

# Biological Systems for Hydrogen Photoproduction Maria L. Ghirardi



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## **Overview**

#### Timeline

Project start date: FY00 Project end date: FY18 Percent complete: N/A

#### **Budget**

Funding received in FY08: \$2,000K

Funding allocated for FY09: \$840K

#### **Barriers**

Production barriers addressed

- Continuity of H<sub>2</sub> production (AI)
- Feedstock cost in an integrated system (AT)

#### **Partners**

Dr. Anatoly Tsygankov, Russian Academy of Sciences, Pushchino, Russia Dr. Michael Flickinger, North Carolina State University Dr. Mace Golden, GoldenBioenergy, CO Dr. Eric Johnson, Johns Hopkins University

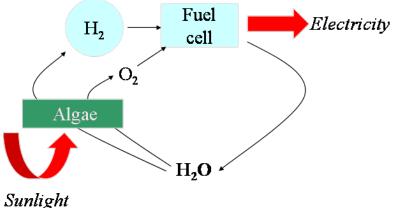
## **Objectives/Relevance**

**General**: Develop photobiological or integrated photobiological/fermentative systems for large-scale H<sub>2</sub> production.

- **Task 1**: Address the O<sub>2</sub>-sensitivity of hydrogenases that prevents continuity of H<sub>2</sub> photoproduction.
- Task 2: Utilize an anaerobic H<sub>2</sub>-producing method (sulfur deprivation) as a platform to address other factors limiting commercial algal H<sub>2</sub> photoproduction.
- **Task 3**: Integrate photobiological and fermentative systems in different configurations for more efficient H<sub>2</sub> production.

### Task 1 – O<sub>2</sub> Sensitivity of Hydrogenases Objectives/Relevance

Develop and optimize *aerobic* photobiological systems for the production of  $H_2$  from water by engineering a  $H_2$ -producing catalyst ([FeFe]-hydrogenase) that has an extended half-life following exposure to  $O_2$ .



#### **Programmatic milestones**

<b>Parameters</b>	Current Status	2013 Target	Maximum Potential
Duration of continuous	90 days (anaerobic)	-	
photoproduction	cycles of 10 days (immobilized, aerobic)	10 min (aerobic)	12 hours (aerobic)
O <sub>2</sub> tolerance (half-	~4 days after exposure to air		
life in air)	(bacterial enzyme)		

### Task 1 – O<sub>2</sub> Sensitivity of Hydrogenases Approach/Milestones

Apply rational, site-directed mutagenesis to a bacterial [FeFe]- and [NiFe]hydrogenases; express mutant enzymes in *E. coli* and test mutants for increased tolerance to  $O_2$  (Subtask 1).

Develop DNA plasmids to express heterologous wild-type or mutated hydrogenases in *Chlamydomonas reinhardtii* in order to test O<sub>2</sub>tolerance in the alga (Subtask 2).

Initiate random mutagenesis/higher-throughput approaches for generation of hydrogenases with increased tolerance to  $O_2$ ; express mutant enzymes in *E. coli* and test mutants for increased tolerance to  $O_2$ (Subtask 3).

Milestones	Completion date	<u>Status</u>
3.3.4 Test the performance of immobilized ATPase mutants	6/08	completed
3.3.5 Test the performance of immobilized antenna mutants	s 10/08	completed
<ul> <li>3.3.6 Introduce and test the expression of a clostridial hydrogenase gene in <i>Chlamydomonas reinhardtii</i></li> <li>3.3.7 Design and test a new DNA construct for <i>E. coli</i></li> </ul>	2/09 (postponed from 08/08)	completed
expression of hydrogenases	12/08	completed

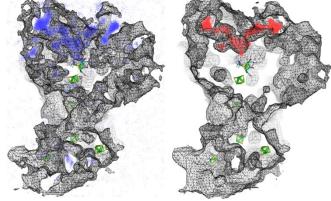
## **Task 1 – Technical Accomplishments**

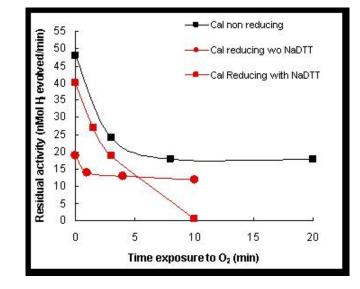
**Subtask 1 – Modeling and Site-Directed Mutagenesis** 

Earlier computational modeling indicated two gas-diffusion pathways in **[FeFe]-hydrogenases** that allow  $O_2$  to access the active site and inhibit their catalytic activity. Site-directed mutagenesis was initiated, aiming at closing those pathways. However, our studies led to the observation that, **depending on the purification procedures, different populations of hydrogenases show different sensitivity to O<sub>2</sub> inactivation.** 

**Results**: Lack of ( $\blacksquare$ ) or short exposure to reductant ( $\blacksquare$ ) results in enzymes that are partially insensitive to O<sub>2</sub> inactivation, whereas enzymes exposed to reductant throughout the purification process exhibit classical O<sub>2</sub> inactivation rates ( $\bullet$ ).

