

# DOE Bioenergy Technologies Office (BETO) 2015 Project Peer Review

2.3.2.103 Fungal Genomics

March 8, 2017
Biochemical Conversion Area Review

Jon Magnuson PNNL

### **Goal Statement**



▶ Goal: Development of efficient and robust fungal biocatalysts and bioprocesses that utilize lignocellulose feedstocks to produce advanced biofuels and bioproducts at lower cost.

### **Quad Chart Overview**



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### **Timeline**

AOP project start date: 10/1/15

Project end date: 9/30/18

### **Budget**

	FY 15 Costs	FY 16 Costs	FY 17 Costs	Total Planned Funding (FY 15- 17Project End Date
DOE Funded	1.5	1.5	1.5	4.5
Project Cost Share (Comp.)*	0	0	0	0

### **Barriers**

#### Barriers addressed

#### **■** Bt-J. Catalyst Development

- Process robustness and productivity to lower cost
  - Higher value bioproducts to support economical biofuel production
- Bt-L. Biochemical/Thermochemical Interface
  - Lipids for catalytic upgrading to fuel
  - Fungal cell mass for HTL
  - Bioproduct precursors for catalytic processing to various chemicals.

### **Partners**

#### Funded Partners

- U. of Kansas, Berl Oakley, 55K
- Collaborators
  - NREL, JBEI, JGI

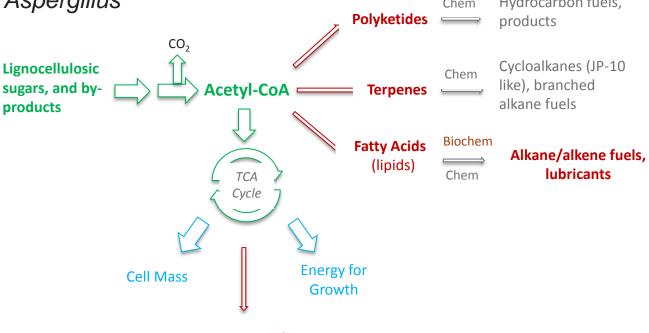
### Industrial Advisory Panel

- Novozymes\*
- POET Research\*
- Mycosynthetix
- \*Cost share or funds-in partners on past projects

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### 1 - Project Overview

- Development of industrially\* relevant fungal biocatalysts & bioprocesses for fuels and bioproducts (chemicals)
  - Hydrocarbon fuels and bioproducts: triacylglycerides (TAGs), terpenes, polyketides
  - Develop and utilize modern genetic, genomic and bioprocess tools to produce the hydrocarbons and maximize TRY in two platform fungi: *Lipomyces* and *Aspergillus*Chem Hydrocarbon fuels,



**Organic Acids** 

\* Robust growth and production in the presence of inhibitors, efficient utilization of different sugars, scalable bioprocess

### 2 – Management Approach



### **Management Approach**

- ► Annual operating plan (AOP) tied to DOE-BETO goals
- PNNL has an internal project management plan (PMP)
- Quarterly milestones & Go/No-Go decisions to direct, focus and measure progress
- Quarterly written reporting and conversations with BETO TM
- Weekly team meetings to maintain focus and tackle technical challenges
- Co-PI (Butcher) to coordinate efforts and maintain team focus
- Work with chemical catalysis experts to identify biomolecules of interest for products/fuels
- Tap into industrial perspective through quarterly meetings with Industrial Advisory Panel: Novozymes, POET, Mycosynthetix
- Input from a variety of internal and external reviews

#### \*Scientific Team

Mark Butcher Jim Collett
Dave Culley Ziyu Dai
Characa Dava Characa Dava Characa Dava Characa Dava Characa Dava Characa Charac

Shuang Deng Beth Hofstad Ellen Panisko Kyle Pomraning

Swarnendu Tripathi

### 2 – Technical Approach



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**Approach**: Develop and *utilize* modern fungal genetic engineering, integrated genomics and bioprocess engineering capabilities to produce robust, efficient organisms (biocatalysts) and bioprocesses for biofuels and bioproducts

#### **Critical Success Factors**

- Maximize TRY:
  - high Titer for downstream processing efficiency
  - high **Rate** to minimize CAPEX/OPEX
  - high Yield to maximize use of costly biomass feedstocks
- ► Robust organisms for conversion of challenging biomass hydrolysates containing inhibitors and mixed sugars
- Development of reproducible, robust and efficient bioprocesses that will scale



# 2 – Technical Approach: Complementary Biocatalyst and Bioprocess Development



### **Genetic Engineering**

- Advanced genetic tools
  - Rational design;
     reverse genetics
- Strains forBioprocess Development

#### **Bioprocess Platforms**

- Lipomyces for lipids
- Aspergillus for bioproducts (terpenes/polyketides)

