

DOE Bioenergy Technologies Office (BETO) 2015 Project Peer Review

Maximizing multi-enzyme synergy in biomass degradation in yeast

March 26
Technology Area Review

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This presentation does not contain any proprietary, confidential, or otherwise restricted information

Goal Statement

- To demonstrate synthetic biology technologies for rapidly developing organisms suitable for industrial lignocellulose processing
- To develop strains for reducing saccharification costs
- To develop American technologies to be commercialized for making biomass-derived fuels and chemicals competitive with those derived from fossil fuels toward energy independence and sustainable development

Quad Chart Overview

Timeline

- 25-Apr-2013
- 25-Apr-2015
- 50% complete

Budget

	Total Costs FY 10 - FY 12	FY 13 Costs	FY 14 Costs	Total Planned Funding (FY 15 - Project End Date)
DOE Funded	\$0	\$60,539	\$430,127	\$775,558
Project Cost Share (Comp.)*	\$0	\$0	\$132,647	\$8,045

Barriers

- Barriers addressed
 - Bt-F (Cellulase Enzyme Production Cost)
 - Bt-G (Cellulase Enzyme Loading)
 - Bt-J (Catalyst Development)from Multi-Year Program Plan

Partners

- Partners
 - NREL (Pin-Ching Maness)
- Other interactions/collaborations
 - Synthetic Genomics, Inc.
 - NREL (Dan Schell, Ling Tao)
 - Novozymes

1 - Project Overview

- Synergism among carbohydrate-active enzymes not sufficiently explored for biofuel production
- Synthetic biology technologies to rapidly construct yeast strains expressing many enzymes to discover novel synergy
- Reducing costs associated with saccharification

2 – Approach (Technical)

1. *Gene synthesis to enable the incorporation of any known cellulase sequence, as well as codon optimization for improved expression in yeast*
 2. *Introduction of the constructs into yeast to confirm activity*
 3. *'Green Monster' process to construct multi-enzyme strains*
 4. *Yeast sexual cycling to shuffle introduced enzymes*
 5. *Viability assay to select strains that contain optimal combinations of saccharification enzymes*
 6. *Demonstration of improvements over the baseline strain in terms of ethanol produced in laboratory-scale SSF and HHF experiments*
- *Critical success factors: >33% reduction in required enzyme load to achieve the same saccharification level in lab-scale cultures*
 - *Go/no-go criterion: functional expression of 20 cellulases (already met)*

2 – Approach (Management)



*Maxim Kostylev, Ph.D.
(David Wilson's lab)*



*Timothy Hanly, Ph.D.
(Mike Henson's lab)*

Small group of motivated researchers with correct skills

Weekly lab meeting, monthly note checking, monthly TC with DOE

- *Critical success factors:*

- Successful completion of all proposed tasks*

- High-impact publications*

- Patent application*

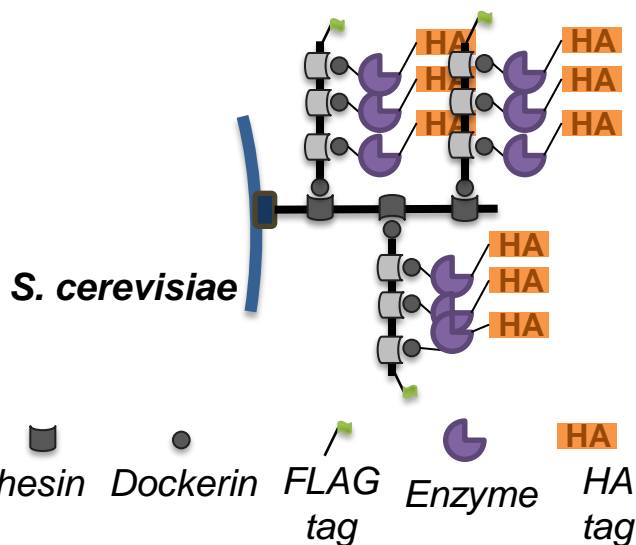
- Identification of funders or corporate partners for subsequent work*

- *Challenges:*

- Initial delays*

3 – Technical Accomplishments/ Progress/Results

- Expression of mini-scaffoldins for accommodating cellulases on the yeast cell surface

