

Second Generation Biofuel, Analytical tools, Automation Challenges and Deconstruction Strategies



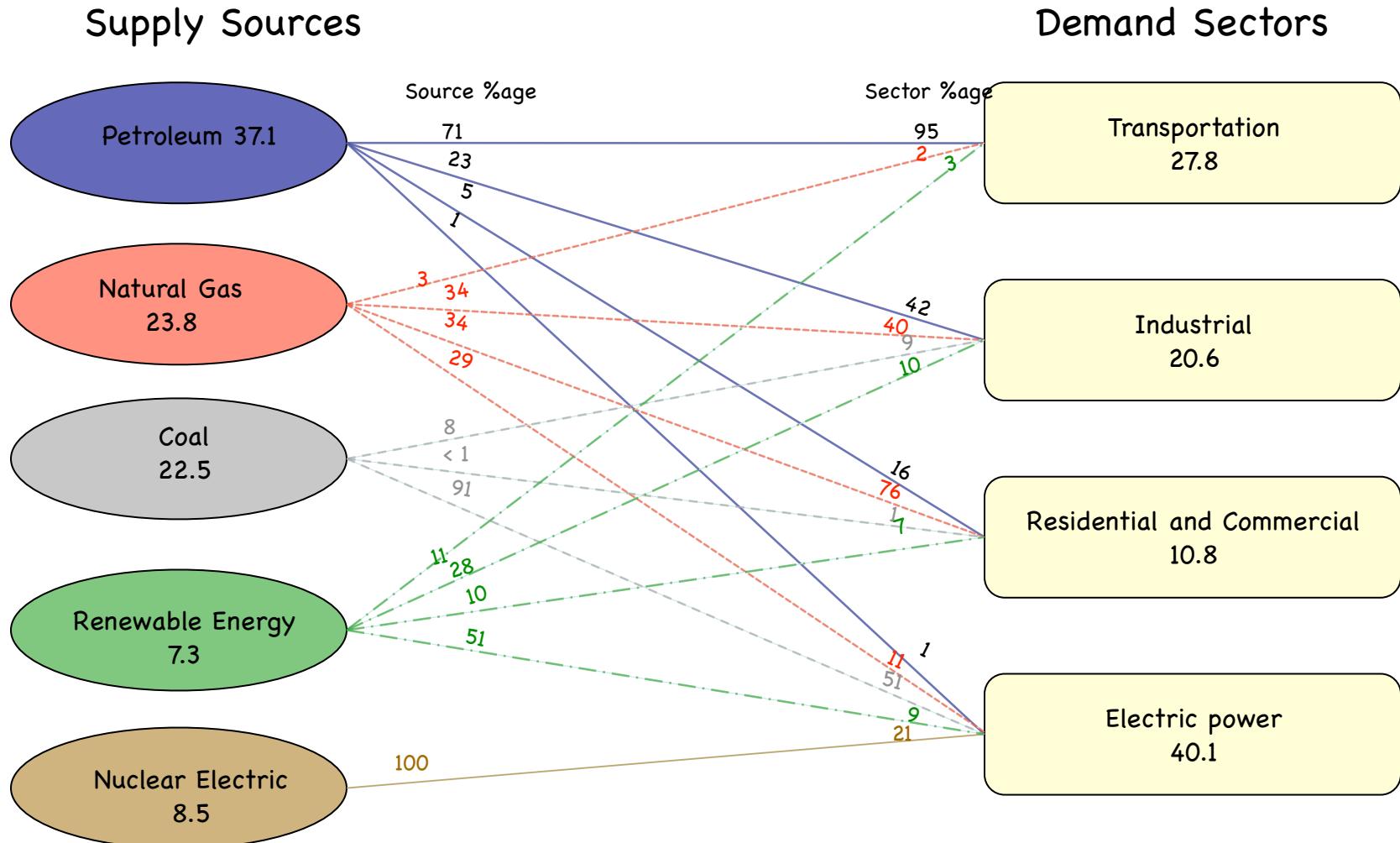
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SAND2011-2606C



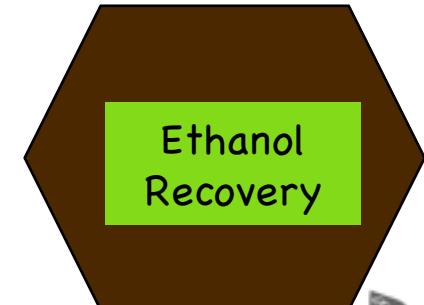
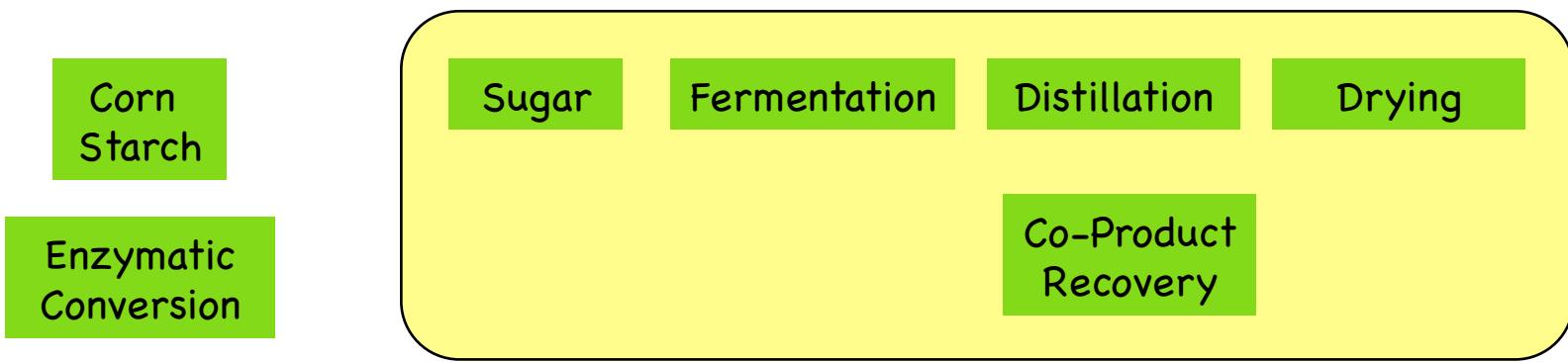
Annual Energy Review 2008 Table 1.3

Rethinking Fuels

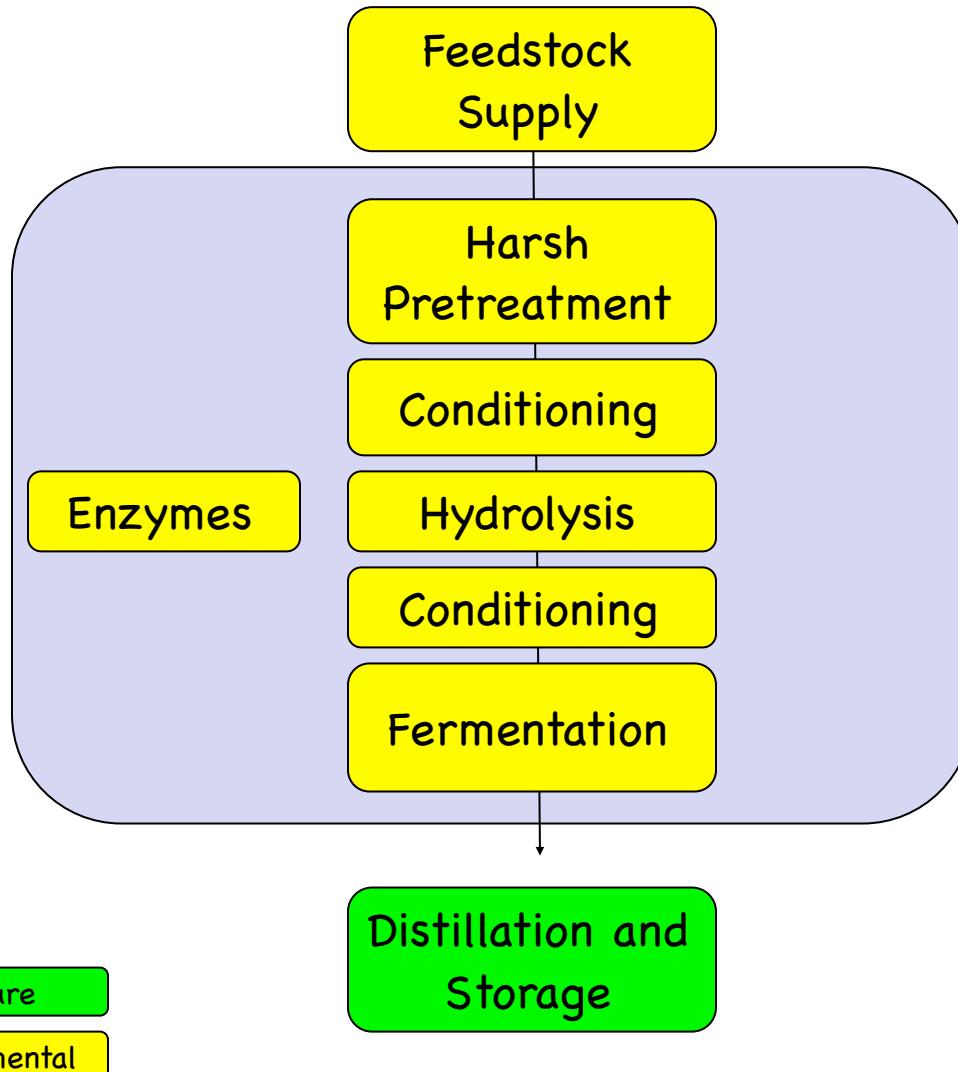
- Energy usage is projected to increase by 55% over the next 20 years
- Transportation is the single largest user of petroleum feedstocks
- There will be an additional 2.3 billion cars worldwide on the roads by 2050
 - 1.9 billion will be in developing countries
- Improvements in mileage standards and alternative vehicles will reduce the need but not eliminate the need for liquid transportation fuels
 - Hybrid systems are expected to dominate new vehicle sales by 2030
- Corn ethanol today can reduce emissions by 30-70% compared to gasoline
- Cellulosic fuels (second-generation) will reduce emissions approximately 90%
(NREL Report)

World Energy Outlook 2007, International Energy Agency, Energy Information Agency,
International Monetary Fund, US DoE, Merrill Lynch, International Energy Agency, UNICA, Renewable Fuel Association, EU Commission

Corn Ethanol Production Processes



Cellulosic Biomass Processing



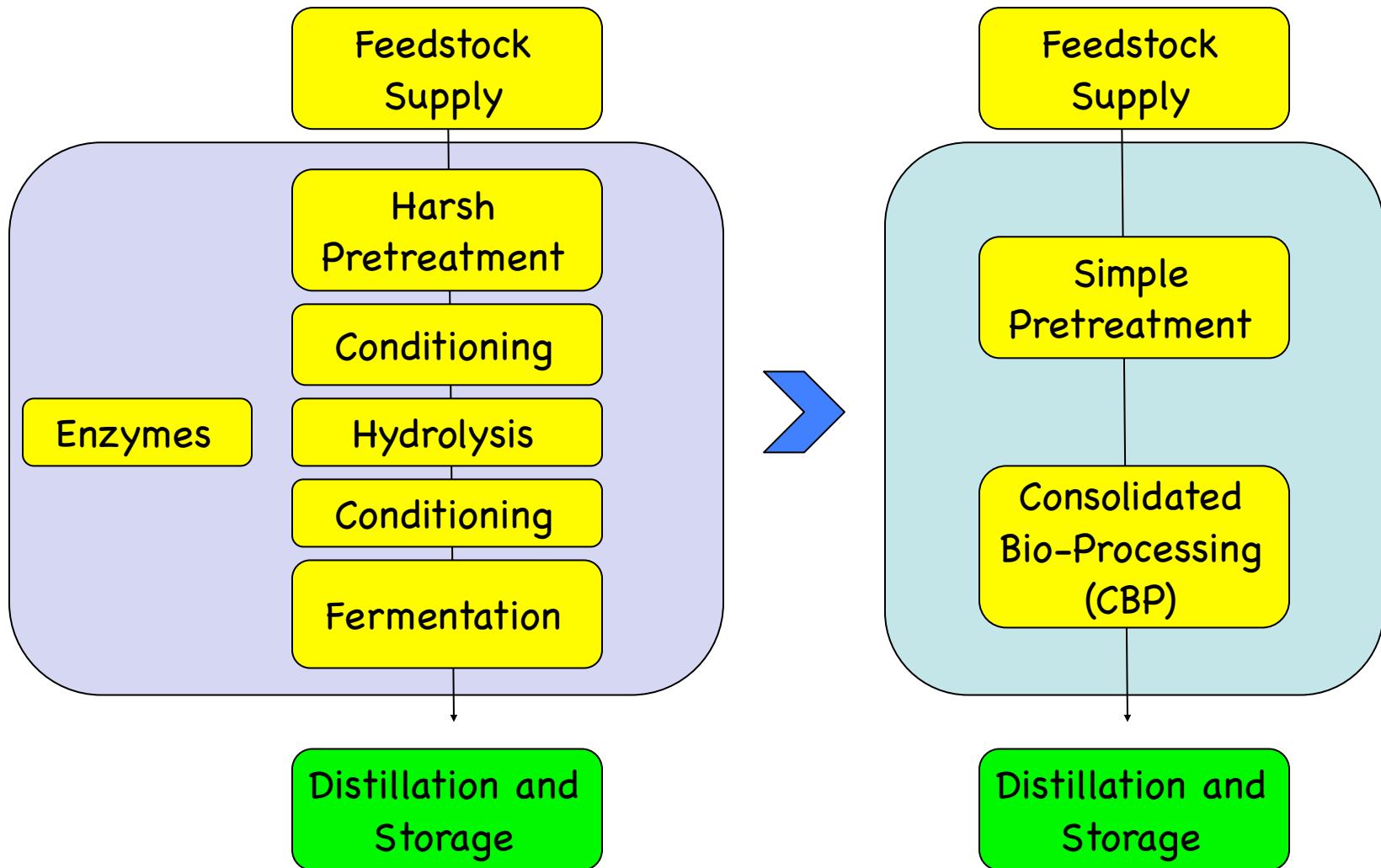
Most processes are experimental and in development