### Systems Biology/ Genomics

- Forward genetics
- Transcriptomics
- •Gene candidates for **Genetic Engineering**



### Bioprocess Development

- Bioreactors
- TRY assessment
- Samples forSystems Biology

#### **Tech Transfer** to

**Bioenergy Industry** 

- Biocatalyst
- Bioprocess
   Description
- Development
   Tools
- TEA

# 3 – Project Accomplishments Why is Lipomyces an excellent choice for an industrial biocatalyst?



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#### **Attributes**

- Highly productive oleaginous yeast: ~65% of cell mass as lipid
- Has a genome sequence from JGI: NRRL Y-11557
- Grows and produces lipids on lignocellullose relevant sugars:
  - Excellent on **glucose**, galactose, mannose, and **xylose**
  - Also utilizes cellobiose and L-arabinose
- We've developed genetic tools
- Behaves well in conventional aerobic bioreactors

MycoCosm Project List Login

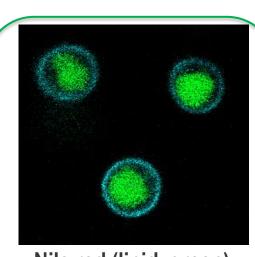
Lipomyces starkeyi NRRL Y-11557\* is an



Service, Forest Products Laboratory

ascomycetous yeast belonging to the order Saccharomycetales. It is known in its telomorphic form with no known anomorphic connections. L. starkeyi NCYC 1436 has been reported to have eleven chromosome-sized DNA molecules ranging from 0.7 to 2.8 kb and a total estimated genome of 15 Mb (4). Most notably from the perspective of biological energy production, L. starkeyi can form more than 60% of its cell dry weight under optimal conditions of carbon source, yeast extract and ferrous sulfate. Lipid production is maximal when glucose and xylose are supplied in a ratio of approximately 2:1 (12). L. starkeyi will produce lipids from various sugars, whey permeate (2), and even sewage sludge (3). Temperature affects lipid composition with the highest lipid production rate reported at 28°C (10, 11). Fatty acid analysis of cells grown on whey permeate showed palmitic, stearic, oleic and linoleic acid; as the predominant fatty acids in the triacylglycerol fractions. The phospholipid fractions

were deminated by alois and linelais aside (1) I



Nile red (lipid, green), Calcofluor (cell wall, blue)

# 3 – Project Accomplishments Why is Aspergillus an excellent choice for an industrial biocatalyst?



#### **Attributes**

- Highly productive fungus for enzymes and biochemicals, including generally recognized as safe (GRAS) products
- ► Has multiple genome sequences: ATCC 1015, 11414
- Great genetic tools
- Grows and produces bioproducts on lignocellullose relevant sugars
- Produces enzymes to deconstruct lignocellulose
- Utilizes simple inorganic nutrients
- Highly acid tolerant (pH 1): minimizes sterility requirements, and advantageous for organic acid production
- Appropriate for conventional aerobic bioreactors



understanding of the molecular mechanisms cortholling carbon niger genome. Finally, A. niger is an important model fungus for general, the effects of various environmental factors on suppre

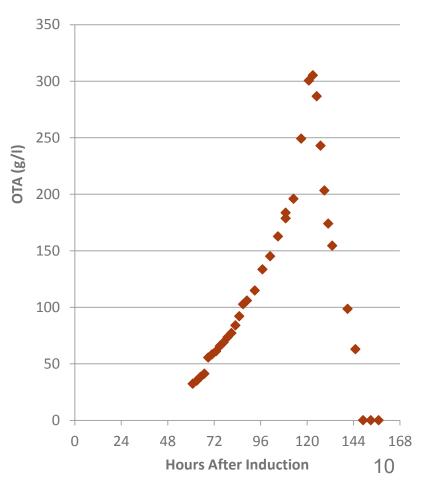
# 3 – Project Accomplishments Aspergillus for Polyketides



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- There are many (est. >100K) different polyketides made by fungi
- We are focused on highly reduced polyketides as potential biofuels and bioproducts precursors
- We have produced 0.7 and 0.5 g/L of two polyketides: asperbenzaldehyde and octatrienoic acid
- 9/30/17 Milestone and a mid FY Go/No-Go dictate concentrating on one for further optimization
- Selected the secreted compound octatrienoic acid for further development as an interesting intermediate to biofuels/bioproducts

