

Biological Upgrading of Sugars WBS 2.3.2.105









2015 DOE BioEnergy Technologies Office (BETO) Project Peer Review

Date: March 25th, 2015

Technology Area Review: Biochemical Conversion

Principal Investigator: Gregg T. Beckham

Organization: National Renewable Energy Laboratory

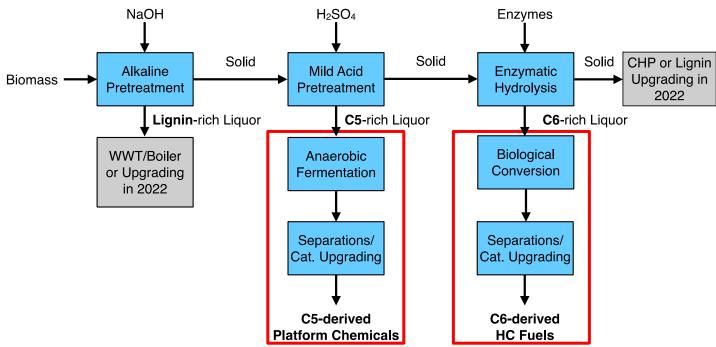
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Goal Statement

Goal: develop strains to produce fuels and co-products for the 2017 and 2022 Biochemical Conversion Platform cost target goals of \$5/gge and \$3/gge

- Fatty acids as fuel precursors, succinic acid as an example product, both aligned with TEA targets
- "Bioproducts are on the Critical Path" DOE BETO



HC fuels alongside co-products will be a major benefit to the US biorefinery infrastructure

- Conduct TEA/LCA to identify cost drivers and data gaps and to refine process options
- Collaborate with industry and academics for joint development of strains and process demonstrations
- Outcome: demonstrated, robust strains for producing HC fuels and co-products in the biorefinery

Quad Chart

Timeline

New Project

Start date: October 2014

End date: September 2017

Percent complete: 10%

Budget

	FY15	Total Planned Funding (FY16- Project End Date)
DOE funded	\$1,800,000	\$4,200,000

Barriers

- Bt-I Catalyst Efficiency
- Bt-J Biochemical Conversion Process Integration
- Bt-H Cleanup/Separation

Partners and Collaborators

- Industry partners: in talks with industrial entities regarding collaborations around both HC and co-product development
- NREL BETO Projects: <u>Biochemical Platform Analysis</u>, <u>Bench-Scale Integration</u>, Separations Development and Application, Catalytic Upgrading of Sugars, Pretreatment and Process Hydrolysis, Pilot Scale Integration, Biochemical Process Modeling and Simulation, Strategic Analysis Platform
- BETO-funded National Lab Projects: Ongoing discussions with PNNL efforts in strain development
- Academic collaborators: University of Pretoria, MIT, UC Davis Phaff Yeast Culture Collection, currently in talks with other groups for collaborations around both HC and co-product development

Project Overview

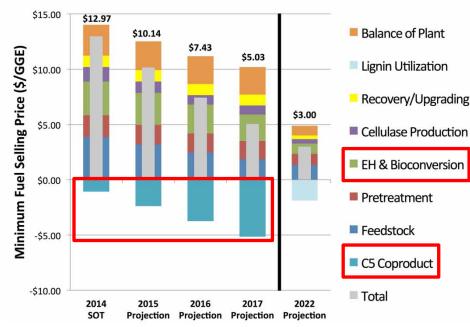
History: HC fuel R&D primarily began at NREL in the Nat'l Adv. Biofuels Consortium

- TEA suggests chemicals are essential to cost-effective HC production
- NREL began developing plans after the 2012 ethanol demonstration to meet 2017 and 2022 cost targets for HC fuels at \$5/aae and \$3/aae



Context: Going "beyond ethanol" to produce a broad portfolio of biofuels

- Produce direct replacements or blendstocks for gasoline, diesel, jet fuel markets
- Move closer to petroleum refinery models with fuel and chemicals production together
- De-risk capital investments in fuels via coproduct manufacturing