**Conclusion and Future Work**: We will focus on understanding the factors that affect the  $O_2$  sensitivity of the enzyme before proceeding with the mutagenesis work. We will conduct additional experiments to understand the nature of the different states of the hydrogenase enzyme as well as their relationship to  $O_2$  tolerance.

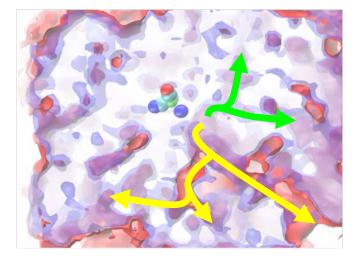




## Task 1 – Technical Accomplishments

**Subtask 1 – Modeling and Site-Directed Mutagenesis** 

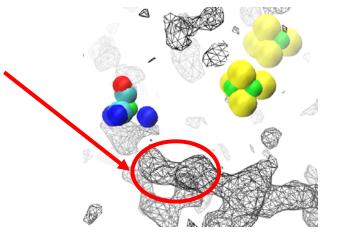
Computational modeling was initiated to determine whether accessibility to the catalytic site was also involved in conferring O<sub>2</sub>-tolerance to **[NiFe]-hydrogenases**.



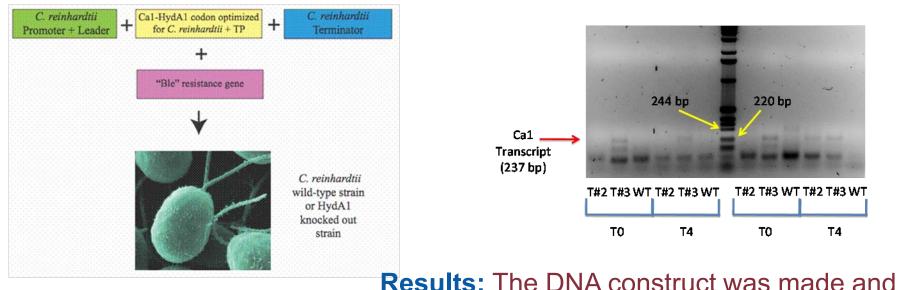
**Results**: Three pathways for  $O_2$  diffusion (yellow) were identified. Two more pathways (green) were found for  $H_2$ , suggesting that  $H_2$  can still migrate out even if all  $O_2$  pathways are blocked.

**Results:** Identified key region for O<sub>2</sub> to further diffuse into the hydrogenase interior and deactivate the [NiFe]-cluster.

**Future Work**: Identify specific targets for mutagenesis; implement them and test for changes in  $O_2$  tolerance *in vitro*.



#### Task 1 – Technical Accomplishments Subtask 2 – Transformation of Green Algae

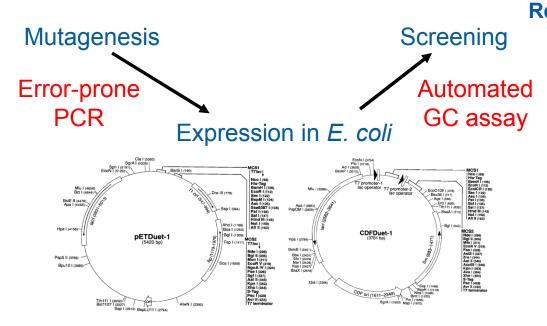


esults: The DNA construct was made and we have demonstrated the presence of Cal gene expression by RT-PCR (see figure above).

**Future work**: Test the activity and  $O_2$ -tolerance of the clostridial hydrogenase in positive transformants and determine physiological effects (if any) or a more  $O_2$ -tolerant hydrogenase in photosynthetic organisms.

#### Task 1 – Technical Accomplishments

Subtask 3 – Random Mutagenesis



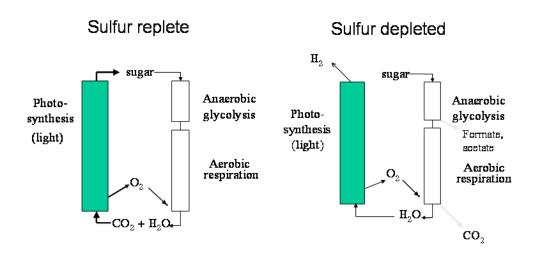
Structural hydrogenase genes and the assembly genes *hydE*, *hydF*, and *hydG* will be incorporated behind the *hya* promoter for expression under anaerobiosis.