## Octatrienoic Acid Bioreactor Run 22

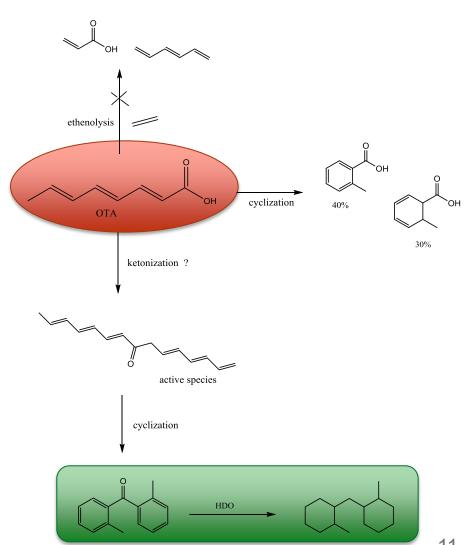


# 3 – Project Accomplishments Chemical conversion of OTA from *Aspergillus*



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- Octatrienoic acid is a potential precursor for biofuels or bioproducts
- ► Ethenolysis/metathesis did not yield the desired acrylic acid and olefin products
- Ketonization will be examined as a possible route to a
   C15 cycloparaffin
- Cyclization is another potential route to aromatics and cyclic chemicals



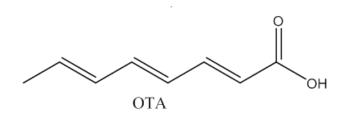
C<sub>15</sub> auto fuel

## 3 – Project Accomplishments Genetic Engineering of *Aspergillus* for Polyketide TRY



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- Maximizing TRY can involve: increasing production and/or decreasing degradation
- OTA-PKS under control of a strong MEK-inducible promoter, which provided 0.5 g/L titers in shake flasks
- Product degradation occurred after a sharp maximum OTA titer in the bioreactor
- ► **Goal**: utilize a different promoter that does not require a volatile or expensive inducer...more practical for a real bioprocess
- Examining two other promoters:
  - Constitutive gpdA promoter
  - Nutrient inducible *nmt1* promoter



- ► Goal: prevent product degradation or modification
- Targeting likely catabolic pathways
  - Beta-oxidation
  - Alpha-oxidation

# 3 – Project Accomplishments Improving Lipomyces– Homologous Transformation

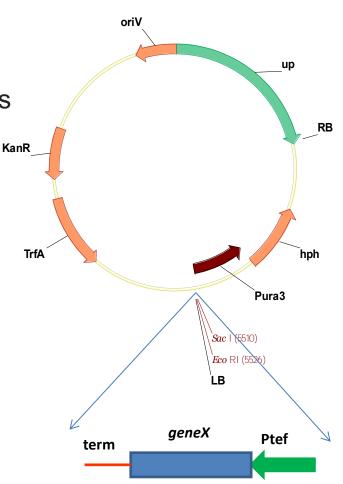


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Challenge: Need a transformation system for gene deletion— to eliminate carbon sinks, increase inhibitor resistance, etc. but...

L. starkeyi didn't have any transformations systems

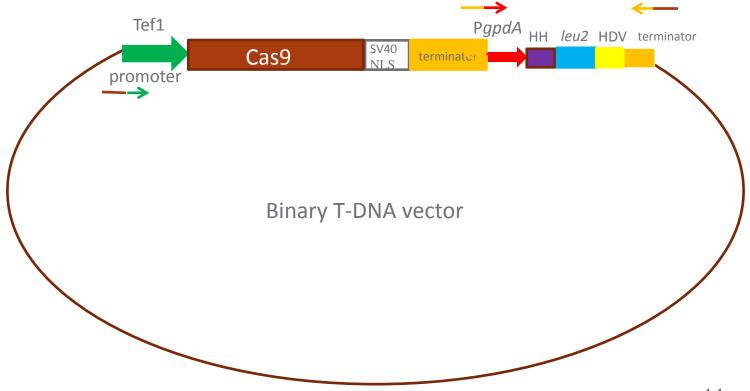
- We previously reported Agrobacterium tumefaciens mediated transformation
- Have since succeeded in using a lithium acetate and electroporation method for gene deletion
- Have disrupted ku70 to obtain homologous recombination!



# 3 – Project Accomplishments Improving *Lipomyces*– CRISPR



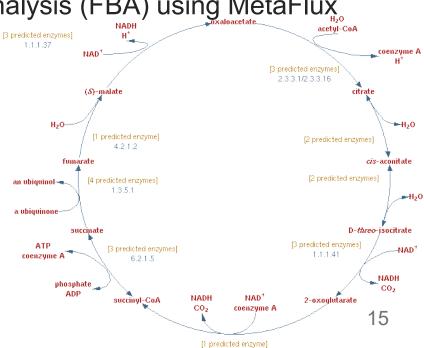
- Goal: faster genome editing to accelerate targeted genetic improvements
- Have succeeded in instituting CRISPR/cas9
- Used CRISPR to generate a leu2 knockout = leucine auxotroph
- Increasing efficiency of CRISPR—examining alternate promoter