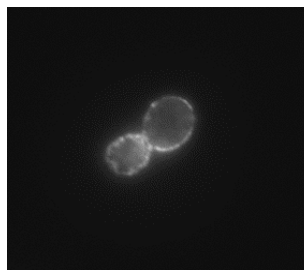


Anti-FLAG staining

Microscopy



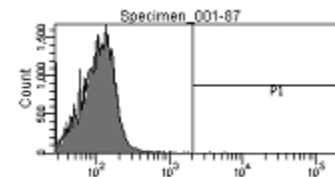
Parent strain



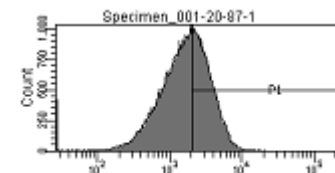
R. flavefaciens
scaffoldins
(codon-optimized
by DNA2.0)

Flow cytometry

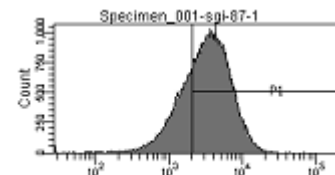
Parent strain



Codon-optimized by DNA2.0



Codon-optimized by SGI-DNA

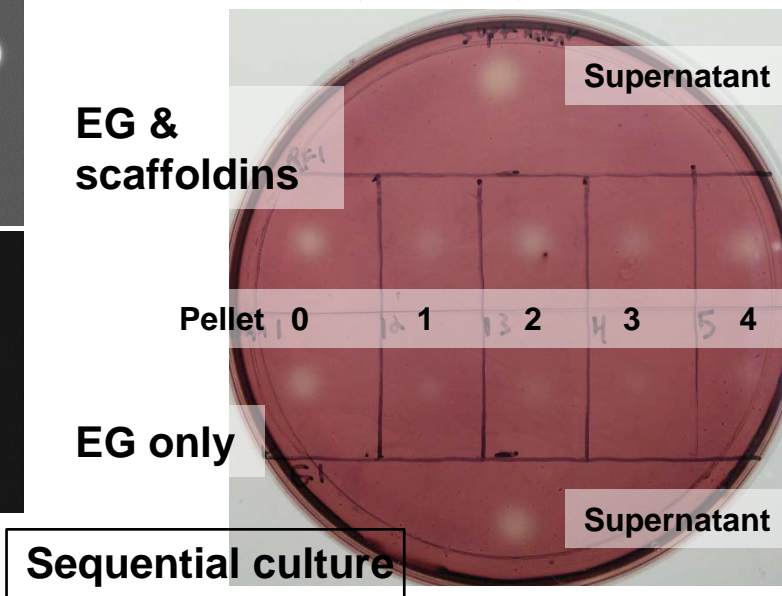
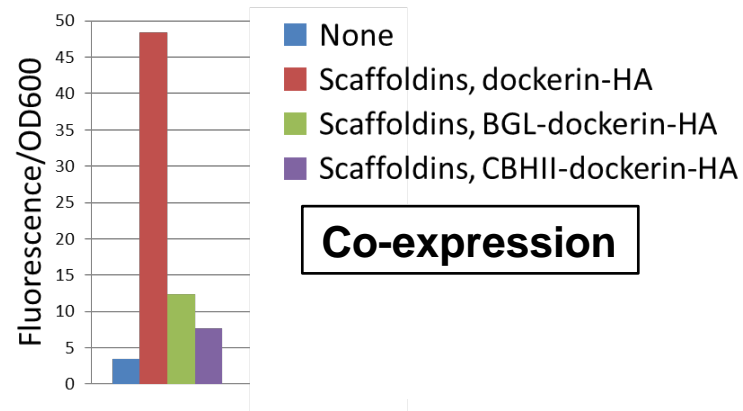
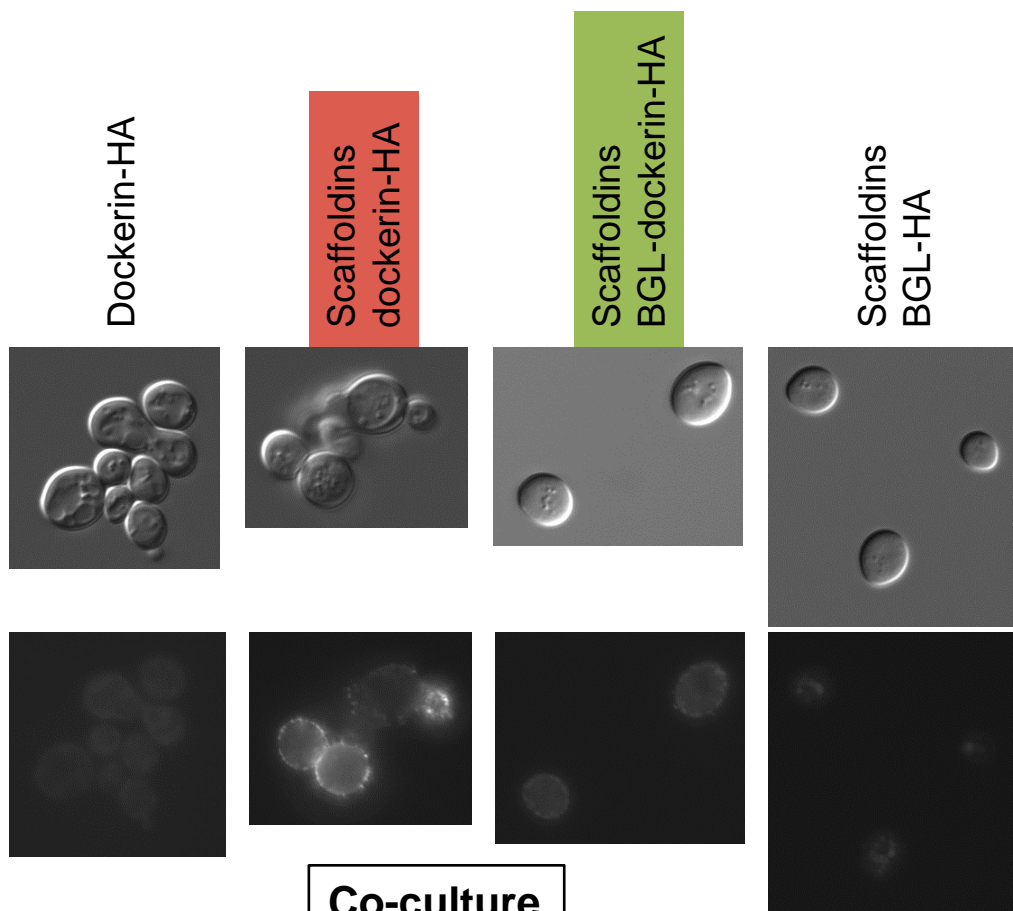