Current approach by companies: POET and Catchlight

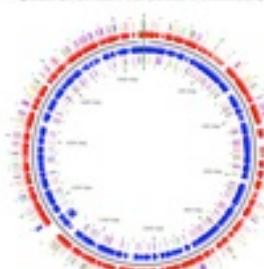
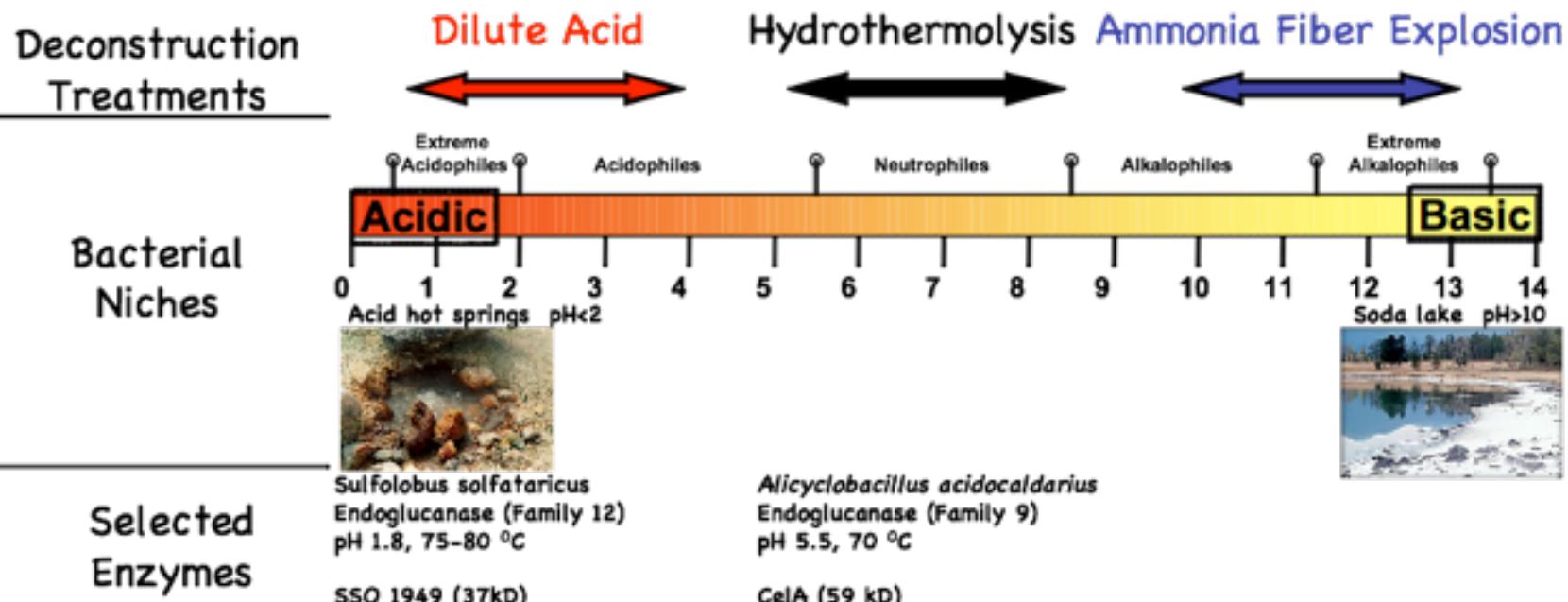


Consolidated Bio-processing

Potentially lower costs through process simplification



Industrially Compatible Enzymes

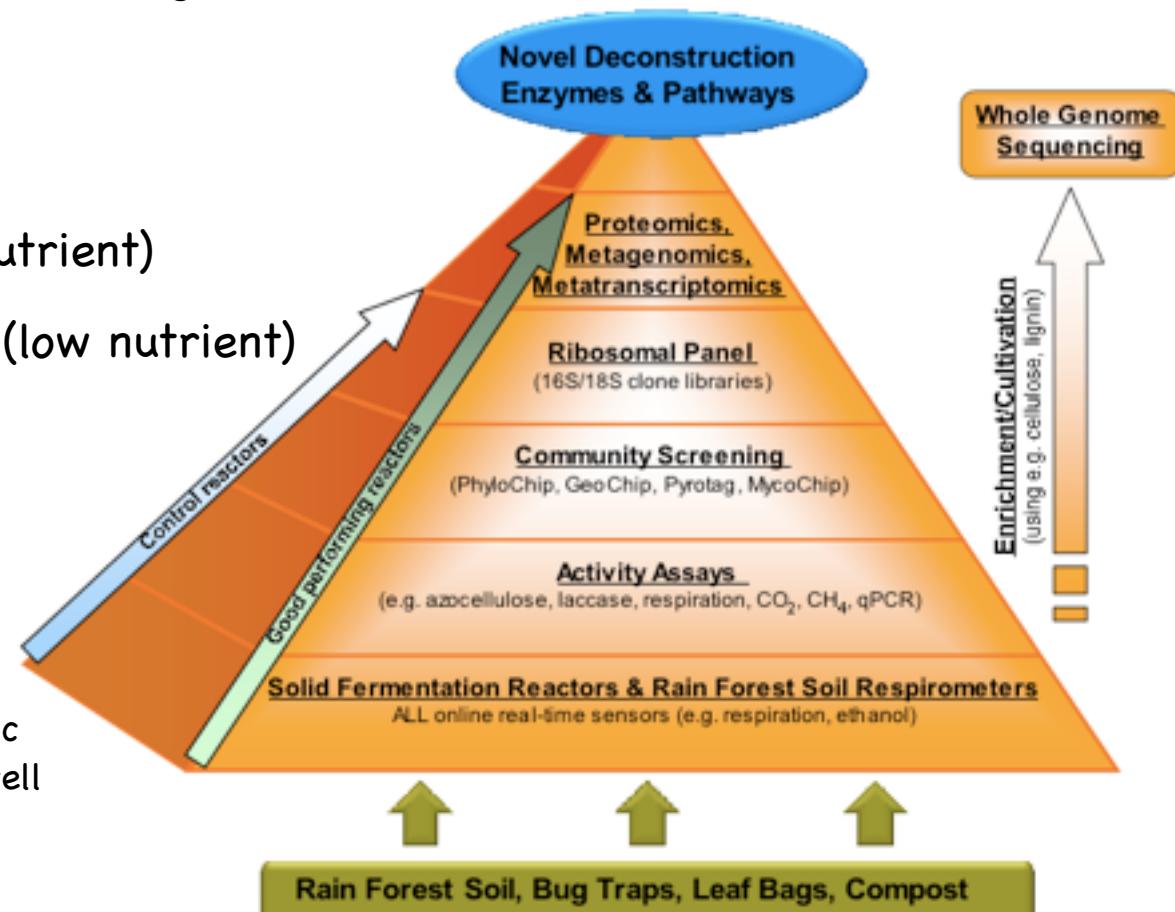


Microbial Communities

Deep and High-Throughput 'Omics' analyses of Microbial Communities in potentially High Return Environments

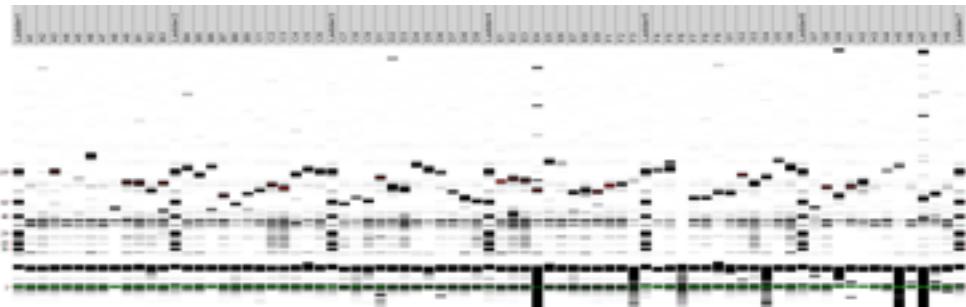
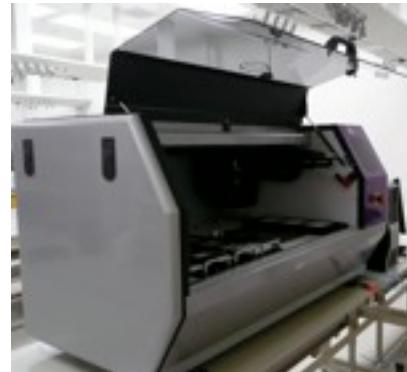
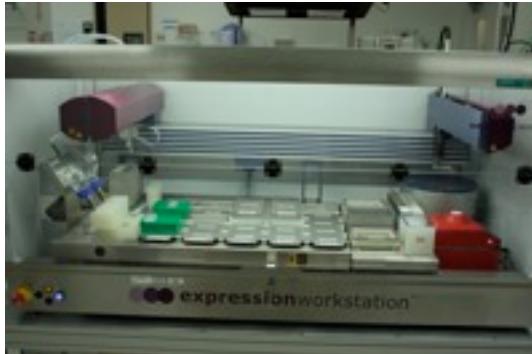
Initial Environments:

- Green Waste Compost (high nutrient)
- Puerto Rican Rain Forest Soil (low nutrient)

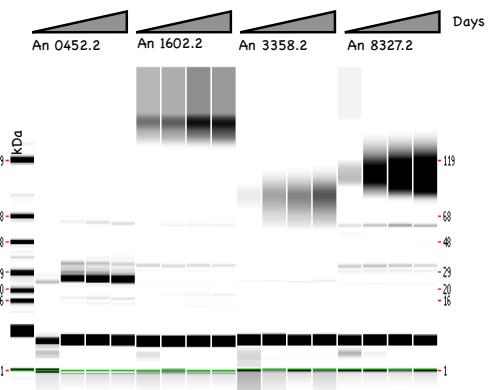


Identified and isolated lignocellulolytic enzymes, metabolic pathways, whole cell biocatalysts, and mixed cultures for deconstruction