### 3 - Project Accomplishments Lipomyces Metabolic Modeling



- Used Pathway Tools and the JGI genome data of L. starkeyi to establish a Pathway/Genome Database (PGDB)
- Using our RNA-Seq data and Pathway-Hole-Filler we closed 107 pathway holes
- ► Ran the Transport-Inference-Parser to annotate 65 unique transport reactions catalyzed by 333 unique transporters
- Currently creating a metabolic model within the Pathway Tools environment to perform Flux Balance Analysis (FBA) using MetaFlux
- Provides a framework for:
  - Understanding the system
  - Making predictions about genes utilizing omics and bioprocess data



## 3 – Project Accomplishments Comparative transcriptomics for gene target ID



- Two bioreactor runs for transcriptomics samples:
  - 1. Saccharified Pre-treated Corn Stover (PCS)
  - 2. Clean Sugars, 2:1 Glucose:Xylose
- Purposes:
  - Time course analysis to examine lipid production, degradation and other C sinks
  - Comparative analysis between runs to identify inhibitor responses

						Lipid		<b>Yield</b> of	
		Final Dry	Specific	Yield of Cell		Synthesis		Lipids from	Lipids as %
		Cell Mass	growth	Mass from	Lipid <b>Titer</b>	Rate	Peak <b>Rate</b>	Sugar	of Dry Cell
Run	Medium	(g/L)	rate (hr <sup>-1</sup> )	Sugar (g/g)	(g/L)	(g/L/h)	(g/L/h)	(wt%)	Mass
	PCS/MM;								
	2.1% Total								
18. PCS	Sugars	18.6	0.11	0.43	6.7	0.05	0.21	22%	36%
	2.7% 2:1								
19. Glc/Xyl	Glc/Xyl/MM	22.0	0.14	0.43	9.7	0.09	0.29	19%	44%

Constants: defined minimal medium components (MM), 2:1 Glc:Xyl ratio, cell inoculum, temperature, aeration, pH

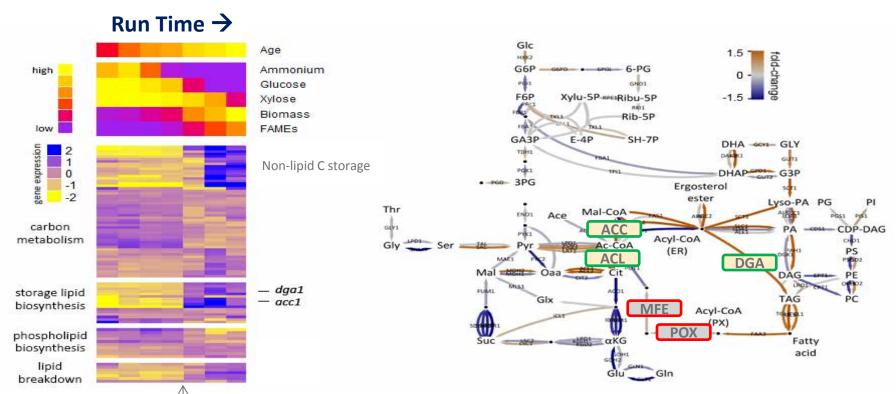
# 3 – Project Accomplishments Comparative transcriptomics for gene target ID



- Nitrogen depletion & lipid biosynthesis conditions
- Gene Targets
  - Overexpression of enzymes for triglyceride biosynthesis
  - Deletion of beta-oxidation or upstream enzymes to increase net productivity
  - ID'd other enzymes in triacylglyceride degradation that may be even better targets
  - ID'd interesting alternative C sink to eliminate

fold-change

Tools: new promoter motifs identified for expressing multiple genes



## 3 – Project Accomplishments Initial Genetic Engineering Targets



- Over-expressed acc1 for acetyl CoA carboxylase and previously reported promising results in shake flasks
- Did not see an improvement in a 30L bioreactor run
- pex10 deletion to disrupt the peroxisome in general, and therefore β-oxidation
- ▶ Did not appear effective in *Lipomyces* under the conditions examined but may manifest an effect under more stressful conditions
- Currently
- ► Targeting multiple gene up-regulation for triglyceride biosynthesis...
- ...plus some new upstream targets in triglyceride degradation from the comparative transcriptomics analysis

# 3 – Technical Accomplishments Objectives for Improvements of the Bioprocess



### **TEA and Design Case Considerations**

- Higher Rate
- Higher Total Mass
- Separation of solids by low cost belt filter

...and/or utilization of those solids downstream Hydrolysis and Fed Batch Biological Conversion Air Seed train To combustor Enzyme From Pretreatment Air blower **Filter** To A500 **Splitter** Storage tank **High-solids hydrolysis** Broth **Batch hydrolysis** (continuous flow) Fed-batch reactor reactor **Evaporator** 