Project Objectives:

- Develop industrially-relevant strains for fatty acids and an example co-product to meet 2017 and 2022 cost targets
- Focus efforts towards titer, rate, and yield targets set by TEA/LCA modeling
- Rapidly test strains with Bench-Scale Integration Project to identify and solve problems in scaling and integration

Davis et al., NREL Design Report, 2014

Technical Approach

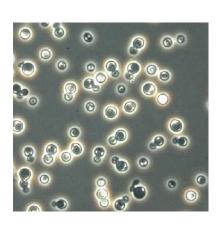
Aim 1: Develop a robust oleaginous strain

Approach:

- Target: 0.4 g/L/hr rate, 60% lipid content, and a 0.27 g/g yield on C6-enriched sugars
- Screen natural oleaginous yeast strains
- Evolve strains to increase lipid yields
- Engineer select strains for high lipid yields

Primary challenges and success factors:

- High yield and productivity of lipids
- Availability of genetic tools in strains for metabolic engineering





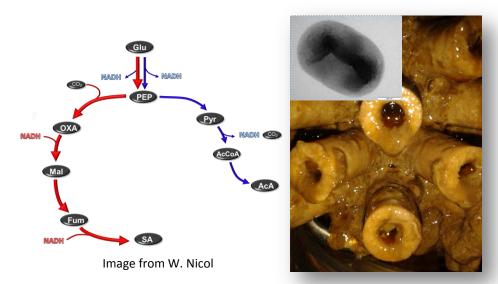
Aim 2: Develop robust succinic-acid strain

Approach:

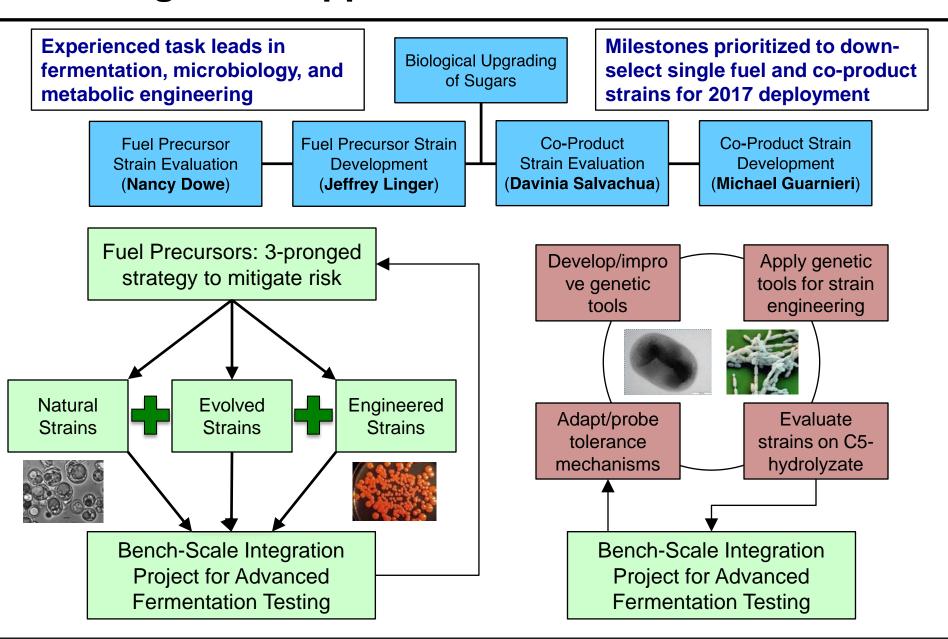
- Target: 2.0 g/L/hr rate, 0.795 g/g yield on C5enriched sugars
- Evaluate natural strains on C5-hydrolyzates
- Adapt strains to tolerate pretreatment inhibitors
- Engineer a strain for higher SA yields

Primary challenges and success factors:

- Overcoming hydrolyzate toxicity
- Increasing carbon flux to SA over side products



Management Approach and Outline



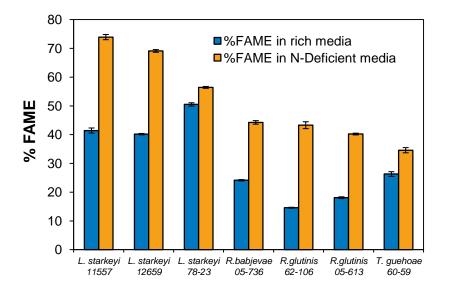
Self-consistent screening of oleaginous yeast

- Obtained oleaginous yeast collection
- Pursuing self-consistent screening results

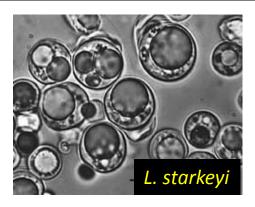
Species being screened:

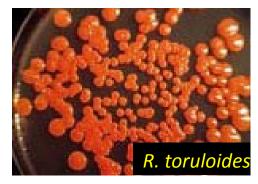
- Cryptococcus curvatus
- Cryptococcus wieringae
- Kurtzmaniella cleridarum
- Leucosporidiella creatinavora
- Lipomyces starkeyi (3)
- Rhodosporidium babjevae (4)
- Rhodosporidium dibovatum
- Rhodosporidium paludigenum

- Rhodosporidium sphaerocarpum
- Rhodosporidium toruloidies (6)
- Rhodotorula glutinis (2)
- Rhodotorula glutinis "like"
- Sporopachydermia opuntiana
- Tremella encepala
- Trichosporon guehoae
- Yarrowia lipolytica (10)









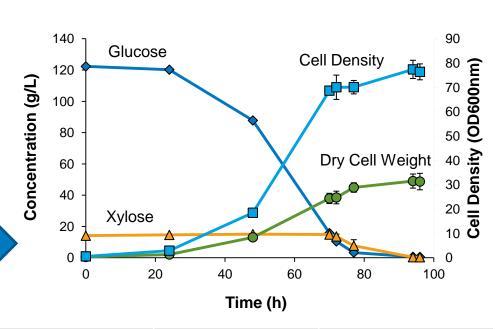


Evaluation of oleaginous yeast

Lipid production by *L.* starkeyi in shake flasks



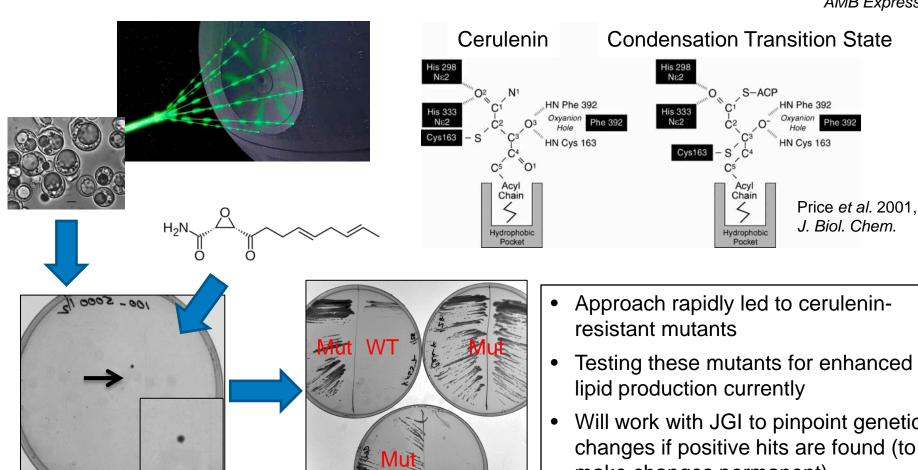
Lipid production by *L. starkeyi* in small fermentors – BSI Early Work