Tiered Screening Strategy



E. coli Detection



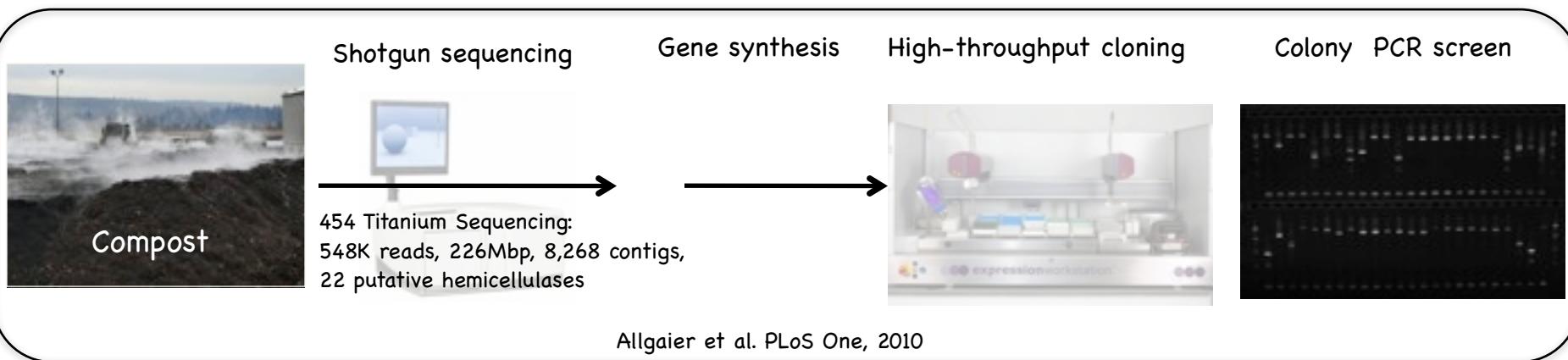
Pichia Optimization



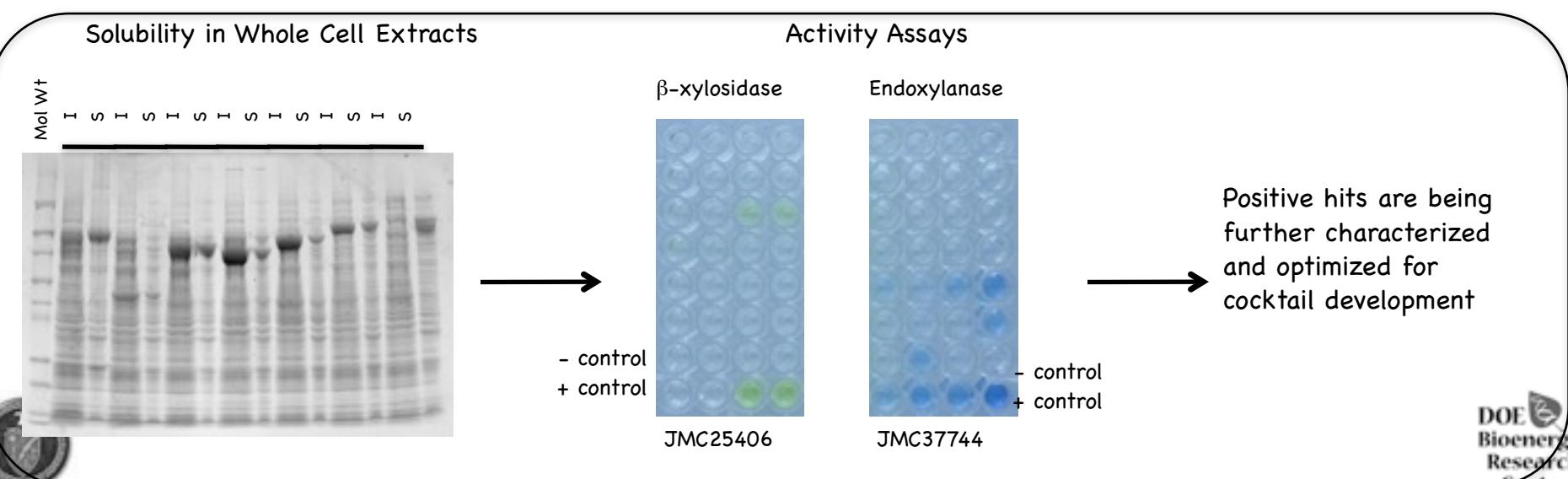
Biocatalyst Discovery

- hemicellulases from compost metagenome

Discovery



Expression and Activity Screening



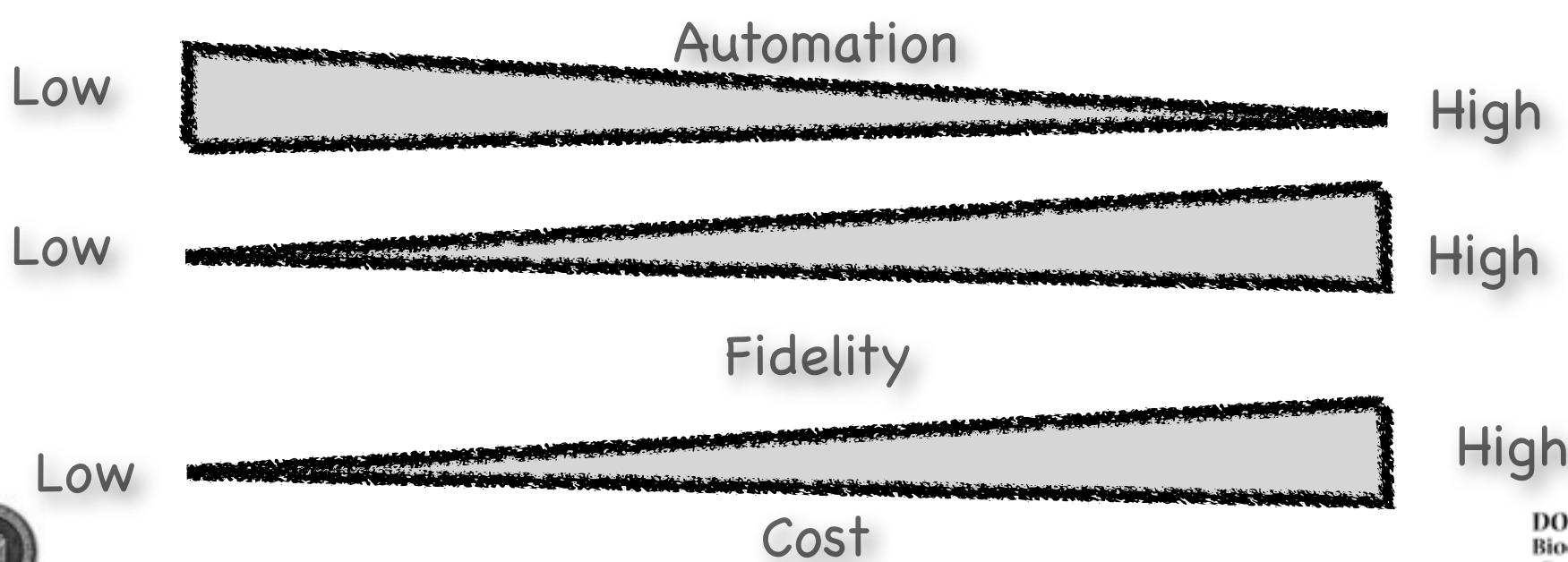
Assay Development

Zone
Clearing
Assay

DNS
Assay

Glucose
Assay

HPLC



Assay Workstation

- Integrated operations for screening and assays
- Reporting and data management
- Various other liquid handling applications

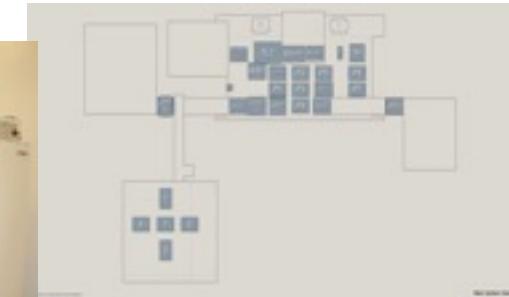
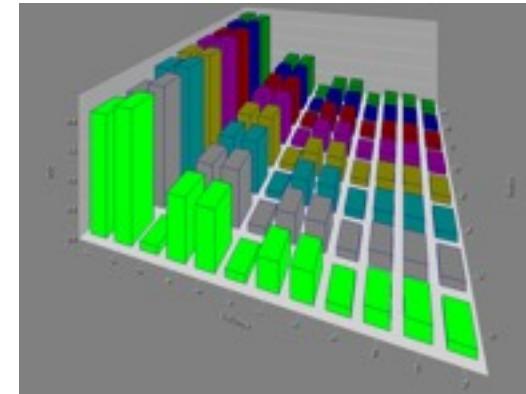
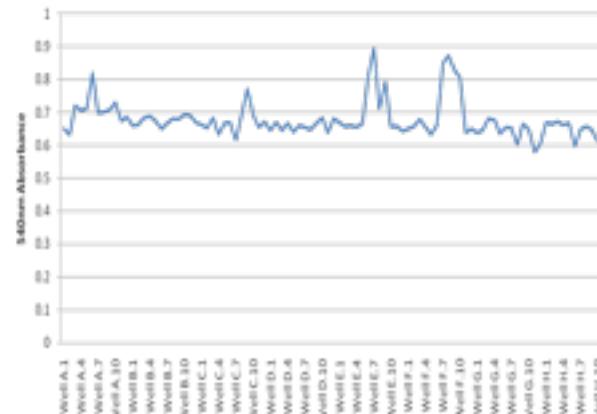
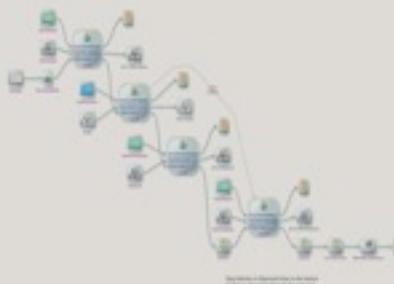
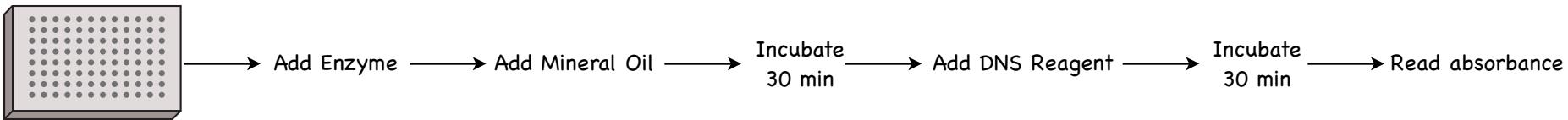
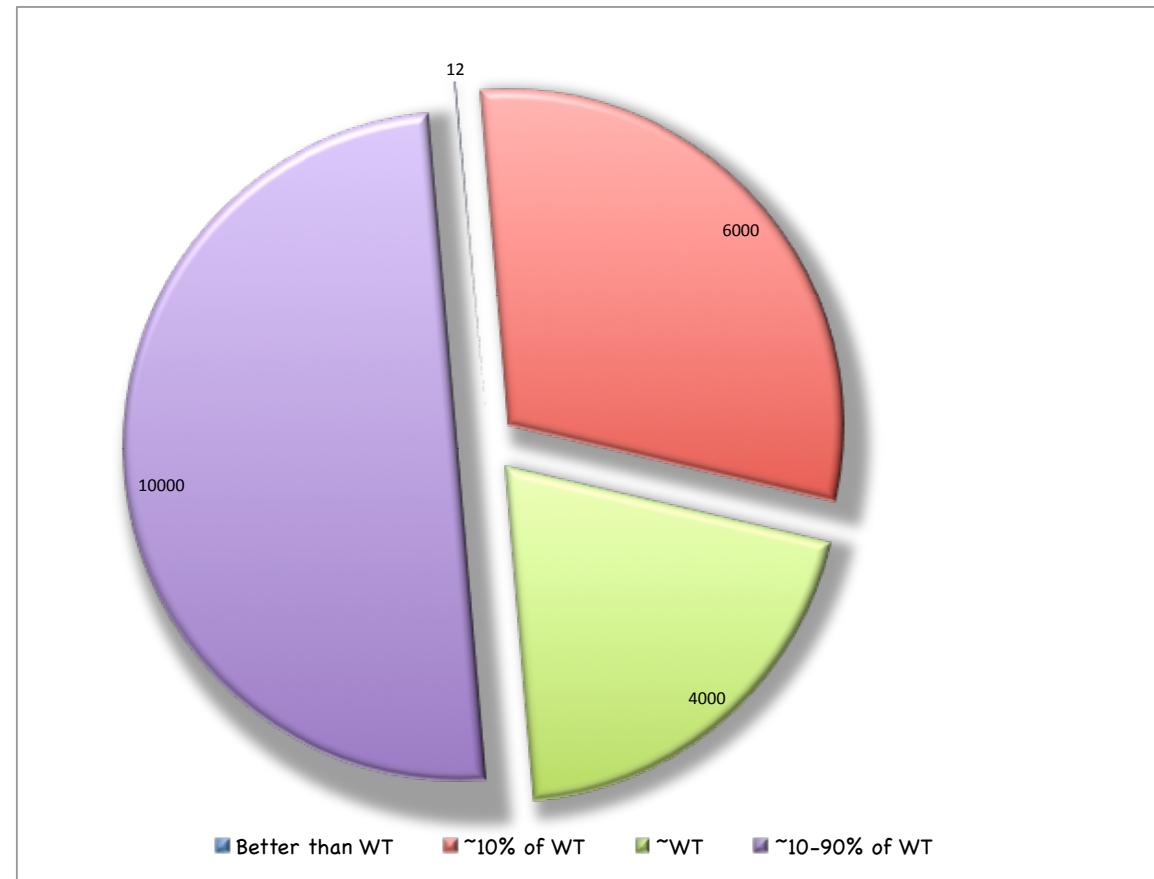


Plate containing
1.25% CMC



Evolution and HT Screening

- Evolve the ORF
- Screen for activity using CMC and DNS
- Most of them are worse than the "WT" enzyme



Solid Substrate Assays

Challenges

Biomass dispensing

- High throughput
- Uniformity
- Particle sizes distribution

Enzyme - biomass reaction

- Mass transfer
- High biomass loadings
- Evaporation

Workflow

Substrate Preparations

- Make up 2% biomass slurry in 2% PEG 20K solution
- Dispense 2% biomass slurry to 96-deepwell plate
- Dry plate over night at 70°C
- Store plate at room temperature



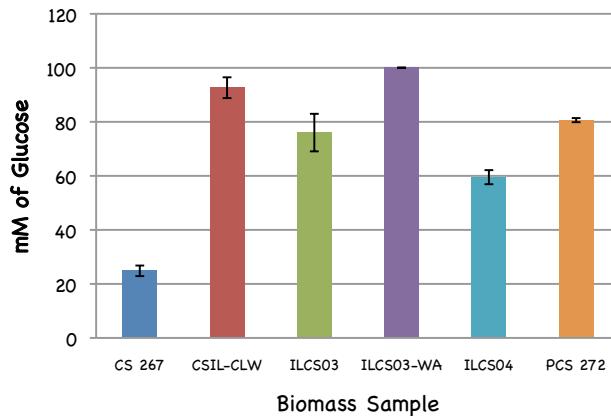
Saccharification

- Add 200µL solution containing enzymes (10% w/w enzymes to glucan content per well)
- Seal and incubate plate for 20 - 24 hrs @ 1000 RPM