To process water

Figure 9. Simplified flow diagram of the enzymatic hydrolysis, hydrolysate conditioning, and bioconversion process

# 3 – Technical Accomplishments Objectives for Improvements of the Bioprocess



- Real World Substrates: dilute acid pre-treated corn stover (PCS)
- Fed-batch to increase total sugar utilized but reduce inhibitor load
- ► Maximize cell mass for hybrid conversion approach: HTL

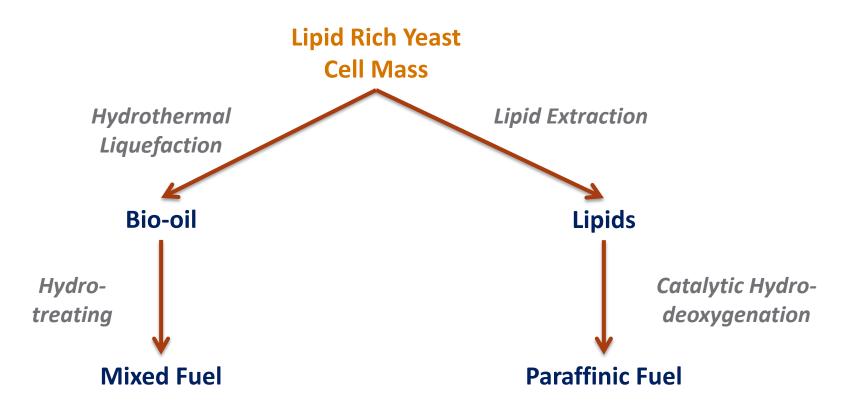
	СО	NDITION	NS	CELLS			LIPIDS				
Expt.	Medium	Inoculum (cells/ml)	~	DCW (g/L)	Specific growth rate (hr <sup>-1</sup> )	Yield: DCW/Sugar (wt%)	<b>Titer</b> (g/L)	Overall Rate (g/L/h)	Peak <b>Rate</b> (g/L/h)	Yield: Lipids from Sugar (wt%)	Lipids as % of DCW
12	CLEAN SUGAR 2.5% 2-1 Glucose, Xylose MM*	1.9E+07	Manual Fed Batch - 46.5% Glucose	20.0	0.08	39%	13.0	0.14	0.90	26%	65%
	PCS only, 2.3% sugars equivalent	1.0E+06	Batch	7.0	0.10	28%	3.1	0.03	0.07	12%	44%
	PCS MM*, 2.1% sugars equivalent	1.0E+06	Batch	18.6	0.11	43%	6.7	0.05	0.21	22%	36%
24	CLEAN SUGAR 6% Glucose MM*	1.2E+06	Manual Fed Batch 100% Glucose, then 76% Xylose	155.7	0.12	38%	56.7	0.46	1.05	14%	36%

<sup>\*</sup> MM = minimal media

# 3 – Technical Accomplishments Oleaginous yeast production alternatives



- HTL (hydrothermal liquefaction): whole cell mass
  - Extraction of lipids and catalytic conversion of triglycerides to alkanes



# 3 – Technical Accomplishments Improvements of the Bioprocess: Maximizing Cell Mass



- High cell mass important for HTL (hydrothermal liquefaction)
- Also important for lipid conversion to alkanes process
- Need to drive up lipid content for the latter

12

0

24

Dry Cell mass (g/L)

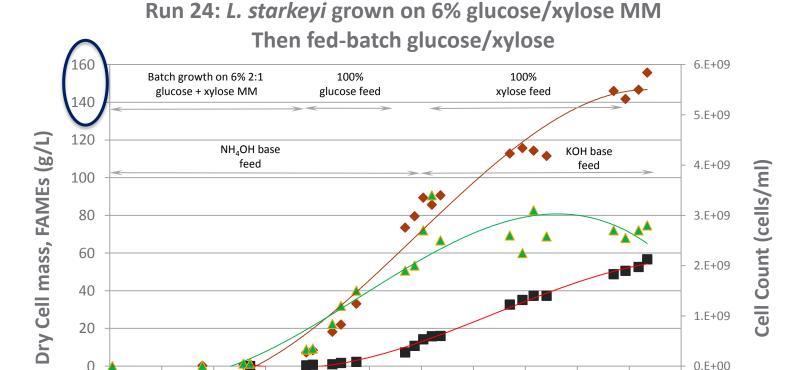
36

48

60

**Culture Age (h)** 

■ FAMEs (g/L)



84

108

96

120

▲ Cell Count (cells/ml)