Fluorescence

Inspired by nature and also:
Bayer EA *et al.* *Trends Biotechnol.* 1994
Wen F *et al.* *Appl. Environ. Microbiol.* 2010
Goyal G *et al.* *Microb. Cell Fact.* 2011
Tsai SL *et al.* *ACS Synth. Biol.* 2012
Fan LH *et al.* *PNAS* 2012

3 – Technical Accomplishments/ Progress/Results

- Functional expression of mini-scaffoldins for accommodating cellulases on the yeast cell surface



3 – Technical Accomplishments/ Progress/Results

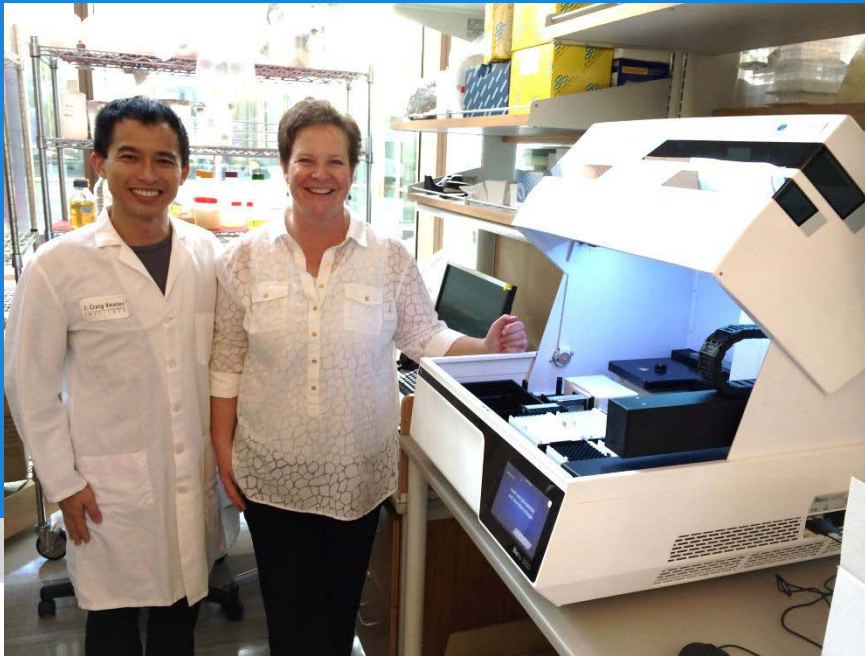
- *Pipeline for generating and characterizing cellulase-expressing yeast strains*