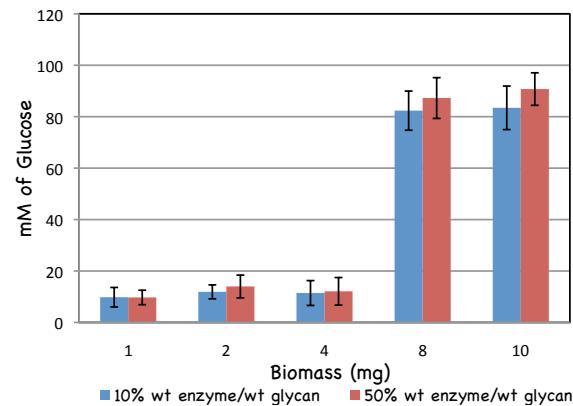


DNS Assay

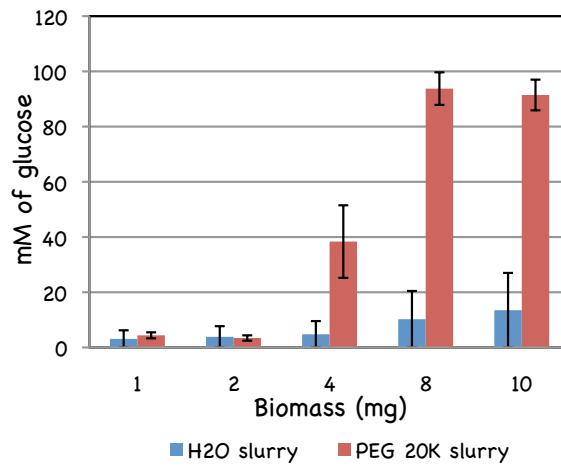
- Spin plate for 30 min, 1500 xg
- Aliquot supernatant for DNS reaction in plate reader plate
- Incubate reaction at 70°C for 30min
- Read absorbance at 540nm



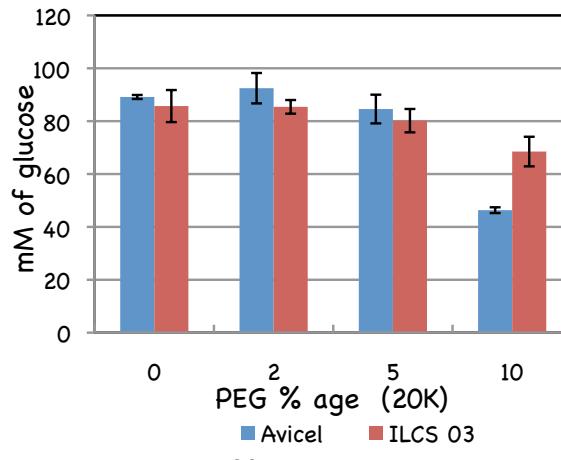
Substrate Source



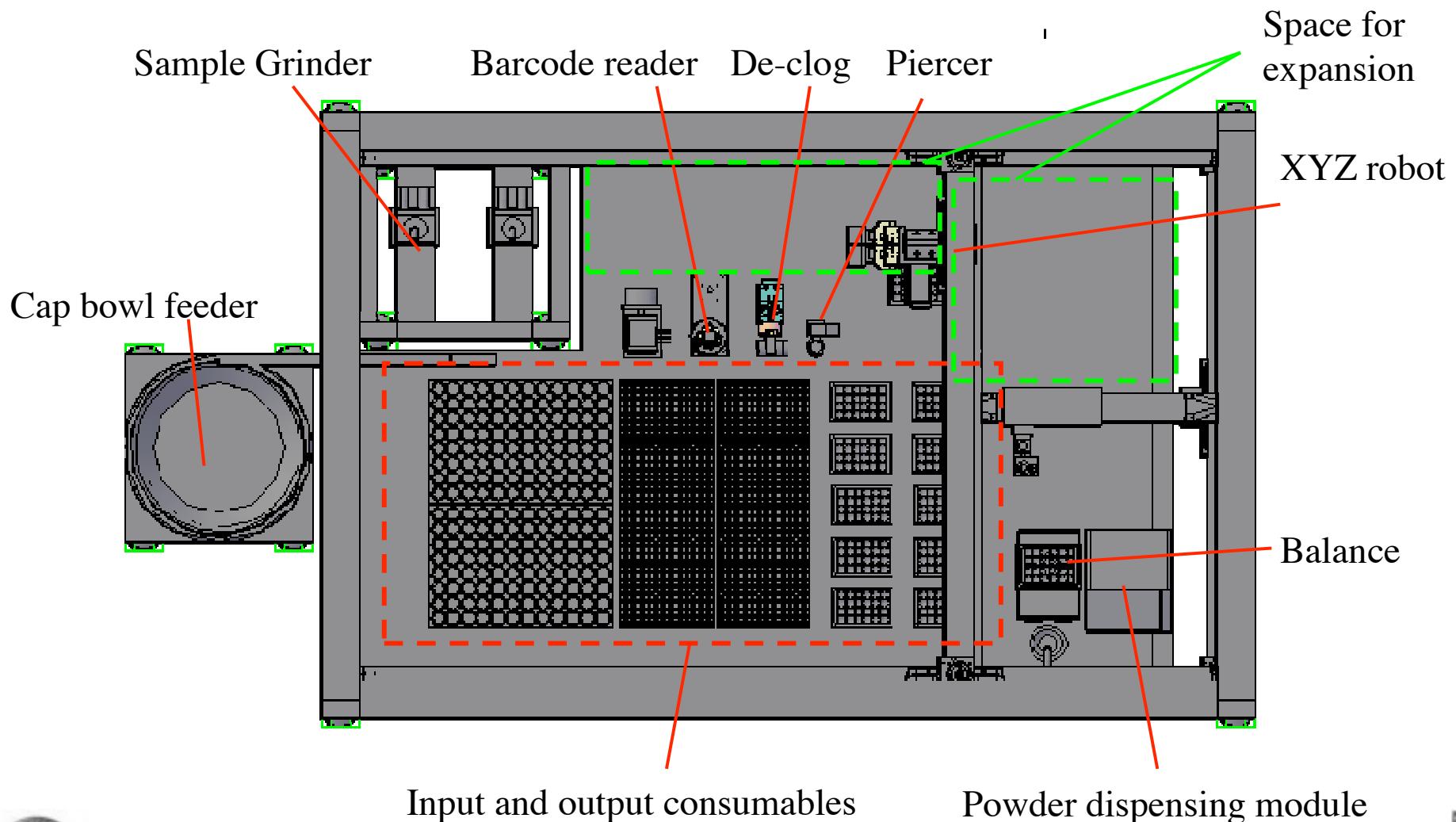
Enzyme Loading



H₂O vs PEG Slurry



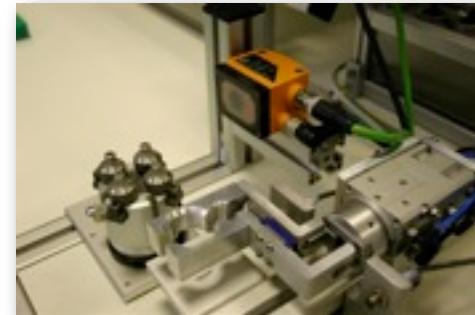
PEG Effects Conversion



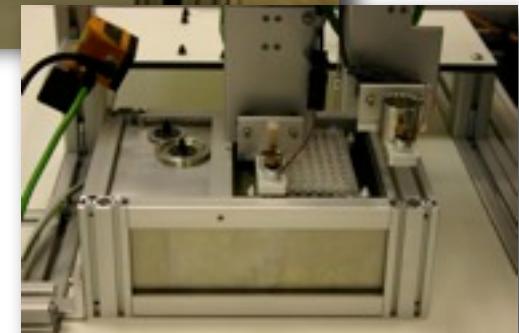
System Image



Large Grinder



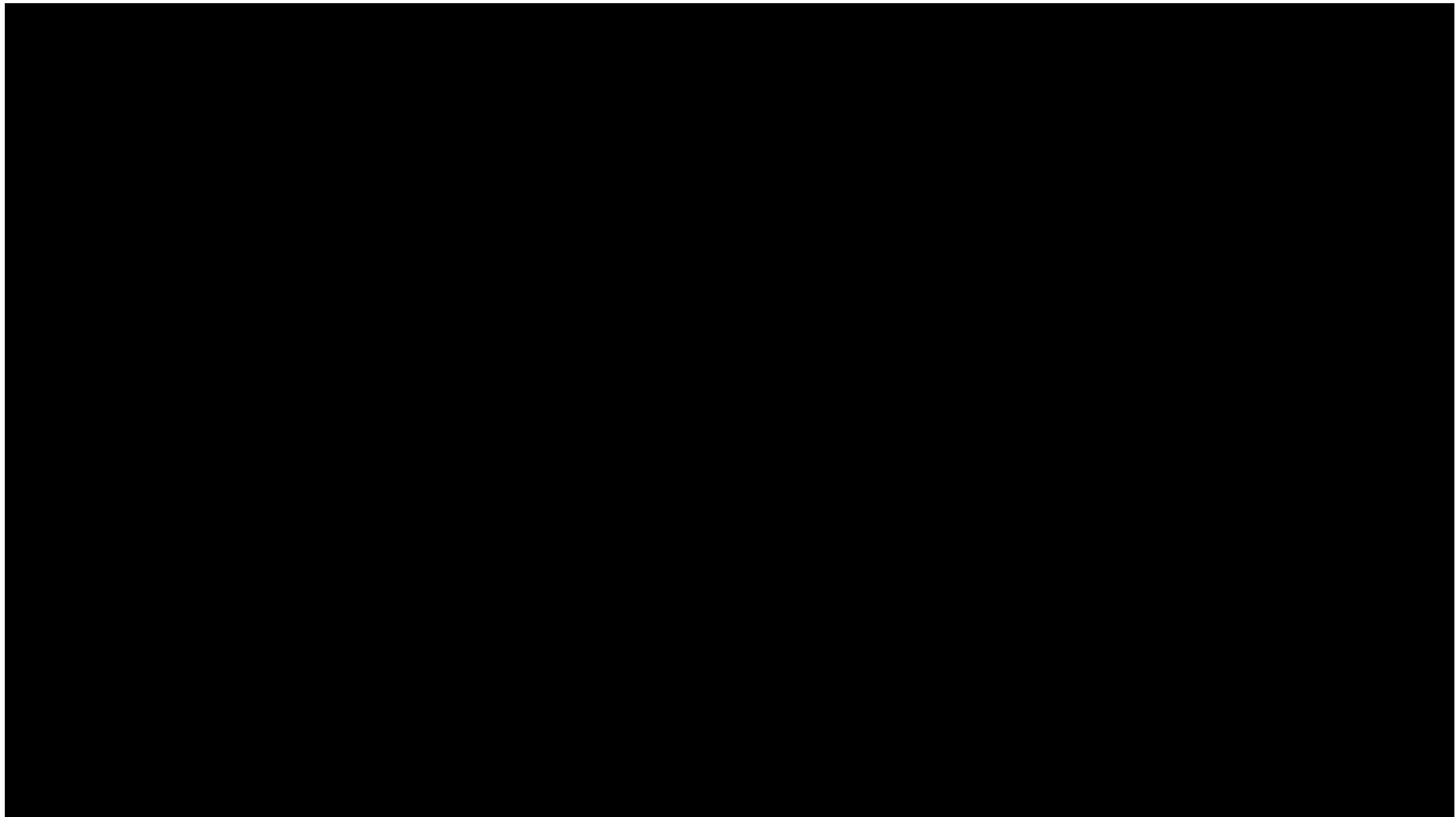
Barcode Scanner



Balance

Large Grinder

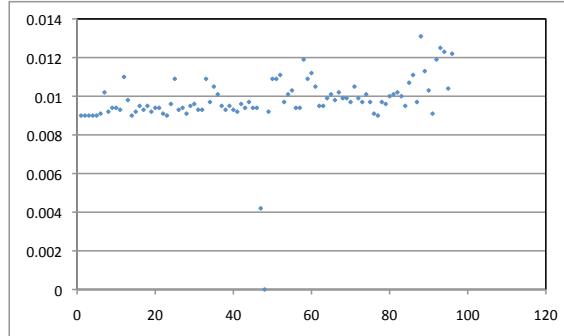
Large Grinder



Uniformity Delivery Across Various Biomass

Switchgrass

oven dried sample
1 x 96 deep well plate
10 mg target, 1 mg tolerance weight



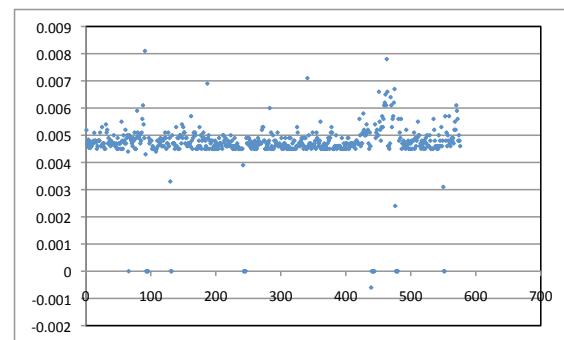
Dispensing Accuracy

2 mg +/- 0.002
5 mg +/- 0.005
10 mg +/- 0.001

Deep 96 Well plates
10 mg / well

Corn Stover

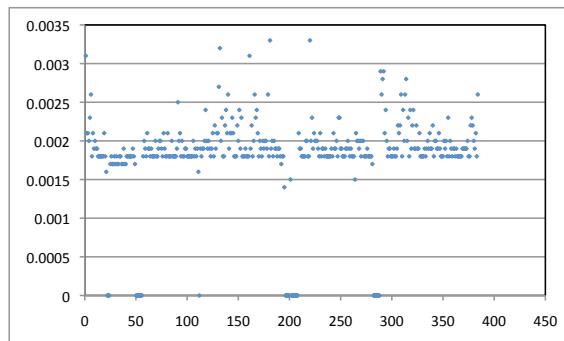
2 X 96 vials to 6 deep well plates
5 mg target, 0.5 mg tolerance



