeling provided an in-depth understanding of organisms in this genus, as well as closely related *Pelobacter* species. Analysis of the regulatory networks of *Geobacter sulfurreducens* gave additional insight into how *Geobacter* species respond to enviornmental changes. Environmental transcriptomic and proteomic studies made it possible to diaganose the *in situ* physiological status of *Geobacter* species in the subsurface and determine what factors were limiting the activity during in situ uranium bioremediation.

Microbial Electrosynthesis

A question about the inefficiency of photosynthesis by our Genomic Sciences program manager led us to consider and develop an artificial form of photosynthesis, known as microbial electrosynthesis. In this novel bioenergy strategy solar energy is captured with photovoltaic technology and the electrical energy obtained is used to extract electrons from water. The electrons are fed to microbial biofilms growing on electrodes that can accept electrons from the electrode for the direct reduction of carbon dioxide to multi-carbon organic molecules that are excreted from the cell. Microbial electrosynthesis is orders of magnitude more efficient in converting solar energy and carbon dioxide to biocommodities that processes depending on natural photosynthesis. Furthermore, microbial electrosynthesis avoids the significant environmental degradation associated with biomass-based bioenergy strategies. Microbial electrosynthesis is now being further developed in the Electrofuels Program of the Department of Energy's ARPA-E.

In summary, this project demonstrated that a systems approach to the study of natural microbial communities could provide the ability to predictively model the response of those communities to environmental perturbations. The computational approach that was developed for genome-scale modeling of microbial activity and the interaction of microbial communities with their environment will be useful not only for bioremediation applications, but also for predicting the

activity of microbial communities in a wide range of other environments. The environmental transcriptomic approach developed for diagnosing the *in situ* physiological status of subsurface microorganisms is expected to become standard practice for in the study of bioremediation. The discovery of metallic-like conductivity in *Geobacter* pili is a paradigm shift in biological electron transport with broad implications not only in microbiology but also for the production of new materials in the emerging field of bioelectronics. The discovery of direct interspecies electron transfer revolutionizes our understanding of the functioning of methanogenic environments and it has already been demonstrated how this new understanding can lead to reactor design modifications that can greatly accelerate conversion of wastes to methane, making this a much more attractive bioenergy strategy. Another unforeseen discovery that emerged from this research was the development of microbial electrosynthesis, a novel bioenergy strategy with substantial potential for efficient, sustainable production of transportation fuels and other organic commodities.

Comprehensive List of Publications

2003 Publications

- 1. Bond, D.R., and D.R. Lovley. 2003. Electricity production by Geobacter sulfurreducens attached to electrodes. Appl. Environ. Microbiol. 69:1548-1555.
- 2. Lovley, D.R. 2003. Cleaning up with genomics: applying molecular biology to bioremediation. Nature Rev. Microbiol. 1:35-44.
- Jara, M., C. Nunez, S. Campoy, A. R. Fernandez de Henestrosa, D.R. Lovley, and J. Barbe. 2003. Geobacter sulfurreducens has two autoregulated lexA genes whose products do not bind the recA promoter: differing responses of lexA and recA to DNA damage. J. Bacteriol. 185:2493-502.

- Butler, J.E., F. Kaufmann, M.V. Coppi, C. Nunez, and D.R. Lovley. 2004. MacA, a diheme c-type cytochrome involved in Fe(III) reduction by Geobacter sulfurreducens. J Bacteriol 186:4042-4045.
- 2. Chin, K.-J., A. Esteve-Núñez, C. Leang, and D.R. Lovley. 2004. Direct correlation between rates of anaerobic respiration and levels of mRNA for key respiratory genes in Geobacter sulfurreducens. Appl. Environ. Microbiol. 70:5183-5189.
- 3. Coppi, M.V., R.O. O'Neil, and D.R. Lovley. 2004. Identification of an uptake hydrogenase required for hydrogen-dependent reduction of Fe(III) and other electron acceptors by Geobacter sulfurreducens. J. Bacteriol. 186:3022-3028.
- 4. Esteve-Núñez, A., C. Núñez, and D.R. Lovley. 2004. Preferential Reduction of Fe(III) over Fumarate by Geobacter sulfurreducens. J. Bacteriol. 186:2897-2899.
- 5. Holmes, D.E., D.R. Bond, R.A. O'Neil, C.E. Reimers, L.R. Tender, and D.R. Lovley. 2004. Microbial communities associated with electrodes harvesting electricity from a variety of aquatic sediments. Microbial Ecol. 48:178-190.
- Holmes, D.E., K.P. Nevin, and D.R. Lovley. 2004. Comparison of 16S rRNA, nifD, recA, rpoB, and fusA genes within the family Geobacteraceae. Int. J. Sys. Evol. Microbiol. 54:1591-1599.
- 7. Holmes, D.E., K.P. Nevin, and D.R. Lovley. 2004. In situ expression of Geobacteraceae nifD in subsurface sediments. Appl. Environ. Microbiol. 70:7251-9.

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