98 carbohydrate-active enzymes

Gene synthesis

Gibson assembly or E. coli assembly

96-well-format yeast transformation

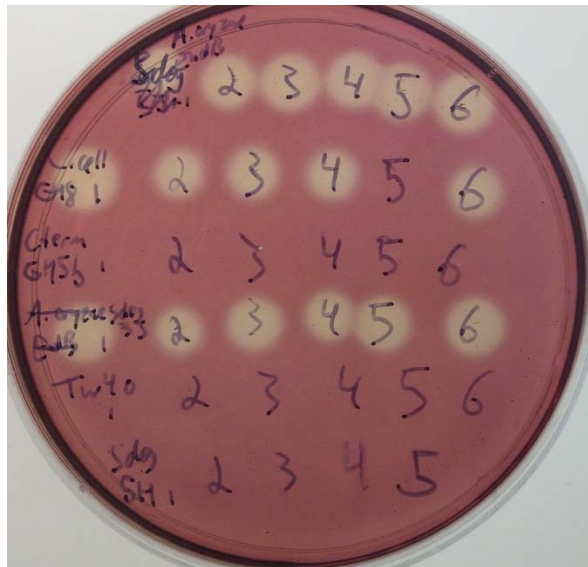


*The first lab in the world to receive
Synthetic Genomics BioXp™ 3200
(for beta-testing)*