Results: Designed DNA constructs for expression of recombinant [FeFe]hydrogenases in *E. coli* and integrated these constructs into an appropriate vector; successfully expressed recombinant hydrogenases in *E. coli* concomitant with their maturation genes, using Novagen's pET-Duet vectors; designed a highthroughput chemochromic assay for screening O<sub>2</sub>-tolerant hydrogenases.

**Future Work**: Test the high-throughput assay; generate random mutagenesis libraries of algal hydrogenases in *E. coli* and screen them for O<sub>2</sub>-tolerant mutants.

## Task 2 – Sulfur-Deprivation Platform Objectives/Relevance

Use the anaerobic, sulfur-deprivation platform (Melis et al., 2000) to address biochemical and engineering issues related to photobiological  $H_2$  production.



Parameters	Current Status	2013 Target	Maximum Potential
Duration of continuous	90 days (anaerobic)		
photoproduction	cycles of 10 days (immobilized, aerobic)	10 min (aerobic)	12 hours (aerobic)
$O_2$ tolerance (half-	~4 days after exposure to air		
life in air)	(bacterial enzyme)		

## Task 2 – Sulfur-Deprivation Platform Approach/Milestones

Determine the light-conversion efficiency of immobilized, H<sub>2</sub>producing *C. reinhardtii* cultures under different growth conditions.

Test the performance of ATPase mutants under sulfur deprivation.

Test the performance of truncated antenna mutants under the same conditions.

Improve the mechanical stability of the alginate film.

Milestones	Completion date	<u>Status</u>
3.3.4 Test the performance of immobilized ATPase mutants	6/08	completed
3.3.5 Test the performance of immobilized antenna mutant	s 10/08	completed
3.3.6 Introduce and test the expression of a clostridial		
hydrogenase gene in Chlamydomonas reinhardtii	2/09 (postponed from 08/08)	completed
3.3.7 Design and test a new DNA construct for <i>E. coli</i>		
expression of hydrogenases	12/08	completed

## Task 2 – Sulfur-Deprivation Platform Technical Accomplishments

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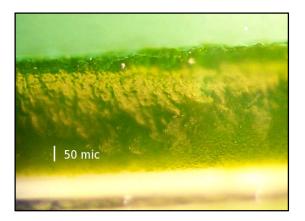
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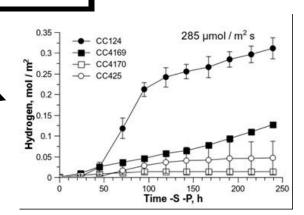


**Results:** In the past year, we have **demonstrated lightconversion efficiencies of about 1% at 29**  $\mu$ E m<sup>-2</sup> s<sup>-1</sup> (solar) **and some H**<sub>2</sub> **production in the presence of O**<sub>2</sub> with cells immobilized in alginate films, underscoring the potential of the technique for higher efficiencies and rates.

#### **Results:**

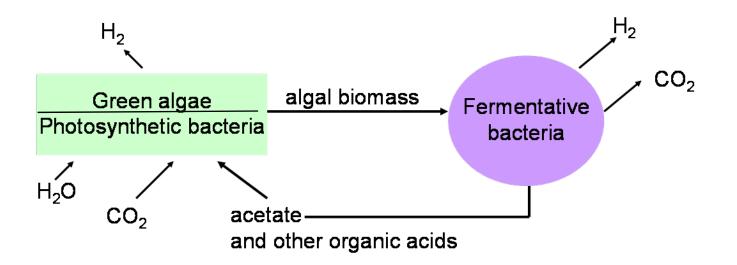
- Demonstrated 30%–45% more H<sub>2</sub> gas production using an ATPase mutant (not limited by the formation of a proton gradient).
- Showed higher and sustained rates of H<sub>2</sub> production by a truncated antenna mutant under 1/10<sup>th</sup> of a sun.

**Future Work:** Further investigate the performance of the ATPase mutants and initiate a new collaboration to utilize them more efficiently; test other truncated antenna mutants; continue to improve the stability of the alginate films.



## Task 3 – Integrated System Objectives/Relevance

Integrate photobiological with fermentative organisms to more efficiently utilize the solar spectrum and the substrates/products from each reaction for  $H_2$  production.



