

Regulation of H₂ and CO₂ Metabolism: Factors Involved in Partitioning of Photosynthetic Reductant in Green Algae

Maria L. Ghirardi (Primary Contact), Mike Seibert, Matthew Posewitz and Matthew Wecker

National Renewable Energy Laboratory, 1617 Cole Blvd., Golden CO 80401
303-386-6312 (phone), 303-384-6150 (Fax)

maria_ghirardi@nrel.gov

DOE Program Officer: Richard Greene

Richard.Greene@science.doe.gov; 301-903-6190

Subcontractors:

Matthew Posewitz, Colorado School of Mines, Golden CO 80401

Objectives

- *The primary objective of this research effort is to develop fundamental understanding about the partitioning of photosynthetic reductant at the level of ferredoxin between the H₂-producing, hydrogenase pathways (active only under anaerobic conditions) and the CO₂-fixing, Calvin-Benson cycle. Specific objectives include: (a) identify protein factors whose expression may be required for optimal hydrogenase expression and activity; (b) identify the promoter regions and transcriptional elements activating the expression of hydrogenase; and (c) determine how *C. reinhardtii* senses O₂ and transduces this signal into gene regulation.*

Technical Barriers

- *Besides the sensitivity of the hydrogenase to O₂, one of the other major barriers to efficient photobiological H₂ production by photosynthetic organisms is the existence of competing metabolic pathways for photosynthetic reductants, such as CO₂ fixation. In order to attain the theoretical maximum light conversion efficiency of 10% from sunlight to H₂, it is essential that most of the photosynthetic reductant be utilized for H₂ production, while concomitantly allowing the cells to store some energy in the form of starch to run their internal metabolism. Once the factors that are involved in this partitioning are known, we expect to learn how to modulate them to achieve efficient H₂ photoproduction and basal cell metabolism occurring simultaneously.*

Abstract

The objective of this proposed research is to continue to develop fundamental understanding about the regulation of partitioning of photosynthetic reductants (at the level of ferredoxin) between the H₂-production and the CO₂-fixation pathways. Our analysis of *C. reinhardtii* mutant libraries in the previous funding periods for strains having attenuated H₂ production has led to the discovery of maturation proteins that are required for the proper assembly of hydrogenases, and to the discovery of the STA7 isoamylase and of the putative 3-hydroxybutyrate dehydrogenase genes, reflecting the importance of starch and lipid metabolic pathways for H₂ production. We have recently shown the presence of heme-binding, FixL-like proteins in *C. reinhardtii*. Such proteins likely play a role in the O₂-sensing mechanism and may mediate components of the anoxic regulatory response. The proposed work will continue to (a) determine what other protein factors may be required for optimal hydrogenase expression and activity, (b) identify O₂-

sensor proteins in *C. reinhardtii* that regulate the expression of the reversible hydrogenase, (c) conduct analyses of the promoter regions for *HYDA1* and *HYDA2* genes, encoding the two algal hydrogenases; and (d) understand the simultaneous or complementary regulation of the competitive CO₂ fixation pathway under anaerobic conditions.