Deep 96 Well plates
5 mg / well

Rice Stem

4 x 96 vials to deep well plates
2 mg target, 0.2 mg tolerance

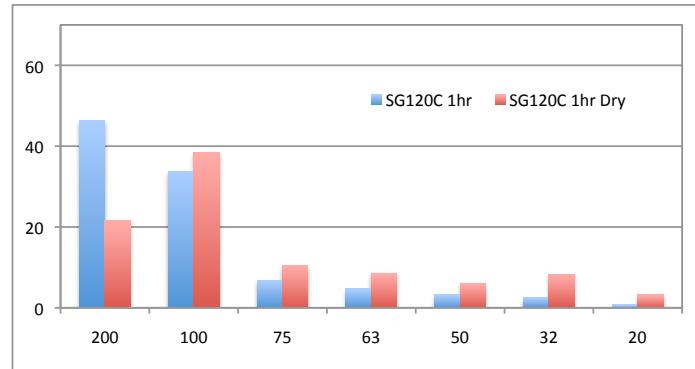


Shallow 96 Well plates
2 mg / well

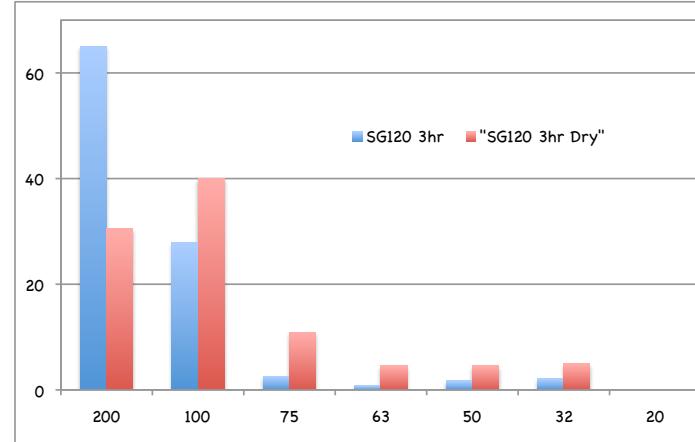
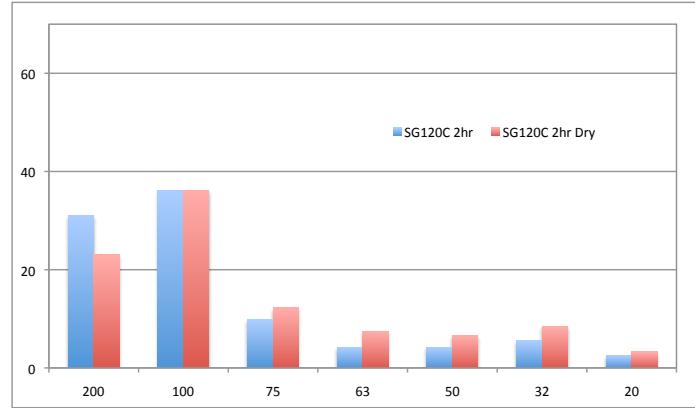


Particle Size Variation

- Particle size varies considerably, depends on source and treatment

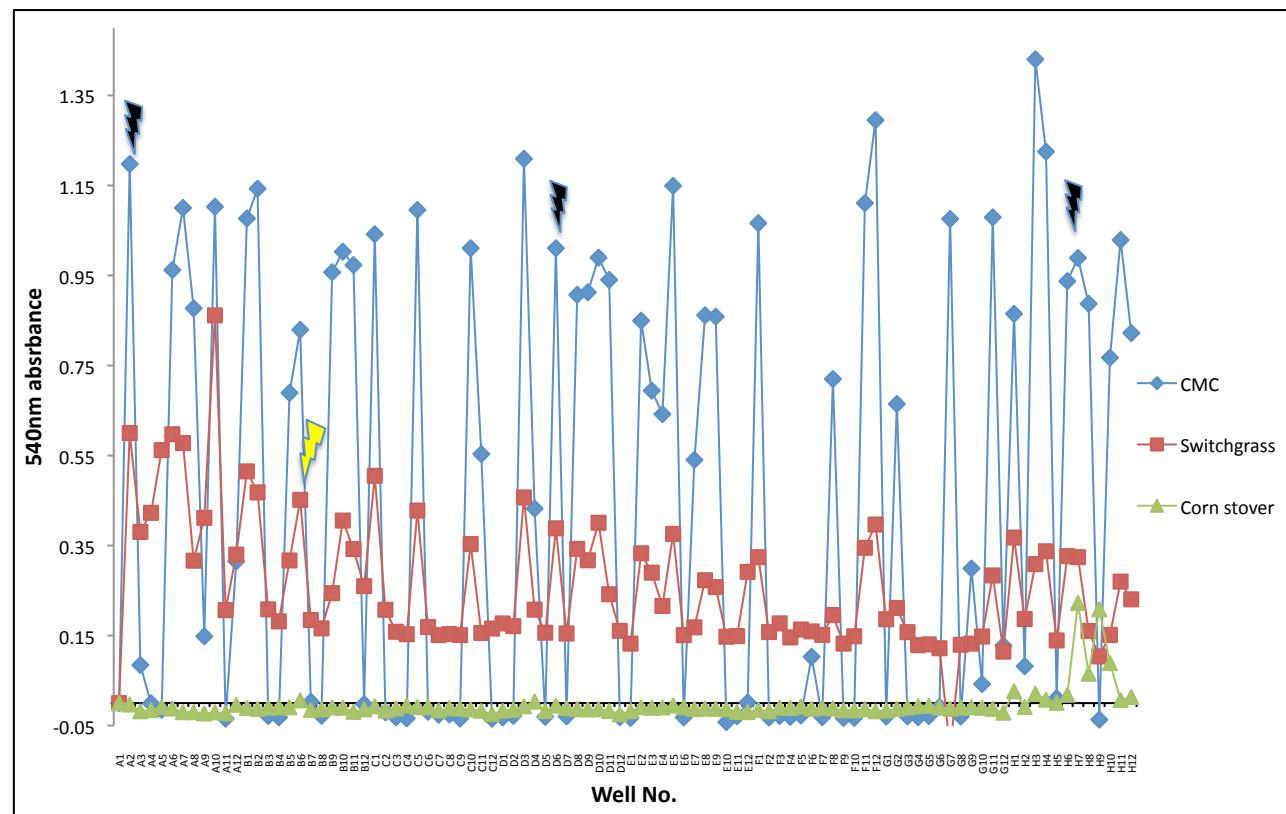


- Drying the sample in the oven helps achieve a more uniform grind and significant differences are due to the readily hygroscopic nature of the substrate



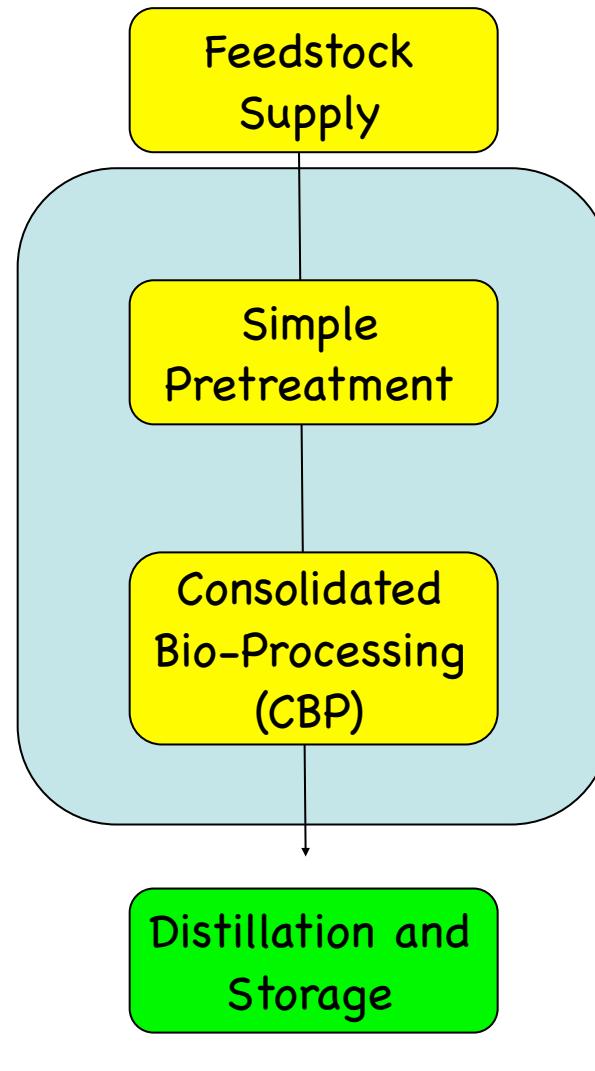
Evaluating on “Real” Substrates

- Re-assay ORFs that were experimentally shown to be active on CMC
- Most of them were dead on real world substrates



Trojan Horse Strategy

Lower costs through process simplification



Engineered Biomass Advantages
Consolidated bio-processing
Steps and cost reduction
Elimination of enzyme costs

About 30-40% of costs are
associated with pretreatment

Mature

Experimental

Plant Transformation:

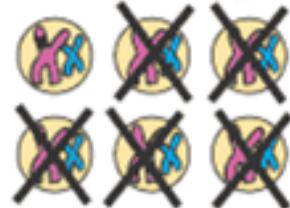
Agrobacterium and Particle Inflow Gun Mediated

Agrobacterium

co-cultivation
with plant cell



Ti plasmid transfer
into plant
chromosome



screening for
transgene(s)

Gene identification

gene insertion
into ti plasmid

gene replication

Particle Inflow Gun

microprojectiles
coated with DNA

Shoot microprojectile
into cells



Recombinant
plant

Hadi et al., 2002, PCR

~30K reports, Vain, P., 2005, Nature
BT Cotton, Roundup Soybean

Bioinformatics Analysis

Optimization Gene Synthesis

- CelA

- CelA from *Alicyclobacillus acidocaldarius* is optimally active and stable at temperatures above 65°C, belongs to glycoside hydrolase family 1 (GH1) and shows wide substrate specificity on different glycosides and cello-oligosaccharides

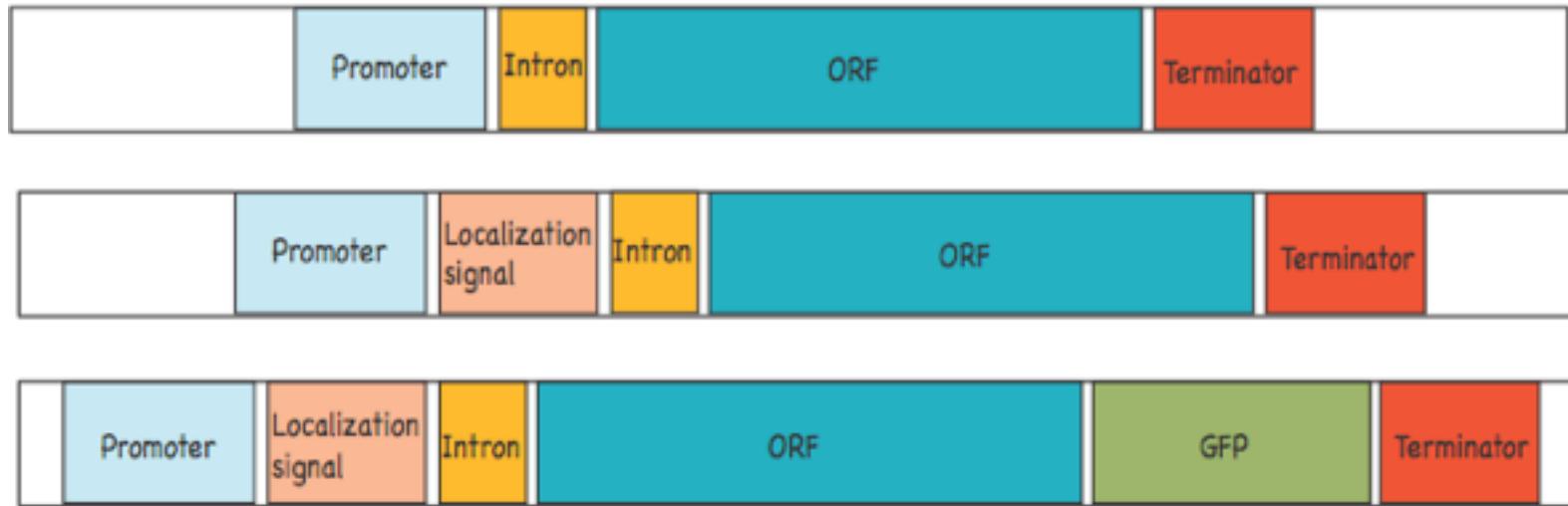
- SSO1949

- SSO1949 gene from thermoacidophilic archae *Sulfolobus solfataricus* encodes a thermostable (GH 12) carboxymethylcellulose as well as cello-oligomers. This enzyme has a pH optimum of 1.8 and a temperature optimum of approx. 80°C. Furthermore, the enzyme has a half-life of approx. 8 hrs at 80°C and pH 1.8