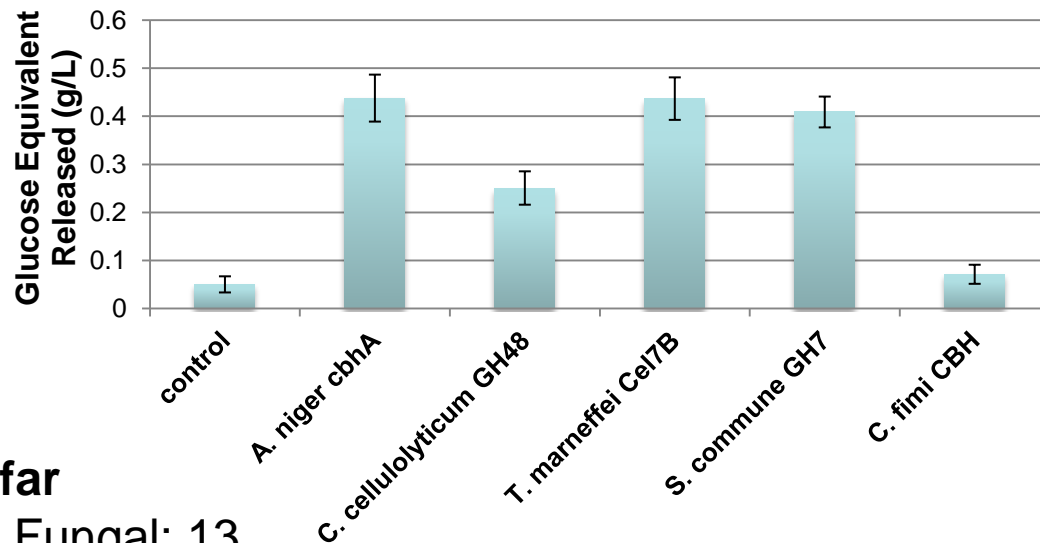
56 kb per day

3 – Technical Accomplishments/ Progress/Results

- Pipeline for generating and characterizing cellulase-expressing yeast strains



CMC- and barley β -glucan-overlay assays
PASC DNS assay
SDS-PAGE and Western



28 with demonstrated activity so far

Kingdom Bacterial: 15 Fungal: 13

Enzyme Endo: 14 Exo: 11 BGL: 3

Glycoside Hydrolase Family

GH1: 1	GH3: 2	GH5: 5	GH6: 4	GH7: 3
GH8: 2	GH9: 5	GH12: 1	GH48: 5	

3 – Technical Accomplishments/ Progress/Results



Non-mutant

- *Multi-enzyme strains being constructed*



Marker 1

Single mutant



**Marker 1
Marker 2**

Double mutant



**Marker 1
Marker 2
Marker 3**

Triple mutant













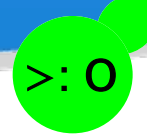


**Marker 1
Marker 2
Marker 3
Marker 4**

Quadruple mutant

The Green Monster process

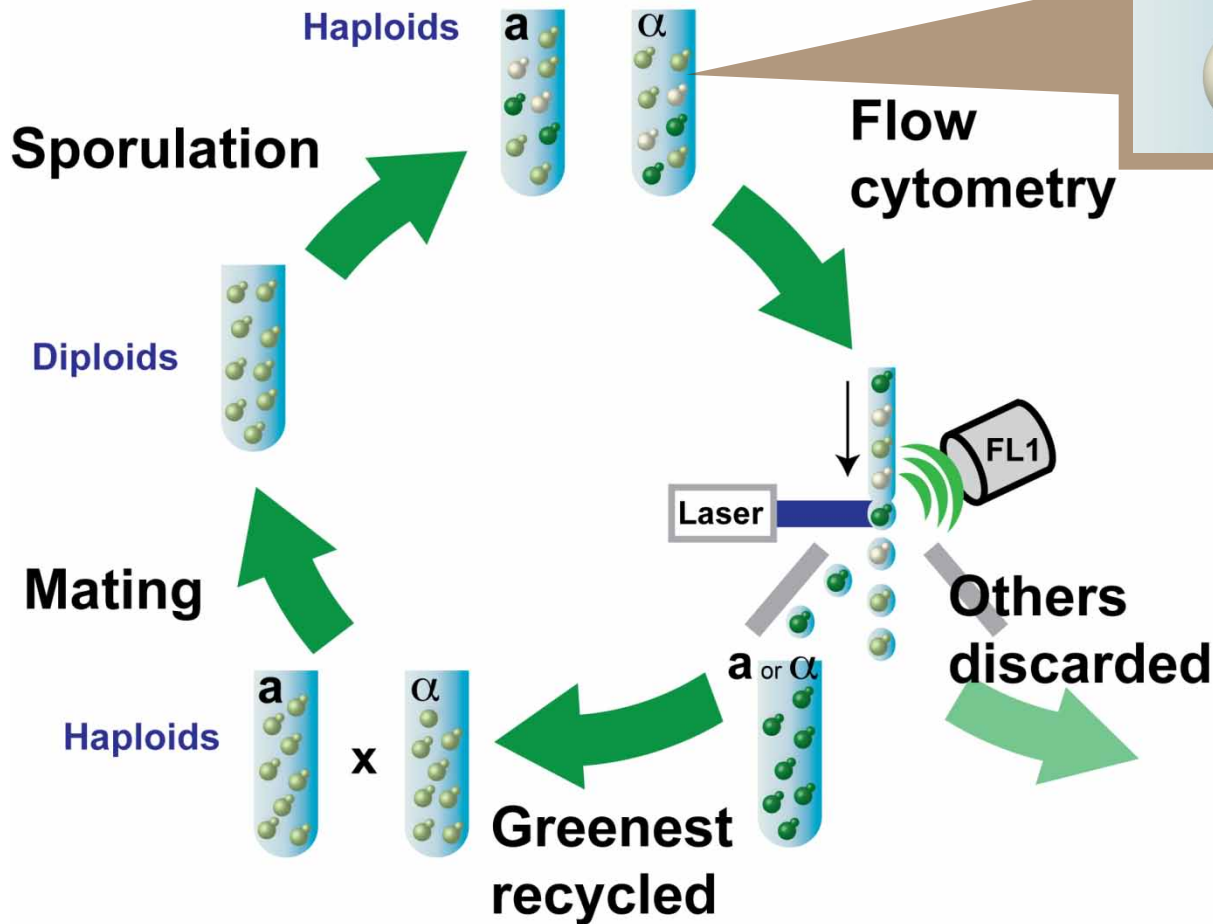
3 – Technical Accomplishments/ Progress/Results