Progress Report

- We have screened through a *C. reinhardtii* mutagenesis library (6,000 transformants) for colonies deficient in H₂-production capability. A bank of eleven distinctly different *C. reinhardtii* mutants were isolated for having attenuated H₂ production, while maintaining wild-type (WT) rates of photosynthetic O₂ evolution and respiration. Among these eleven mutants, two mutants have been fully characterized. One mutant contained a disrupted isoamylase gene (*STA7*) and its characteristics were described in detail previously. The other mutant that we characterized contained a disrupted novel [FeFe]-hydrogenase assembly protein gene, *HYDEF*, and has also been previously reported. The flanking DNA for three additional mutants has been obtained and the disrupted genes appear to include: 1) a putative 3-hydroxybutyrate dehydrogenase (*3-HBD*); 2) a potential quinone oxidoreductase; and, 3) a disruption neighboring a potential transcriptional regulator, ferredoxin, or kinase. A mutation in 3-HBD indicates that lipid metabolism is involved in H₂ production, a finding that could correlate with chloroplast membrane lipid degradation upon sulfur deprivation and ensuing H₂ production in *C. reinhardtii* [64]. This mutant has attenuated hydrogen production in early to mid exponential growth phase, but normal H₂ production in older cultures. PCR and reverse transcription PCR assays indicate a duplication of the *3-HBD* gene during insertion mutagenesis. One of the duplicated genes is disrupted by the insert, while the other gene appears to be intact, with mRNA for *3-HBD* at approximately wild-type levels. This mutant is currently being back-crossed by Patrice Hamel (Ohio State University) against a WT cell line prior to further analysis. An additional library of insertion *ApaH* paromycin mutants is being created in order to streamline some of the difficulties encountered in the original library. These experiments will help to further define the biochemical pathways required for H₂ production in *C. reinhardtii*.
- As a second approach to finding other regulatory genes, *C. reinhardtii* proteins with homology to O₂-sensing proteins were identified by our group. Analysis of the *Chlamydomonas reinhardtii* genome indicates a number of closely-related homologs to eubacterial FixL proteins. Nine of these FixL like homologs (FXL) have a core PAS domain that is homologous to the FixL O₂-sensing PAS domains of the nitrogen-fixing bacteria *Bradyrhizobium japonicum*, *Sinorhizobium meliloti* and *Rhizobium leguminosarum*. Each of the putative homologs has multiple transmembrane-spanning domains, which are typical of the bacterial FixL homologs. Additional homology includes conserved α -helical loops, β -sheet structures, and critical residues required for binding a heme moiety transmitting the presence of heme-bound O₂ to an autophosphorylation site of a conserved histidine residue within a neighboring histidine kinase domain. However, the *Chlamydomonas* FixL homologs do not have the typical histidine autophosphorylation site. Two of the *Chlamydomonas* FixL heme-binding domains were cloned as truncated genes (*FXL1PAS* and *FXL5PAS*) and the corresponding expressed proteins in *E. coli* were shown to coordinate heme. The heme moiety is visible on an *o*-dianisidine-stained, SDS-PAGE denaturing gel, as either free heme or bound to the truncated FXL proteins. Purified cell extracts of the background strain of *E. coli* harboring only the vector plasmid did not heme-stain prominently when the cells were grown under identical conditions, nor do truncated FXL proteins stain when purified under denaturing conditions, although upon reconstitution with 100 μ M hemin, the heme group again migrated with the protein band. The spectral properties of *FXL1PAS* and *FXL5PAS* reveal absorbance peaks at 415 nm and 530/560 nm that are the characteristic bands of protein-bound heme and similar to that of oxy-*RmFixL*, although typically the peak at 560 nm is more intense than that at 530 nm. Upon reduction with 10 mM sodium dithionite, the primary 415 nm Soret bands of both *FXL1PAS* and *FXL5PAS* shift about 15 nm downfield, and the ratio of the absorbance of the 560 nm band relative to the 530 nm band increases, as is typical of heme-binding proteins. Preliminary characterization of the *FXL1* and *FXL5* heme-binding domains indicates that these proteins are able to coordinate heme. We are currently testing the ligand binding characteristics of these domains to determine the effects of O₂ coordination. These data will be correlated with the transcriptional level of the FixL homologs resulting from exposure to O₂ and other gases during culture. Using microarray analysis, two of the FixL homologs (*FXL1* and *FXL2*) were observed to have increased transcript levels upon dark, anerobic adaptation. To date there have been

no other reports of O₂-sensing regulatory proteins in *Chlamydomonas*. Analysis of these FixL homologous genes may prove invaluable for understanding the regulation of fermentative metabolism and the production of H₂ under conditions of low O₂ tension.

Future Directions

- Identify additional protein factors whose expression may be required for optimal hydrogenase expression and activity;
- Identify the promoter regions and transcriptional elements activating the expression of hydrogenase in *C. reinhardtii*;
- Determine whether the FXL proteins sense O₂, and establish how the signal for O₂ is transmitted from the sensing proteins to cellular regulation. In particular, determine whether these sensing proteins relate to hydrogenase gene expression and H₂ production in *Chlamydomonas reinhardtii*.

Publications (including patents) acknowledging the grant or contract in 2007:

- Ghirardi, ML, MC Posewitz, PC Maness, A Dubini, J Yu and M Seibert. **2007**. Hydrogenases and hydrogen photoproduction in oxygenic photosynthetic organisms. *Ann. Rev. Plant Biol.* 58, 71-91.
- Nagy, LE, JE Meuser, S Plummer, M Seibert, ML Ghirardi, PW King, D Ahmann and MC Posewitz. **2007**. Application of gene-shuffling for the rapid generation of novel [FeFe]-hydrogenase libraries. *Biotechnol. Lett.* 29: 431-430.