 $B30\ 24\_Dry\ wts\_FAMEs\_mgb\_jrc.xlsx$ 

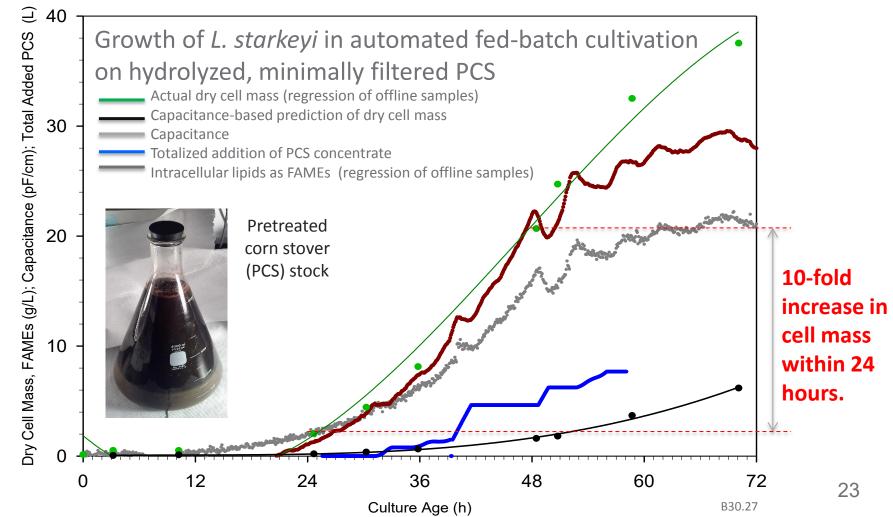
132

# 3 – Technical Accomplishments Improvements of the Bioprocess: Rate of Growth for Seed



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- Examining the seed train
- Design case: requires 10 x increase in cells per day in the seed bioreactor
- Have achieved that mark



### 4 – Relevance



▶ Goal: Development of efficient and robust fungal biocatalysts and bioprocesses that utilize lignocellulose feedstocks to produce advanced biofuels and bioproducts at lower cost.

### Why?

- Fungi, Saccharomyces and Aspergillus, are already the key players in the 1<sup>st</sup> generation biofuel/bioproduct industry—biofuels, bioproducts, enzymes
- Pre-competitive R&D to generate robust industrially-relevant fungal platforms for utilization of real world biomass substrates is our emphasis to meet BETO programmatic and 2<sup>nd</sup> generation biorefinery industry needs
- Parallel & iterative development of the organisms & the bioprocesses in an environment that can scale to biorefineries is emphasized to encourage tech to market

### 4 – Relevance



#### **BETO Program Relevance**

- ▶ BETO cost target of MFSP = \$3 per GGE is challenging for advanced biofuels in general
- ► We are contributing pathways for biofuels and bioproducts to **decrease risk**
- In *Lipomyces* need to increase TRY of lipids and/or cell mass for biofuels to decrease bioprocess costs
- ► TEA indicates that Rate is very important...effects on process time and capital cost
- ▶ **Bioproducts** needed to enable achievement of this goal...and *Aspergillus* is a good platform in this area...coupled with upgrading chemistry
- ► Integration with BETO Projects: 2.5.3.104-12 ABF (9 NLs), 2.5.1.102 SCADA, 2.1.0.301 Anal. & Sustain. Interface, 2.2.3.102-3 "Thermoascus" (LBNL), 2.4.1.102 Process Scale Integration (NREL)



### 4 – Relevance



#### **Industrial Relevance**

- Our focus on development of biocatalysts and bioprocesses in bioreactors and use of authentic feedstocks maximizes their potential usefulness for industrial bioenergy and bioproducts
- Industry is currently producing lipids for fuel and animal feed applications—a fungal system that produces triglycerides with a fatty acid profile similar to plant derived lipids (akin to palm oil) could allow integration into the same product stream
- Active communication with industrial partners in the bioenergy marketplace helps us test the relevance of our research and provides potential tech transfer points
- ► Industry's biocatalyst needs: cheap, fast, easy
  - produce fuels and bioproducts of value
  - at high TRY
  - with reproducible bioprocess characteristics
  - able to utilize different pre-treated biomass sources
  - tolerant of inhibitors
  - tools available to genetically manipulate the organism

### 4 – Future Work



#### **FY18**

- A focus on automated fed-batch and seed train mimic runs with PCS: increasing Rate, with simultaneous optimization of Titer and Yield of lipid
- Use our understanding of lipid production and inhibitor resistance from transcriptomics and mutagenesis studies to obtain improved strains through genetic engineering and/or selection
- Focus on improving TRY from PCS of a highly reduced polyketide produced by Aspergillus for bioproducts/biofuels
- ► Integrate with catalytic chemists to investigate the bioproduct potential of the polyketide
- Continue to communicate our fungal engineering lipid, cell mass and bioproduct advances to our IAP and others with T2M goal