Actuator Construction

Targeting and Gene Regulatory Sequences



- **Cytoplasmic Expression**
Maize Ubiquitin promoter + intron Cellulase-nos cassette inserted into pCAMBIA 1305.1.
- **Apoplast Expression**
Maize Ubiquitin promoter + intron-SP-Cellulase-nos cassette in pCAMBIA1305.2 (translational fusion)
- **Apoplast Expression of GUSPlus Fusion Protein**
Maize Ubiquitin promoter + intron-SP-Cellulase-GUSPlus-nos cassette in pCAMBIA1305.2
(translational fusion)



Plant Model Systems

Arabidopsis

- Brassicaceae family, are small flowering plants related to cabbage and mustard. This genus is of great interest since it contains Thale Cress (*Arabidopsis thaliana*), one of the model organisms used for studying plant biology and the first plant to have its entire genome sequenced. Changes in the plant are easily observed, making it a very useful model system



Brachypodium distachyon (L)

- Has many qualities that make it a model for functional genomics studies in temperate grasses, cereals, and dedicated biofuel crops such as Switchgrass. These attributes include small genome diploid accessions, short life cycle, and simple growth requirements





CelA



SSO 1949



Sub-cellular Protein Localization

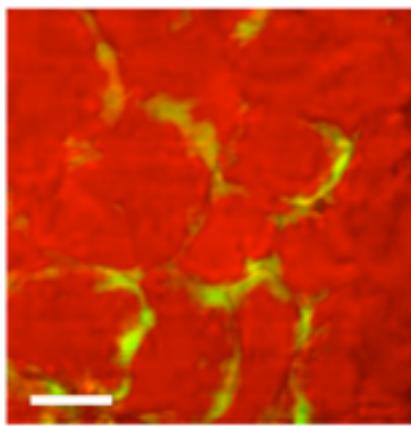
Arabidopsis Seedling (Hyperspectral Imaging)



Cytoplasmic

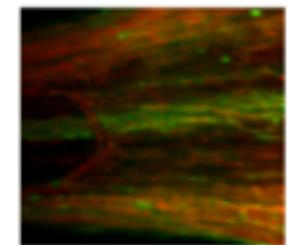
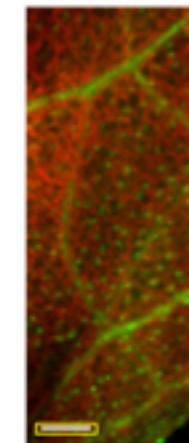
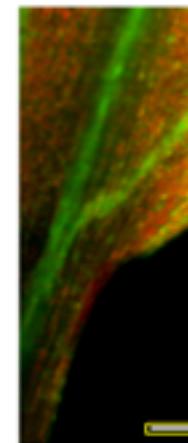
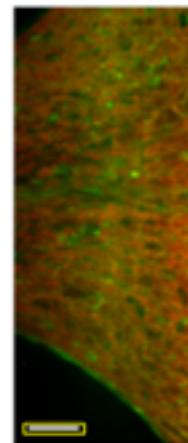


Cajal Body



Scale bar is 10 μ m

GFP fused to the apoplast targeting signal is localized to the apoplast in leaf tissue.



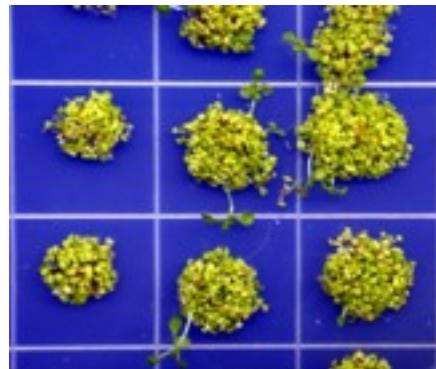
Images scanned with 5 μ m pixels resulting in image size of 515 μ m \times 1.0 mm

All color channels have been adjusted independently for contrast.

All scale bars 100 μ m



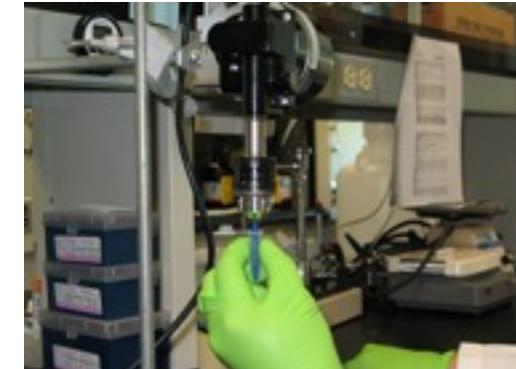
Arabidopsis Containing the Genetic Circuit Were Selected



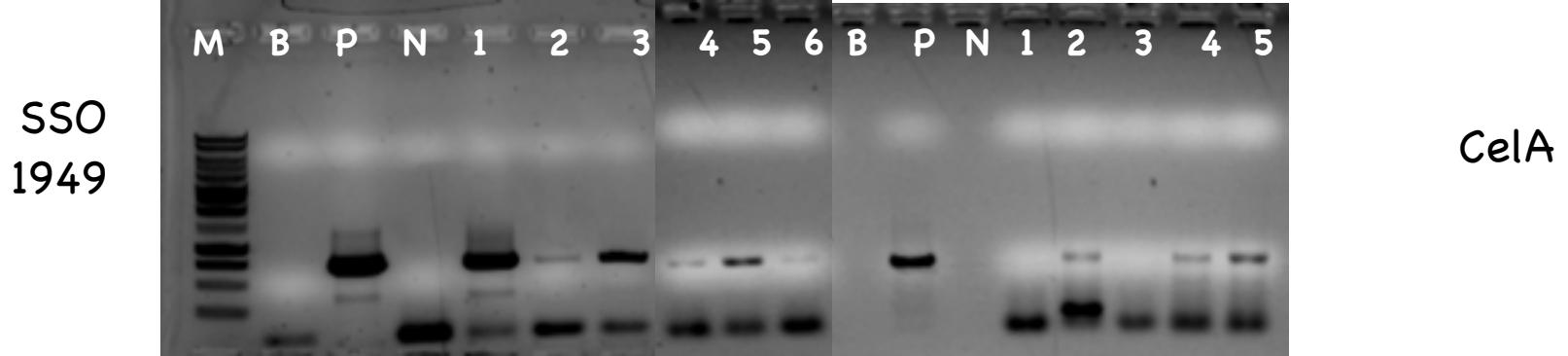
Seed Selection



Transfer to Soil



Grinding & DNA Extraction

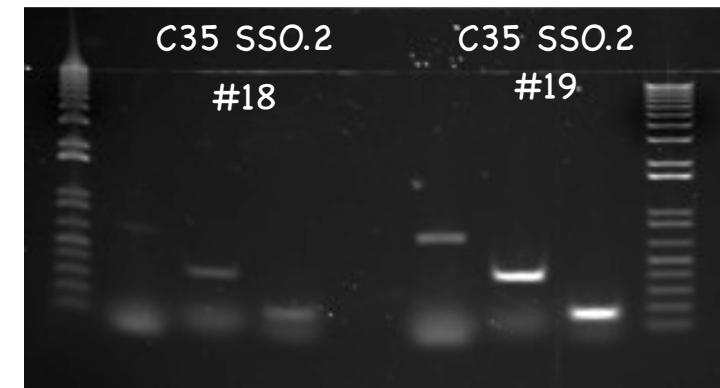
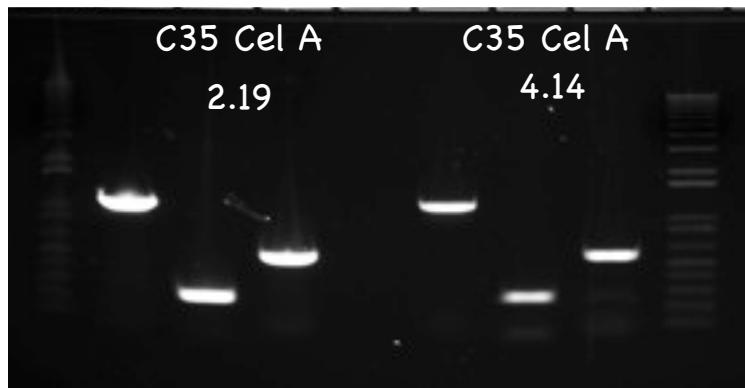


PCR analysis to confirm the presence of actuator in plants



Transcript Analysis

RTPCR in *Arabidopsis* Transgenics



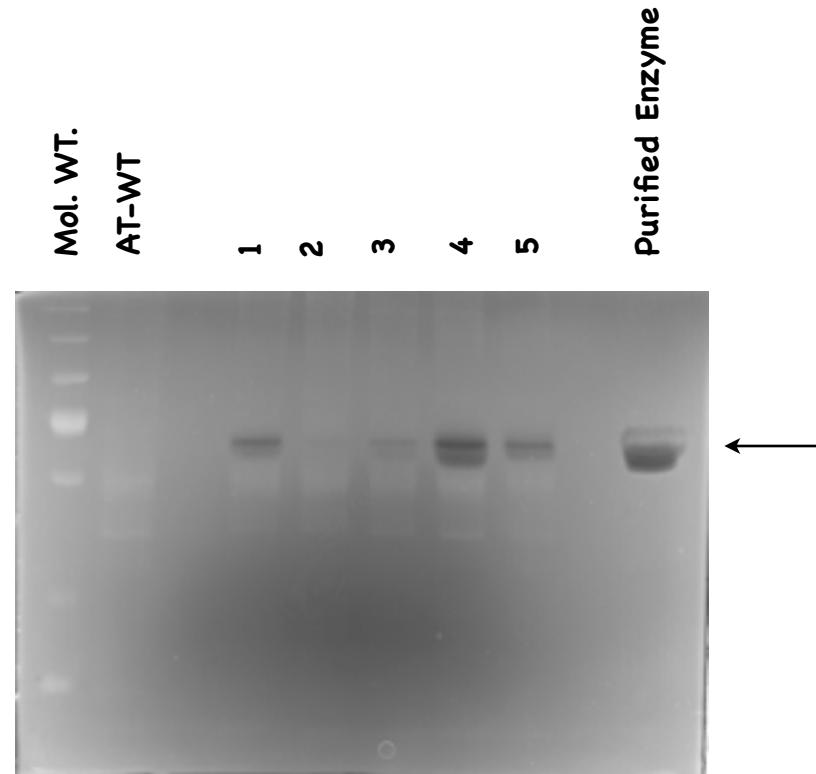
1. CelA F2 + CelA R1 (1194 bp)
2. CelA F1 + CelA R2 (269 bp)
3. CelA F3 + CelA R1 (576 bp)



1. 1949 Plant F1 + 1949 Plant R1 (713 bp)
2. 1949 Plant F2 + 1949 Plant R1 (393 bp)
3. 1949 Plant F3 + 1949 Plant R1 (176 bp)

We were able to confirm expression of both actuators in all transgenics

Zymograms Confirm Enzyme Activity



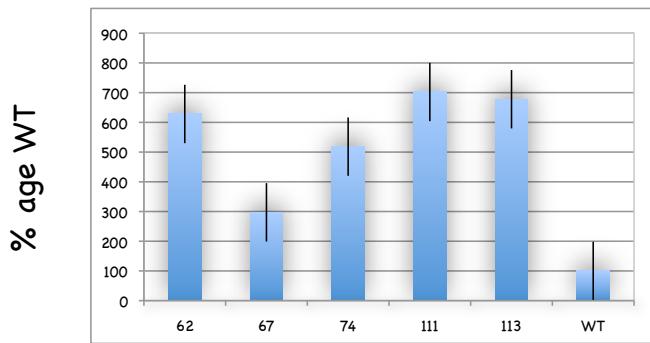
Zymograms were used to assay for protein activity in *Arabidopsis* extracts. We were able to confirm activity with whole cell lysates prepared from plants containing CelA