## Task 3 – Integrated System Approach/Milestones

- Determine whether a H<sub>2</sub>-producing, fermentative consortium can utilize spent algal and photosynthetic bacterial biomass (Subtask 1).
- Find a consortium of organisms that is able to ferment organic wastes, produce organic acids to support photosynthetic bacteria growth, and produce H<sub>2</sub> at high efficiency (Subtask 2).

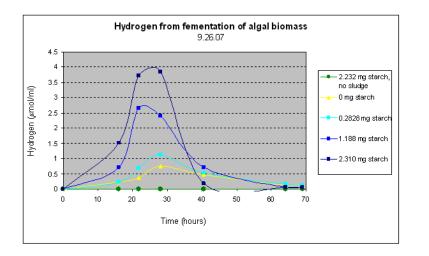


The continuation of this subtask will be determined by the results of a techno-economic analysis by Directed Technologies, Inc., that is being completed.

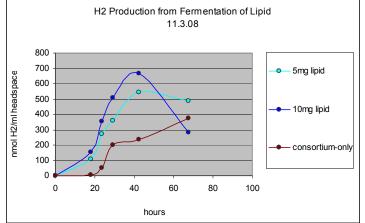
#### (No milestones in FY09)

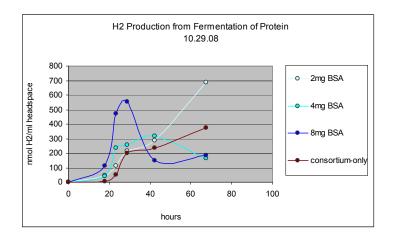
#### Task 3 – Technical Accomplishments Subtask 1 – Fermentation of Algal Biomass

**Results**: A fermentative consortium was shown to be capable of metabolizing algal biomass, purified algal lipids (DGDG), and purified proteins, co-producing H<sub>2</sub> gas and organic acids, with a final yield of 0.45  $\mu$ g H<sub>2</sub>/mg biomass (nonoptimized).



**Future work**: Test whether the consortium can metabolize alginate films; scale up fermentation to 200 ml and optimize it.

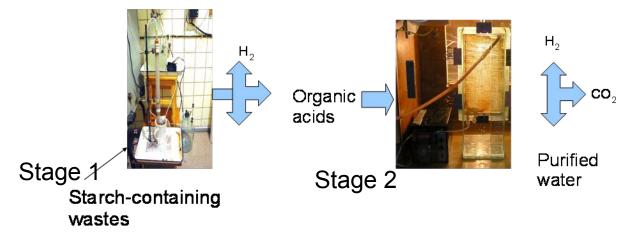




#### Task 3 – Technical Accomplishments Subtask 2 – Fermentative and Photosynthetic Bacteria

#### **Results:**

- 1. Demonstrated H<sub>2</sub> production by fermentative organisms using starch-rich potato wastes, accompanied by production of organic acids.
- 2. Showed H<sub>2</sub> production by photosynthetic bacteria using organic acids from fermentation of potato wastes.



**Future work:** Integrate fermentation of potato waste with photosynthetic bacterial  $H_2$  production and determine the total efficiency of the process, using dilute wastes.

#### **Collaborations**

#### • Task 1:

Dr. Mace Golden, Golden Bioenergy, CO (random mutagenesis and high-throughput assay).

• Task 2:

Dr. Eric Johnson, Johns Hopkins University (ATPase mutants).

• Task 3:

Dr. Anatoly Tsygankov, Russian Academy of Sciences, Pushchino, Russia (fermentation of potato wastes, photosynthetic bacterial H<sub>2</sub> production).

## Summary

- **Task 1:** (1) We continued to investigate the  $O_2$  sensitivity of the two redox states of the [FeFe]-hydrogenase using recombinant enzymes; (2) the expression of a clostridial hydrogenase gene in *C. reinhardtii* was successful, and we will test the expressed enzyme's activity and  $O_2$  tolerance next; and (3) a high-throughput screening for  $O_2$ -tolerant recombinant hydrogenases was developed and will be tested.
- **Task 2:** (1) The alginate-immobilization process was used to successfully test the H<sub>2</sub>-producing performance of ATPase and truncated antenna mutants.
- **Task 3:** (1)The fermentative consortium at NREL was shown to metabolize algal starch, lipid, and protein at a non-optimal yield of 0.45 μg H<sub>2</sub>/mg biomass; and (2) the consortium is also able to utilize algal biomass isolated from a variety of growth conditions, both fresh and frozen (damaged), without the need for pretreatment.