Metric	Pure Sugar - Flasks	Pure Sugar - Fermentor	C6 Biomass Sugars from Enz Hyd Fermentor		
Glucose utilization (total)	98%	80%	100%		
Lipid content	59%	60%	57%		
Volumetric productivity (g/L-hr) at 72 h	0.05 (batch culture)	0.18 (batch culture)	0.29 (batch culture)		
Lipid process yield (total sugar-to-product , g/g)	0.07	0.13	0.20		

- β-ketoacyl-acyl carrier protein synthases (KS) regulate FA synthesis and are inhibited by cerulenin
- Cells can overcome this inhibition by increasing FA synthase production Tapia et al. 2012, AMB Express

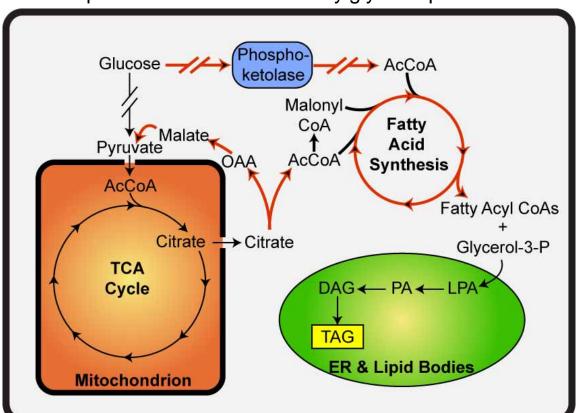


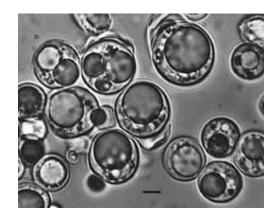
- Approach rapidly led to cerulenin-
- Testing these mutants for enhanced
- Will work with JGI to pinpoint genetic changes if positive hits are found (to make changes permanent)

Chose L. starkeyi as initial strain for engineering

- Very high lipid productivities and titers
- Strain NRRL Y-11557 genome sequenced (Tom Jeffries/JGI)
- DNA Transformation established (Calvey et al. 2014)

Simplified metabolism for triacylglycerol production





RED lines represent initial focal points for engineering

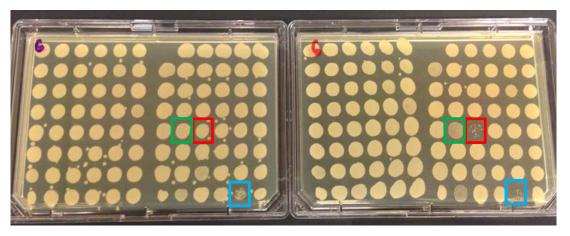
Overexpression of native biosynthetic genes and heterologous expression of a phosphoketolase to increase acetyl-CoA (AcCoA) pools

Leveraging S. cerevisae for rapid gene identification

Engineered Strains







Hypersensitive mutant

Slightly sensitive mutant

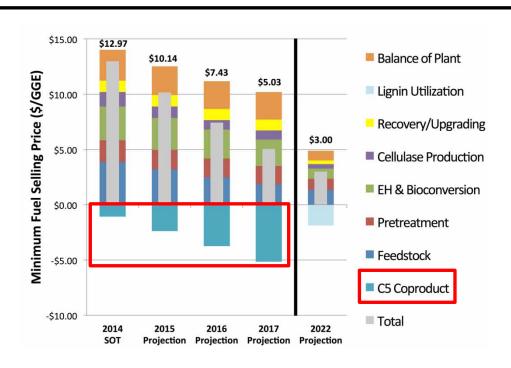
Intrinsically weak mutant

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Hypersensitive mutants	77
Sensitive mutants	63
Intrinsically weak mutants	23

- Leverage single gene deletion and single gene overexpression collections developed in S. cerevisiae
- Developed, validated HTP method to screen for enhanced lipid production
- Currently screening ~5,000 single gene deletion strains and ~5,000 single gene overexpression strains to identify genes whose alteration increases lipid production
- Leverage these results to apply to more process-relevant but less genetically malleable strains, e.g., L. starkeyi

Why a C5-derived co-product? Why succinic acid?