		Non-mutant				
	Marker 1	Single mutant		1 GFP		
	Marker 1 Marker 2	Double mutant		2 GFP		5 GFP
	Marker 1 Marker 2 Marker 3	Triple mutant		3 GFP		6 GFP
	Marker 1 Marker 2 Marker 3 Marker 4	Quadruple mutant		4 GFP		7 GFP

Monstah!

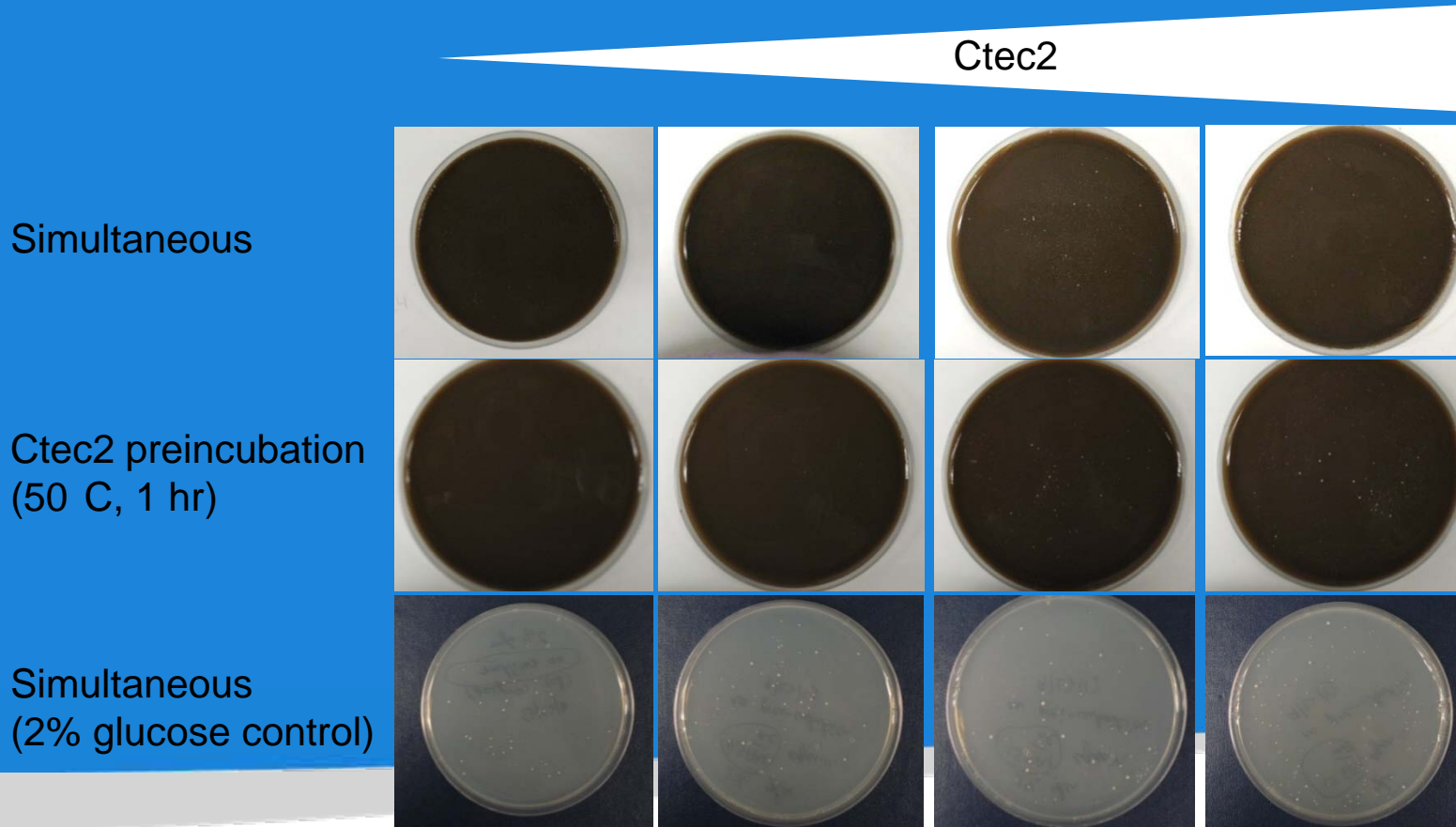
The Green Monster process

3 – Technical Accomplishments/ Progress/Results



3 – Technical Accomplishments/ Progress/Results

- *Screening method being developed - colony growth on corn stover agar plates*



3 – Technical Accomplishments/ Progress/Results

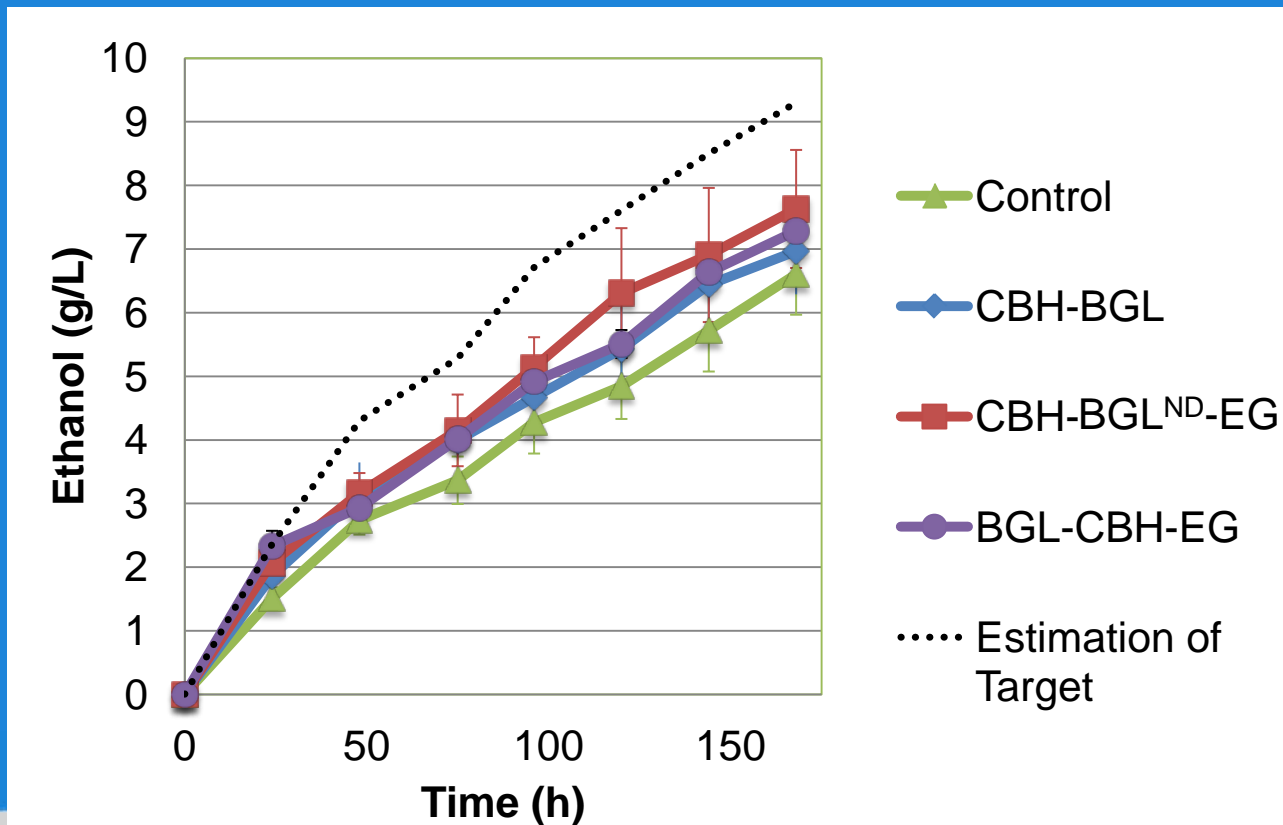
- Very preliminary corn stover result

SSF

Enzyme loading:
1 FPU/g cellulose
10% w/w solids

% conversion

Control	20	2
CBH-BGL	21	2
CBH-BGL ND -EG	23	3
CBH-BGL-EG	22	1



4 – Relevance

- *This project addresses barriers Bt-F (Cellulase Enzyme Production Cost), Bt-G (Cellulase Enzyme Loading), and Bt-J (Catalyst Development) identified in the BETO Multi-Year Program Plan*
- *Strains with superior saccharification properties will be licensed to or further developed with industrial partners*
- *Yeast strains that require less enzyme loading will result in reduced cost for enzyme cocktail to positively impact the commercial viability of biomass and/or biofuels*
- *Preparation is ongoing for IP protection*