### Summary



- 1. Overview: fungi are proven platforms for biofuels and bioproducts to meet the needs of BETO and the biorefinery industry
- 2. Approach: parallel fungal genetic & bioprocess engineering drive faster development and improvement of industrially relevant biocatalysts/bioprocesses
- 3. Technical Accomplishments:
  - Improved genetic, genomic and bioprocess development tool box for two fungi: the well understood lipid producer *Lipomyces*, and the workhorse bioproduct platform *Aspergillus*
  - Bioprocess development has realized large Rate and Titer improvement in cell mass from PCS using Lipomyces
- 4. Relevance: engagement with Industrial Advisory Panel to guide our research and produce relevant biocatalysts and bioprocesses
- 5. Future work: maintain focus on improving TRY on lignocellulose and building organism robustness, expansion in regard to bioproducts made



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### **Additional Slides**

### **NEEDS REVISION/INPUT**

### 3 – Status Summary from 2015 Peer Review

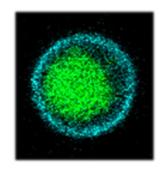


We had made significant improvements in TRY over the previous two years

■ Titer: 2.3x improvement to 5.5 → 13 g/L lipids

Rate, **5x** improvement in *peak* rate 0.18 to 0.90 g/L/h

■ Yield: **3x** improvement 9 to 27% (100% of theoretical)



- Had observed theoretical Yield. Had observed high Titers
- Room to improve on Rate and simultaneous high TRY
- ► TEA indicates rate has a major impact on MFSP
- ► Had just begun work on biomass hydrolysates so most of our emphasis since has been on hydrolysates
- We had developed the minimum required genetic tools needed to express genes in the organism
- Still needed improvements in genetic tools, especially gene deletion capability

### 4 – Future Work



### **FY17 Milestones**

- ▶ Go/No-Go to determine if promising titers can be obtained of a polyketide product (3/31)
- Demonstrate engineering of Lipomyces for improved lipid TRY and/or inhibitor tolerance (6/30)
- ▶ Demonstrate engineering a significant advance in titers of a polyketide product (9/30)

Due Date	Remaining FY17 Milestones
March 31	Over-express or delete four (4) gene targets implicated by transcriptomics or other results as improving lipid TRY, or enhancing robustness to inhibitor rich feedstocks in <i>L. starkeyi</i>
March 31	Obtain at least 1 g/L of 1 of the 2 target polyketides/terpenes selected in M1. GO/NO-GO
June 30	Measure TRY for each of the genetic modifications obtained in M2 and demonstrate a 20% improvement in either titer, rate, or yield vs. the wild type strain of L. starkeyi in lignocellulosic hydrolysates
Sept. 30	Obtain 2.5 g/L of a polyketide or terpene in a scaled (20L) bioprocess



#### **Publications**

- ▶ Bredeweg EL, Pomraning KR, Dai Z, Nielsen J, Kerkhoven EJ, Baker SE. A molecular genetic toolbox for Yarrowia lipolytica. Biotechnol Biofuels 2017 Jan 3; 10:2.
- Butcher, M., Pimphan, M., Hallen, R., Magnuson, J., Karl Albrecht, Clayton, C., Polikarpov, E., Jones, S. 2017. "Fungal Metabolites as Precursors to Renewable Transportation Fuels" (to be submitted, Applied Energy, March 2017)
- Dai Z, S Deng, DE Culley, KS Bruno, and JK Magnuson. 2017. Agrobacterium tumefaciens-mediated transformation of oleaginous yeast Lipomyces species (in review, Applied Microbiol and Biotechnology, Feb. 2017)
- ▶ Goodwin S, CB McCorison, JR Cavaletto, DE Culley, KM LaButti, SE Baker, and IV Grigoriev. 2016. "The mitochondrial genome of the ethanol-metabolizing, wine cellar mold Zasmidium cellare is the smallest for a filamentous ascomycete." Fungal Biology 120(8):961-974. doi:10.1016/j.funbio.2016.05.003
- Gunsalus R, LE Cook, BR Crable, L Rohlin, E McDonald, H Mouttaki, JR Sieber, N Poweleit, H Zhou, A Lapidus, HE Daligault, ML Land, P Gilna, N Ivanova, N Kyripides, DE Culley, and MJ McInerney. 2016. "Complete genome sequence of Methanospirillum hungatei type strain JF1." Standards in Genomic Sciences 11:Article No. 2.