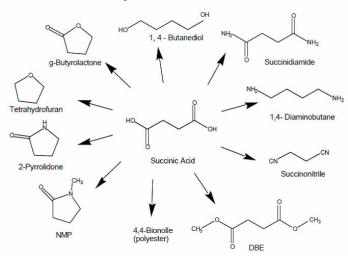


Direct and **functional replacement** markets for SA

- Potential for 4 MM tons/year (Top Ten Report)

 Disseminated results will aid industrial transition from starch to lignocellulosic sugars
- Similar to track record with ethanol demonstration **Acid functionality** common to products of interest
- Broadly applicable insights in integrated process

Significant industrial interest already in this molecule



Top-Ten Value Added Chemicals from Biomass, Vol. 1, 2004

Robust strains exist, enabling an aggressive timeline to an integrated 2017 demonstration

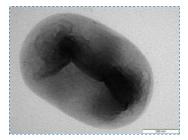




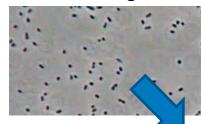
Image from BASF

Strain down-selection

Species examined from the literature

- Anaerobiospirillum succiniciproducens
- Bacteroides fragilis
- Enterococcus faecalis RKY1
- Succinivibrio dextrinosolvens
- Fibrobacter succinogenes
- Mannheimia succiniciproducens
- Actinobacillus succinogenes
- Basfia succiniciproducens

A. succinogenes



B. succiniciproducens



Image from BASF

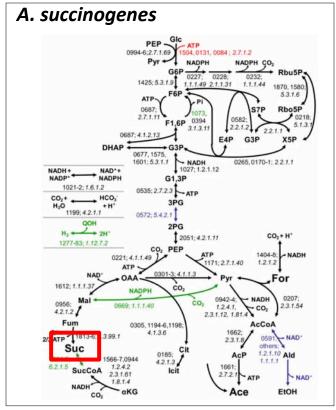


0.5 L fermentors

	Lignin	Monomeric sugars				Acetic acid	HMF	Furfural	
All in g/L		Cellobiose	Glucose	Xylose	Galactose	Arabinose			
DCS-hydrolyzate	7.6	1.7	13.1	93.4	6.5	15.8	3.8	0.26	1.8

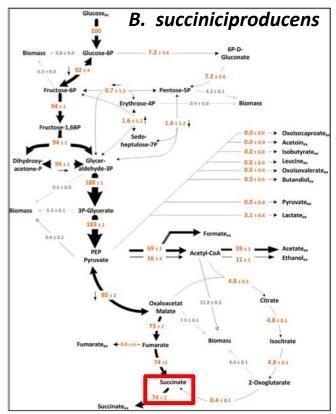
- Three strains were Biosafety Level 2 (in blue), two strains did not consume xylose (in red), and M. succiniciproducens is not publically available
- Rapidly down-selected to *B. succiniciproducens* and *A. succinogenes*
- Initially screening strains in batch reactors on C5-rich hydrolyzates

Two leading strains for SA production



McKinlay JB, et al. (2010) BMC Genomics

- Facultative anaerobe, CO₂ fixer
- Produces formate, acetate, ethanol
- Does not have oxidative TCA cycle branch
- Forms biofilm
- Extensive information

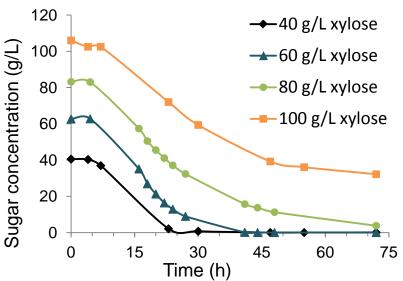


Becker, J. et al (2013) Biotechnol Bioeng.