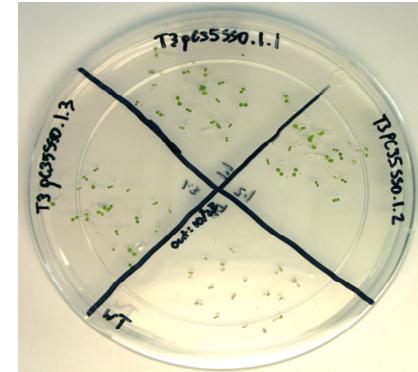
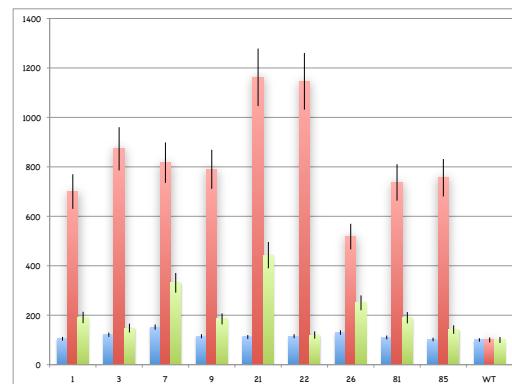
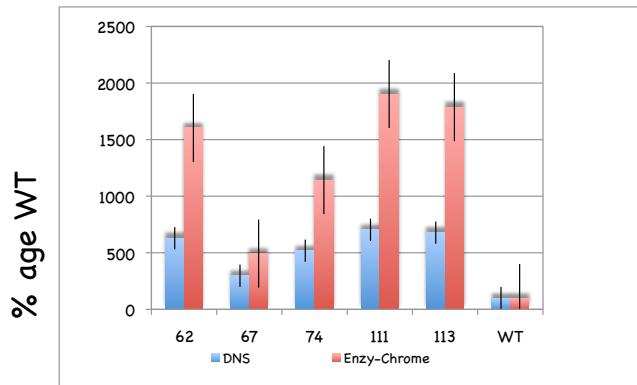
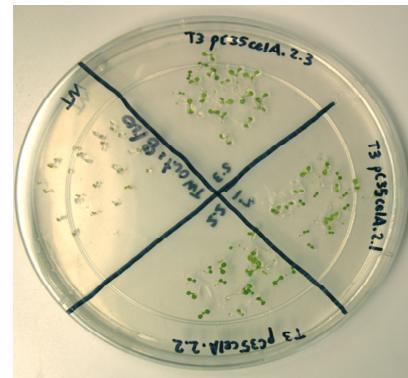
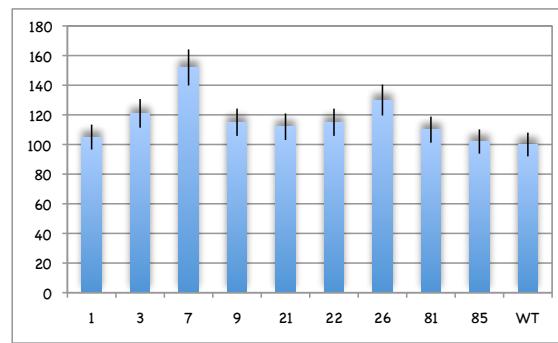
T3 Homozygous Plants

Crossed to Pyramid Genes

CelA



SSO-1949



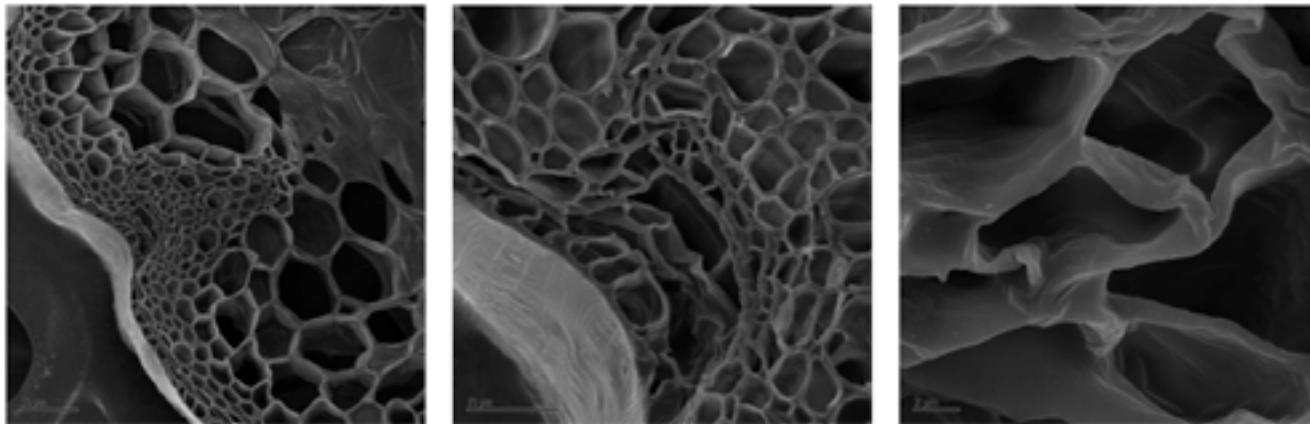
SSO 1949 containing plants are slower growing compared to wild type and/or CelA harboring

Homozygous SSO 1949 plants have been crossed with homozygous CelA plants in order to pyramid the genes

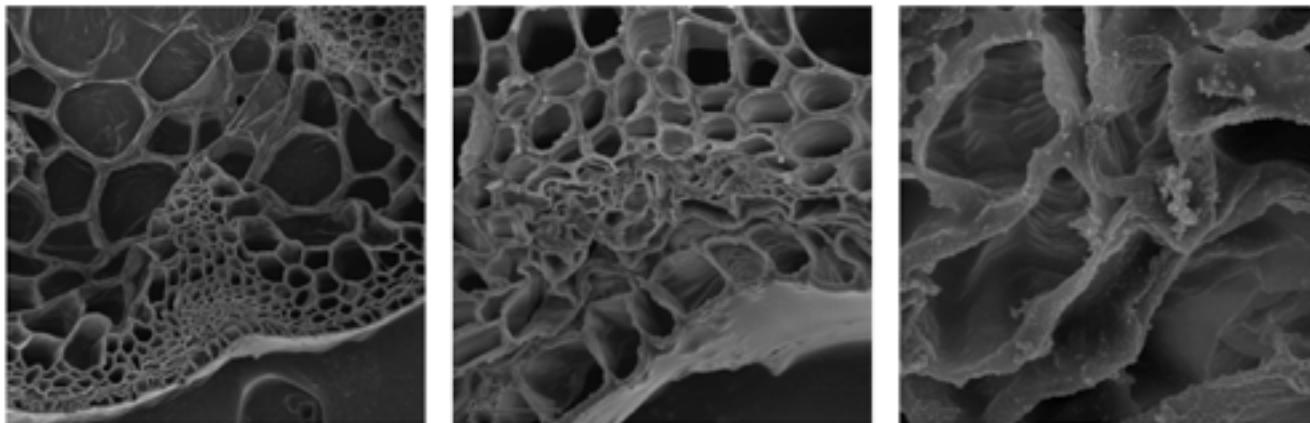


SEM after Hydrothermolysis Pre-treatment

Wild Type



Cel A

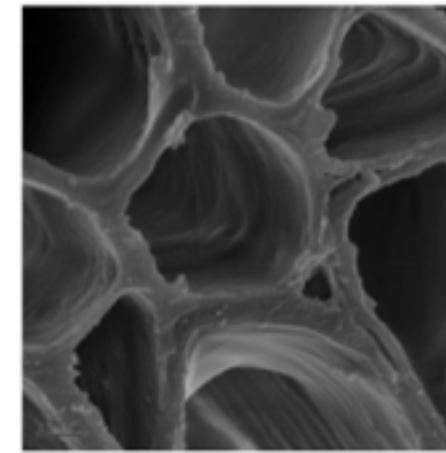
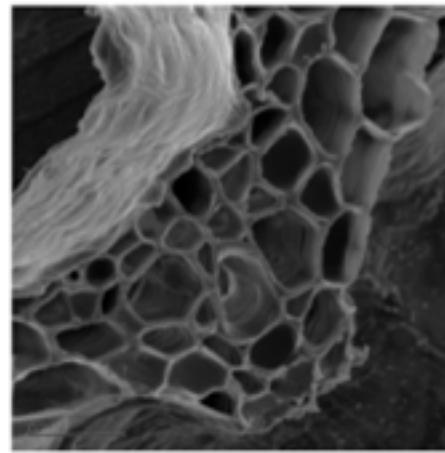
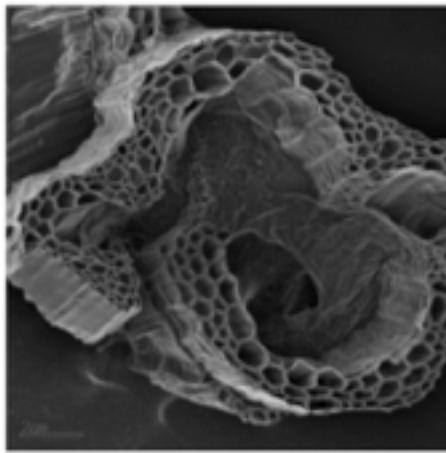


Transgenic Arabidopsis containing Cel A treated under hydrothermolysis conditions for 1 hours

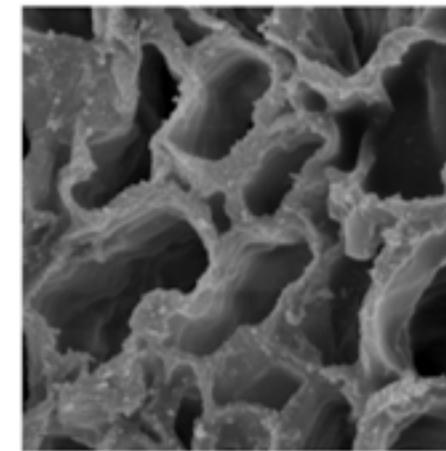
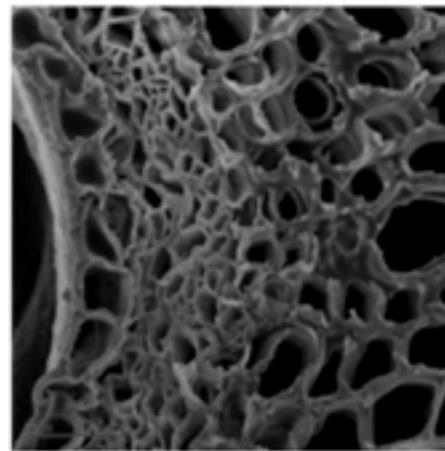
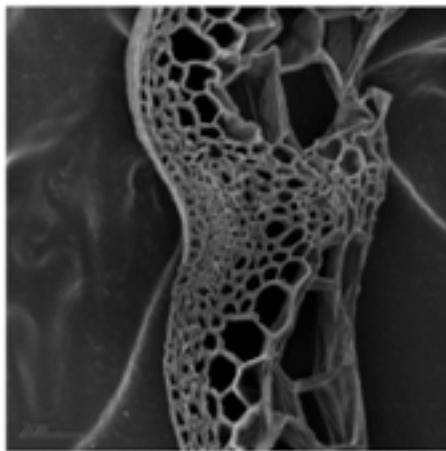


SEM after Dilute Acid Pre-treatment

Wild Type



SSO 1949



Transgenic *Arabidopsis* containing SSO 1949 were pretreated with dilute acid for 2 hours

Brachypodium Transformation

Seed to seed 8 months



Green Seeds



Dissected embryos
(<0.3-0.7 mm)



Callus Induction



Agrobacterium Cocultivation
3 days

Subculture
Callus 2X
~3 weeks



Transgenic Plants
12-20 Weeks



Regeneration
2-6 weeks



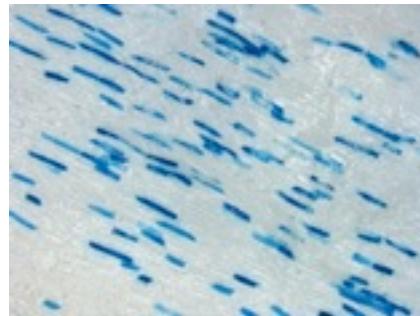
Selection
3-5 weeks



CelA and SSO1949 in Brachypodium

Transient Actuator Testing Using Particle Inflow Gun

Cel A



SSO 1949

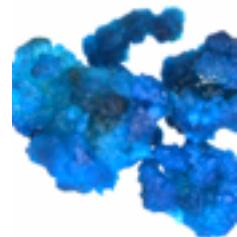
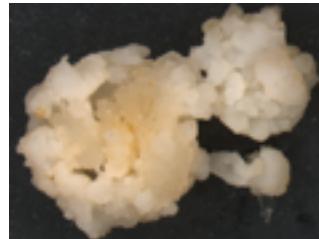


Onion cells were transformed using particle inflow gun.
Cells were assayed for reporter protein expression after
three days
CelA and SSO 1949 fusion was detected in onion cells.

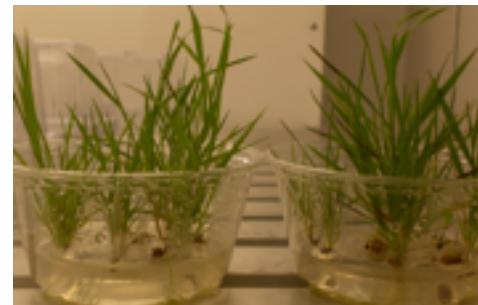
Brachypodium leaf tissue was transformed using particle
inflow gun.
Cells were assayed for reporter protein expression after
three days
CelA and SSO 1949 fusions was detected in leaf tissue.