### **Publications (cont.)**

- Kerkhoven E, Pomraning KR, Baker SE, Nielsen J. Regulation of amino acid metabolism controls flux to lipid accumulation in Yarrowia lipolytica. npj Systems Biology and Applications 2016 2. Published online 3/3/16.
- Mondo, S. J., R. O. Dannebaum, R. C. Kuo, K. Louie, K. LaButti, S. Haridas, A. Kuo, A. Salamov, S. R. Ahrendt, A.J. Bewick, R. Lau, B. Bowen, A. Lipzen, W. Sullivan, W. B. Andreopoulos, A. Clum, E. Lindquist, C. Daum, T. R. Northen, G. Ramamoorthy, R. J. Schmitz, A. Gryganskyi, D. Culley, J. Magnuson, T. Y. James, M. A. O'Malley, J. E. Stajich, J. W. Spatafora, A. Visel, I. V. Grigoriev "Pervasive Adenine N6-methylation of Active Genes in Fungi" (accepted, in revisions, Feb 2017)
- Mäkelä MR, Bredeweg EL, Magnuson JK, Baker SE, de Vries RP, Hildén K. "Fungal Ligninolytic Enzymes and Their Applications" Microbiol Spectr. 2016 Dec; 4(6).
- Pomraning KR, Kim YM, Nicora CD, Chu RK, Bredeweg EL, Purvine SO, Hu D, Metz TO, Baker SE. Multi-omics analysis reveals regulators of the response to nitrogen limitation in Yarrowia lipolytica. BMC Genomics. 2016 Feb 25;17(1):138.
- Tamano, K., Bruno, K.S., Koike, H., Ishii, T., Miura, A., Umemura, M., Culley, D., Baker, S. and Machida, M., 2015. "Increased production of free fatty acids in Aspergillus oryzae by disruption of a predicted acyl-CoA synthetase gene", Appl Microbiol Biotechnol 99: 3103.



### **Intellectual Property**

 Agrobacterium tumefaciens mediated transformation of oleaginous (oil-producting) yeast Lipomyces 30396-E 23-91636-01 (2014) Ziyu Dai, Jon K. Magnuson, Shuang Deng, Kenneth S. Bruno and David E. Culley

#### **Presentations**

- Collett JR, PA Meyer, Y Zhu, ER Hawley, Z Dai, MG Butcher, and JK Magnuson. 2015. "Bioreactor performance data and preliminary biorefinery technoeconomics for the production of distillate fuels via bioconversion of pretreated corn stover by Lipomyces starkeyi." Poster presentation at 37th Symposium on Biotechnology for Fuels and Chemicals, San Diego, CA on April 27, 2015. PNNL-SA-107273.
- Culley DE, MG Butcher, BA Hofstad, JK Magnuson, IV Grigoriev, and KW Barry. 2015. "1000 Fungal DNA Samples for the 1000 Fungal Genome Project." Presented by David Culley at 28th Fungal Genetics Conference, Pacific Grove, CA on March 19, 2015. PNNL-SA-108790.



### **Presentations (cont.)**

- Culley DE, MG Butcher, BA Hofstad, JK Magnuson, KW Barry, and IV Grigoriev. 2015. "ETOP Project: Development and Implementation of High Throughput Methods for Fungal Culturing and Nucleic Acid Isolation." Presented by Beth A. Hofstad (Invited Speaker) at The 10th Annual DOE Joint Genome Institute / Genomics of Energy & Environment Meeting on March 24, 2015. PNNL-SA-108949.
- ▶ Dai Z, S Deng, DE Culley, KS Bruno, and JK Magnuson. 2015. "Agrobacterium tumefaciens-mediated transformation of the oleaginous yeast genus Lipomyces." Presented by Ziyu Dai at The 37th Symposium on Biotechnology for Fuels and Chemicals, San Diego, CA on April 28, 2015. PNNL-SA-107519.
- ▶ Joo H, and DE Culley. 2015. "Determining the reliability of fluorometric analyses to rapidly quantify the lipid content in Lipomyces starkeyi NRRL Y-11558." Presented by Heena Joo (Invited Speaker) at SULI Symposium, Richland, WA on July 23, 2015. PNNL-SA-111657.
- Collett JR. 2015. "Process Analytical Technologies in the New Bioeconomy for Fuels and Chemicals." Presented by James R. Collett (Invited Speaker) at Sartorius Upstream/Downstream Technology Forum, Foster City, CA on October 6, 2015. PNNL-SA-113501.



### **Presentations (cont.)**

- ➤ Ziyu Dai, Shuang Deng, David E. Culley, Kenneth S. Bruno, and Jon K. Magnuson (2015) Agrobacterium tumefaciens-mediated transformation of oleaginous yeast Lipomyces species. (37th Symposium on Biotechnology for Fuels and Chemicals, San Diego, CA)
- ➤ Ziyu Dai, Shuang Deng, Kyle R. Pomraning, David E. Culley, Kenneth S. Bruno, and Jon K. Magnuson (2017) Deletion of Lipomyces starkeyi Ku70 homologue augments platform stain generation for gene expression and functional analysis. (39th Symposium on Biotechnology for Fuels and Chemicals, San Francisco, CA)