- Facultative anaerobe, CO₂ fixer
- Produces formic, acetic, ethanol, lactate
- Produce SA via oxidative TCA cycle branch
- Does not form biofilm
- Limited information about this bacterium

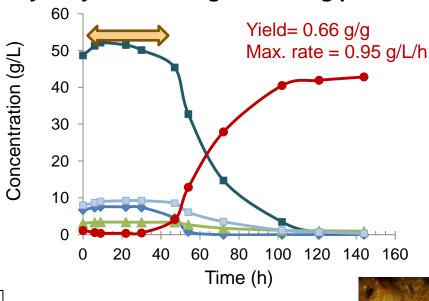
Testing inhibition in A. succinogenes

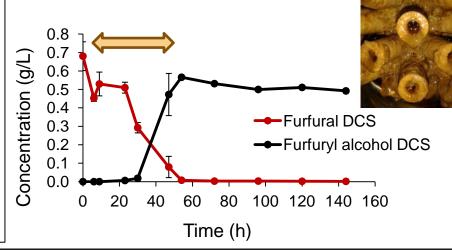
Tolerates sugar concentrations up to 80 g/L



- Early work in BSI in FY14
- Furfural and HMF reduction correspond to lag
- Transferred to BSI Project for continuous fermentation to obtain high yield and rate
- Cleanup ongoing to overcome rate limitations
- Ongoing: transcriptomics, proteomics, metabolomics, metabolic flux analysis
- Similar work ongoing in *B. succiniciproducens*

Reasonable yield and rate on C5-rich hydrolyzate with significant lag phase





Metabolic Engineering for Improved SA Biosynthesis

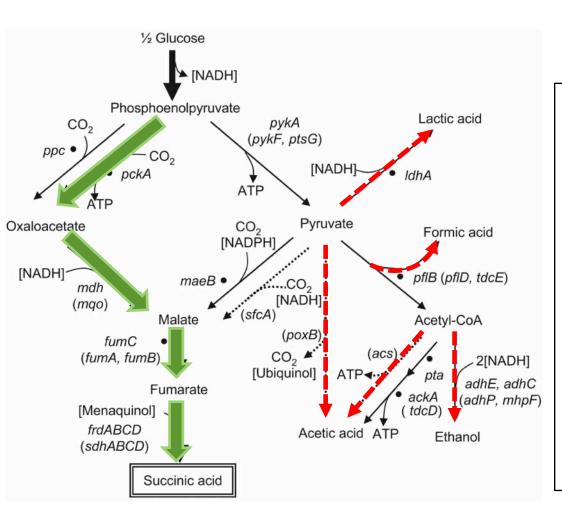


Image from S. Vaswani, 2010

Genetic tools will enable two parallel approaches to enhance flux to succinate:

- Overexpression of succinate biosynthetic components (green arrows)
- Down-regulation and/or knockout of competitive fermentation pathways: lactate, acetate, formate, and ethanol (red arrows)

Relevance

This project is essential for 2017 HC fuel cost targets of \$5/gge

Key MYPP areas targeted by the Biological Upgrading of Sugars Project:

Catalyst Efficiency

- Developing efficient bio-catalysts to produce advanced fuels and chemicals
- Improvement in titer, rate, yield key to economic viability

Biochemical Conversion Process Integration

- Coupling process considerations with organism development
- Working with BSI task to iterate on fermentation needs and organism modifications/evolution

Cleanup/Separation

 Elucidating inhibitor effects on biocatalysts and downstream processing

Key Stakeholders and Impacts:

- Industrial and academic research focused on carbohydrate utilization in both HC fuel production and co-product manufacturing including chemical and polymer precursors from biomass
- Will enable demonstration of C5-rich stream to chemicals in a scalable manner
- Co-products impact the "Whole Barrel of Oil"
- Portfolio of chemicals will diversify and accelerate development of the biomass value chain
- Significant amounts of peer-reviewed science and IP will be generated from this work
- Methods to upgrade sugars to organics acids can be leveraged well beyond succinic acid