5 – Future Work

- *Generation and identification of strains carrying optimal combinations of enzymes using corn stover as a feedstock*
- *Identification of characteristic features of combinations that result in efficient saccharification*
- *Demonstration of increase in saccharification efficiency and decrease in necessary enzyme load*
- *Preliminary assessment of the effect of scale-up using a bench-top bioreactor*
- *Final validation*
- *No more go/no-go point*

Summary

1. Overview: Powerful synthetic biology methods enable the reconstitution of natural synergism among enzymes in laboratory/industrial processes
2. Approach: Mating and meiosis in yeast are used to construct numerous multi-enzyme strains
3. Technical Accomplishments/Progress/Results: We have designed and built a mini-cellulosome system, generated synthetic constructs for 98 enzyme genes, and so far confirmed enzyme activity for 28 enzymes
4. Relevance: Our research targets reducing costs associated with enzymes by reducing enzyme loading
5. Future work: We will generate and screen multi-enzyme strains to identify those containing optimal sets of enzymes

Additional Slides

Publications, Patents, Presentations, Awards, and Commercialization

Publications fully or partly supported by DE-EE0006109

(1) Karas, B.J., Jablanovic, J., Irvine, E., Sun, L., Ma, L., Weyman, P.D., Gibson, D.G., Glass, J.I., Venter, J.C., Hutchison, C.A. 3rd, Smith, H.O. & **Suzuki, Y.** Transferring whole genomes from bacteria to yeast spheroplasts using entire bacterial cells to reduce DNA shearing. *Nature Protocols*. 2014 Apr; 9(4):743-750.

(2) Labunskyy, V.M., **Suzuki, Y.** (co-first author), **Hanly, T.J.**, Murao, A., Roth, F.P. & Gladyshev, V.N. The insertion Green Monster (iGM) method for expression of multiple exogenous genes in yeast. *G3: Genes, Genomes, Genetics*. 2014 Apr 28; 4(7):1183-1191.

(3) Karas, B.J., Wise, K.S., Sun, L., Venter, J.C., Glass, J.I., Hutchison, C.A. 3rd, Smith, H.O. & **Suzuki, Y.** Rescue of mutant fitness defects using *in vitro* reconstituted designer transposons in *Mycoplasma mycoides*. *Frontiers in Microbiology*. 2014 Jul 23; 5:369.

(4) Karas, B.J., **Suzuki, Y.** & Weyman, P.D. Strategies for cloning and manipulating natural and synthetic chromosomes. *Chromosome Research*. Published online.

(5) **Suzuki, Y.**, Assad-Garcia, N., **Kostylev, M.**, Noskov, V.N., Wise, K.S., Karas, B.J., Stam, J., Montague, M.G., **Hanly, T.J.**, Enriquez, N.J., Ramon, A., Goldgof, G.M., Richter, R.A., Vashee, S., Chuang, R.Y., Winzeler, E.A., Hutchison, C.A. 3rd, Gibson, D.G., Smith, H.O., Glass, J.I. & Venter, J.C. Bacterial genome reduction using the progressive clustering of deletions via yeast sexual cycling. *Genome Research*. 2015 Mar;25(3):435-444.

Three more papers in preparation

Meeting presentations

Kostylev, M., Hanly, T.J. & Suzuki, Y. Synthetic biology for biofuels: the engineering of a multivalent cellulosome on the cell surface of *Saccharomyces cerevisiae*. American Society for Microbiology 114th General Meeting (Boston, MA). 2014 May17-20.

Two meeting presentations in preparation for 37th Symposium on Biotechnology for Fuels and Chemicals

Technology transfer and commercialization efforts

Preparing for IP protection