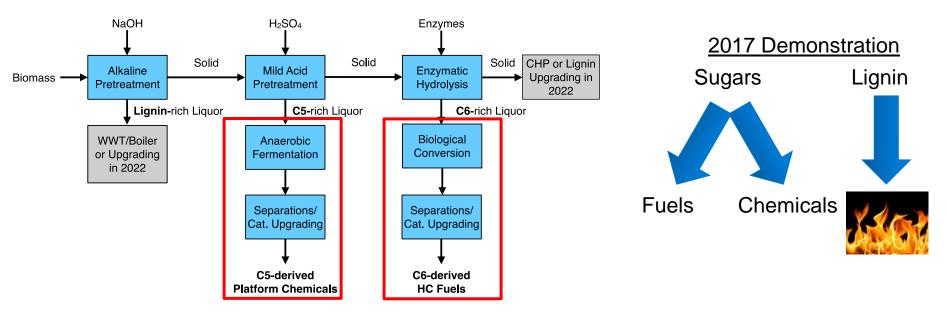
Future Work

Fatty Acid Production

- Define 2-3 strains by end of FY15 with BSI
- Target a "final" strain by end of FY16
- 0.4 g/L/hr rate, 60% lipid content, and a 0.27 g/g yield on C6-enriched sugars

Succinic Acid Production

- Down-select strain by end of FY15 with BSI
- Target a "final" strain by end of FY16
- Target: 2 g/L/hr, 0.795 g/g yield on C5enriched sugars



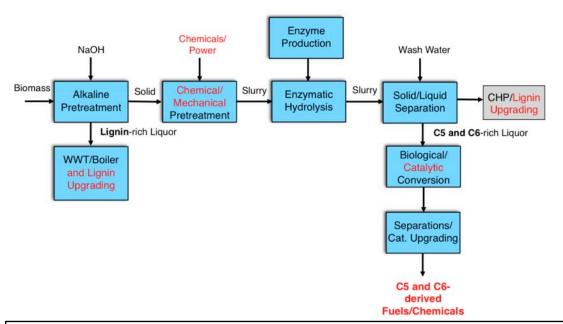
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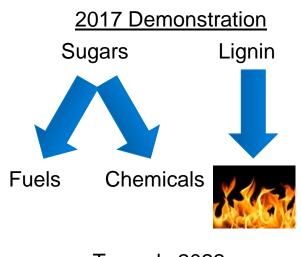
Succinic Acid Production

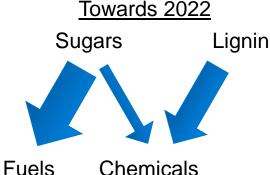
- Down-select strain by end of FY15 with BSI
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Towards 2022 demonstration

- Emphasize step changes in lipid recovery through cell wall engineering and improved carbon flux
- Explore fuel precursors with higher C-efficiency pathways
- Divert more carbon to fuels through more efficient strains





Summary

1) Approach:

- Develop oleaginous yeast for lipid production for renewable diesel blends from C6-rich streams
- Develop example co-product train (succinic acid) from C5-rich streams from dilute-acid pretreatment

2) Technical accomplishments (4 months of work thus far)

- Screening large collection of oleaginous yeast in a self-consistent manner
- Demonstrated ability to rapidly evolve L. starkeyi strains towards higher lipid production
- Developed a HTP method for screening for gene candidates for lipid production in a model system.
- Demonstrated high yields of succinic acid on process-relevant hydrolysate
- Identified multiple inhibitors that cause a lag phase in A. succinogenes growth and SA production
- Metabolic engineering in progress for both FA and SA industrial production hosts

3) Relevance

- Directly impacts the 2017 and 2022 HC fuel cost target demonstrations through strain development
- Addresses Whole Barrel of Oil Initiative and bolsters the biomass value chain

4) Critical success factors and challenges

Economic and sustainable production of co-products, high yields of FAs and products needed

5) Future work:

 Continue all fronts towards down-selection of strains for 2017 demonstration, partial transition of efforts to 2022 targets in mid- to late-FY16

6) Technology transfer:

Initiating contact with industry to build commercialization path for both fuel and co-product trains

Acknowledgements

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- Bill Michener
- Davinia Salvachua
- Holly Smith
- Thieny Trinh
- Min Zhang



BIOMASS PROGRAM

External collaborators

- Willie Nicol, University of Pretoria,
- School of Chemical Engineering Practice, MIT
- Kyria Boundy-Mills, UC Davis Phaff Yeast Culture Collection

Acronyms

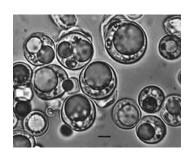
- FA: Fatty Acid
- LCA: Life-Cycle Analysis
- NHEJ: Non Homologous End Joining
- SA: Succinic Acid
- TEA: Techno-Economic Analysis

L. starkeyi: Initial strain for engineering

Engineered Strains

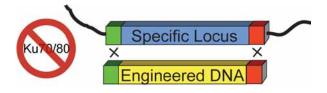
Strain Highlights:

- Very high lipid productivities and titers
- Strain NRRL Y-11557 genome sequenced (Tom Jeffries/JGI)
- DNA Transformation established (Calvey et al. 2014)

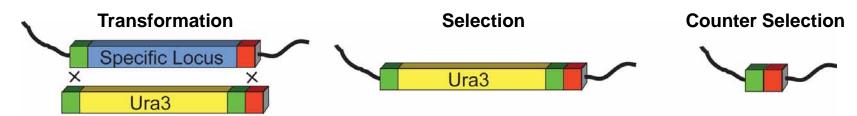


Initial Genetic Tool Development goals:

- Increasing the genetic engineer-ability: Disruption of Ku70/80 genes should increase the efficiency of gene targeting by eliminating NHEJ for DNA repair
- Currently screening hundreds of transformants to identify ku70 deletion mutants



Reusable selectable/counter-selectable marker: Generated random mutant *ura3* auxotrophic strains and are screening transformants for "clean" deletions to enable marker recycling:



Genetic Tool Development in *A. succinogenes*

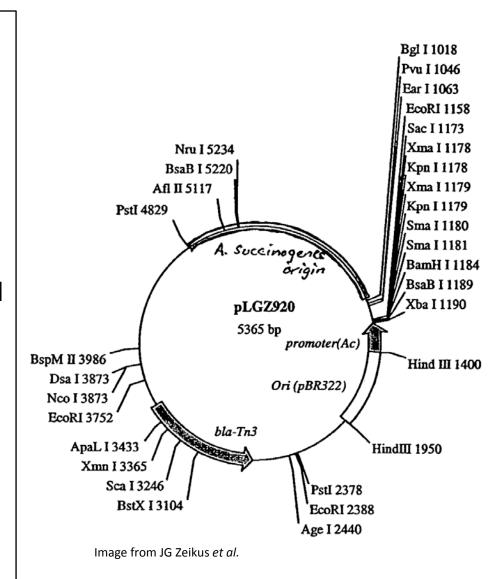
Replicative plasmid (pLGZ920) obtained for facile gene expression

 Complete plasmid re-sequenced to facilitate construct design

Efficient electroporation transformation method developed

- 9 x 10⁴ cfu/µg plasmid
- Sufficient for plasmid transformation and good starting point for linear DNA transformation (for gene knockout)

Similar tools in place for *B.* succiniciproducens



A. succinogenes -omic Analyses

Identify promoters across an array of expression levels

 Facilitate fined-tuned expression of strain-engineering targets

Comparative analyses between solution state and biofilm (production) state

 Identify novel targets for induction of biofilm formation and temporal regulation of succinate biosynthesis