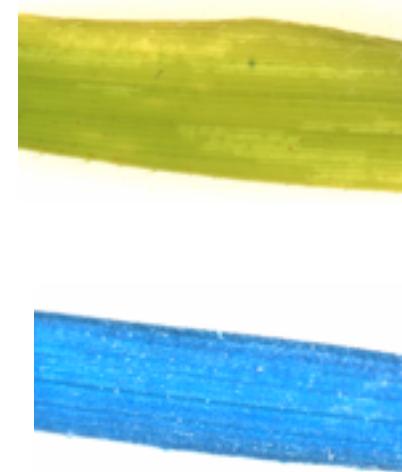
Brachypodium Transformation



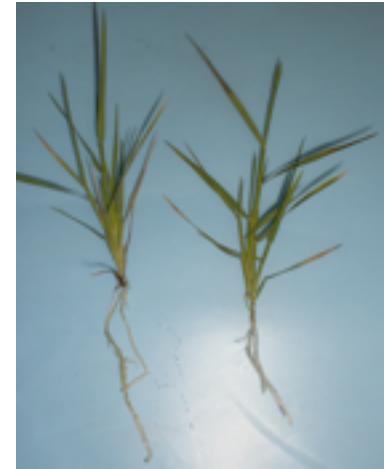
Callus
Screening



Shoot
Regeneration



Shoot-tip
Screening



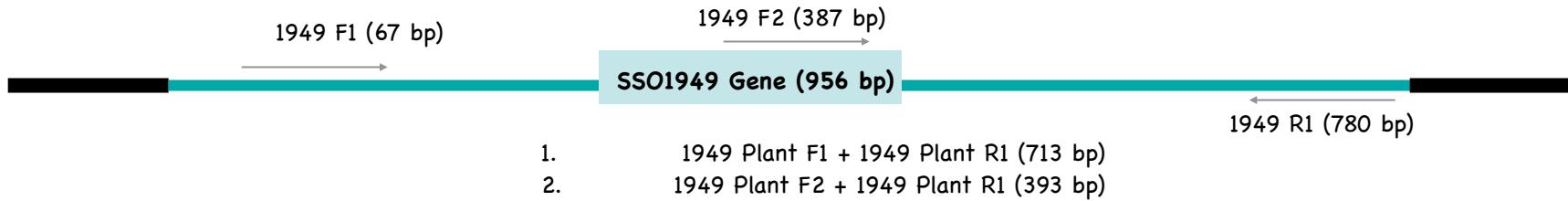
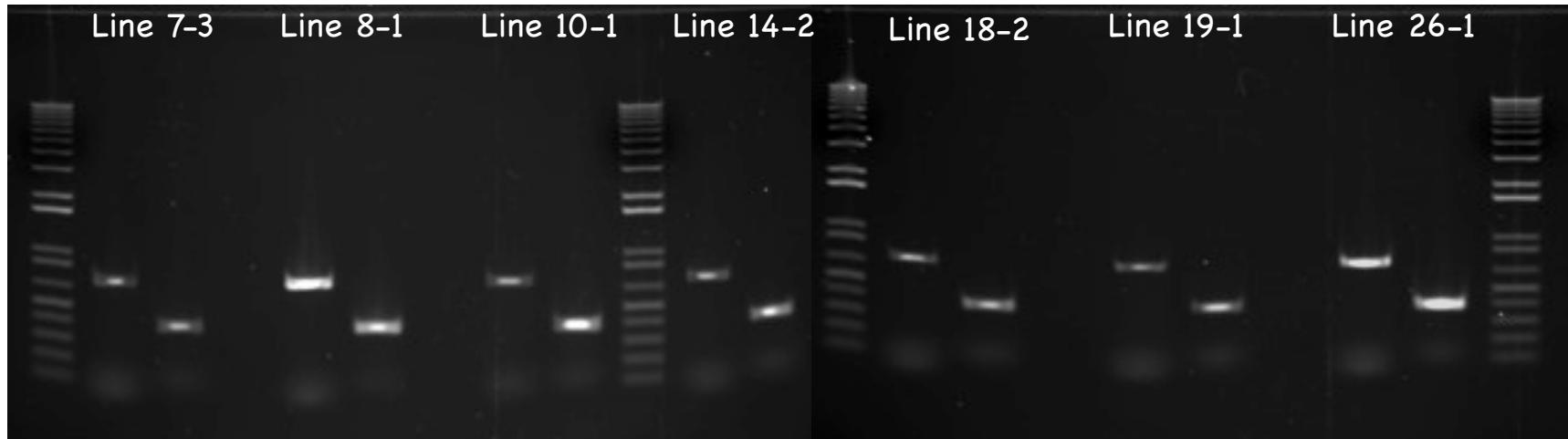
Plantlet
Acclimatization



Plantlet
Regeneration

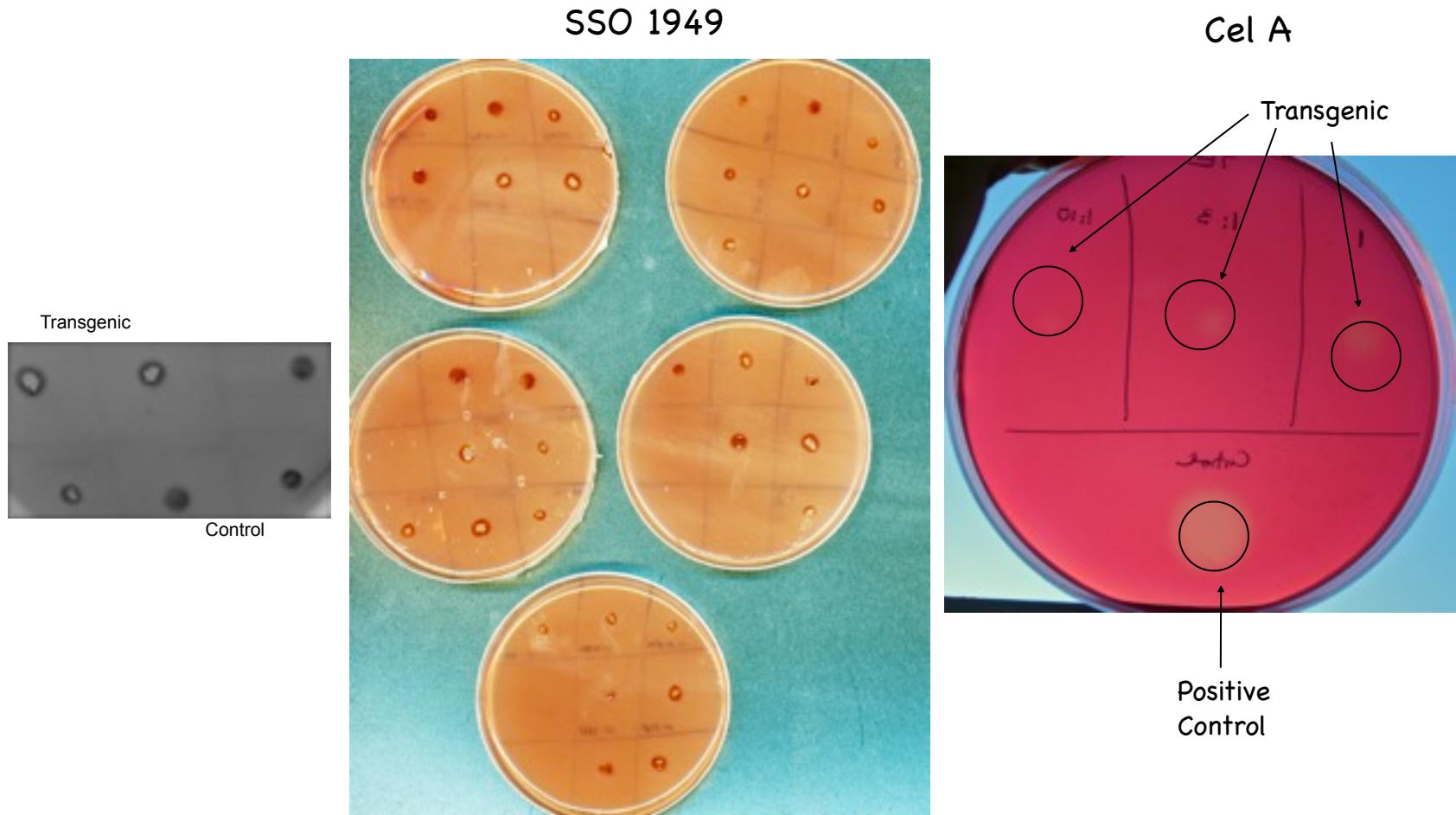


Expression Analysis - RTPCR



RT-PCR analysis confirms expression of actuators in *Brachypodium*.

Screening for Enzyme Activity



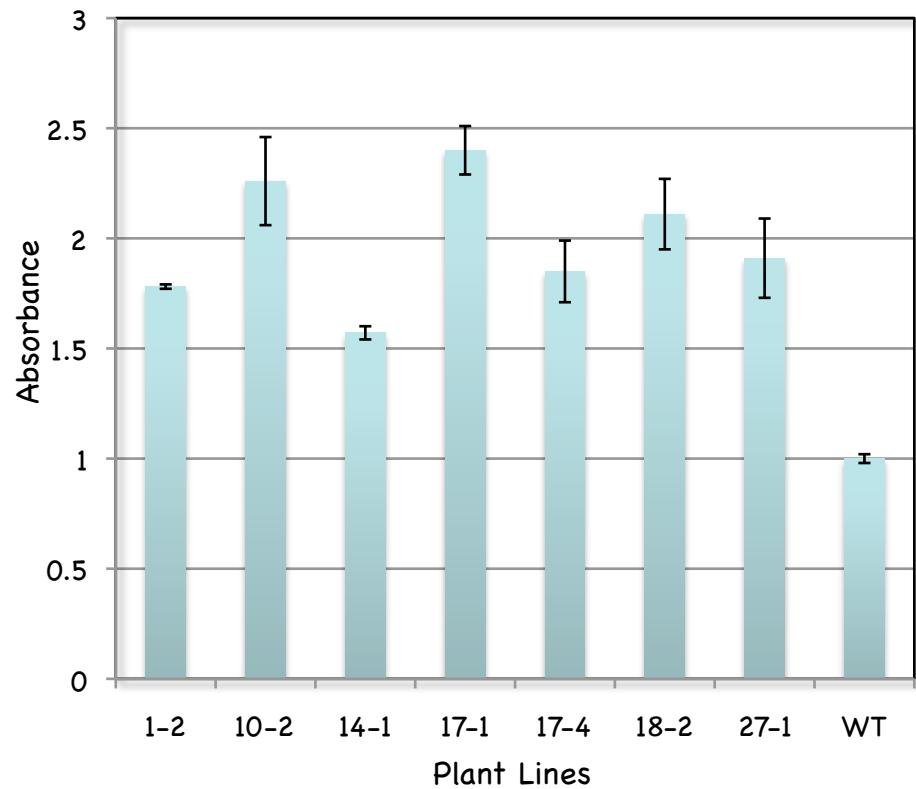
Congo red assay was used to screen for enzyme activity in transgenic callus

Enzyme Activity in Plant Extracts

Extract total protein and quantify

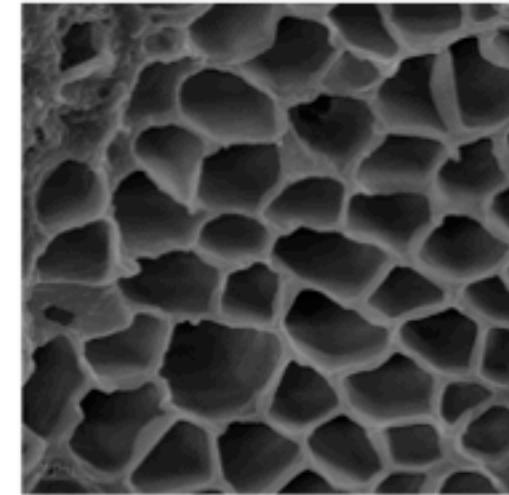
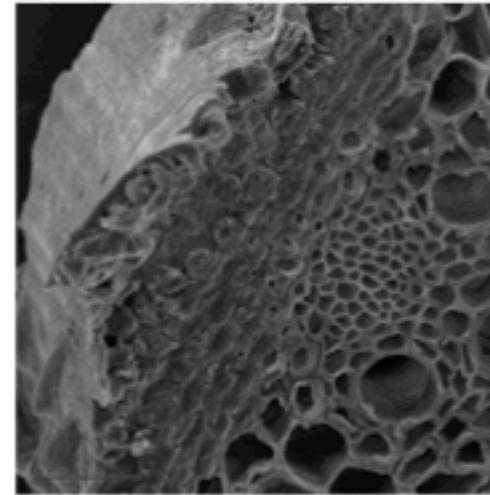
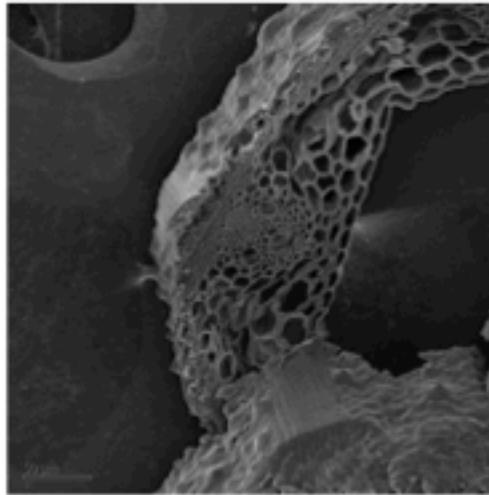
Assay for enzyme activity using
CMC

Determine reducing end formation
using 3,5-dinitrosalicylic acid (DNS)
assay

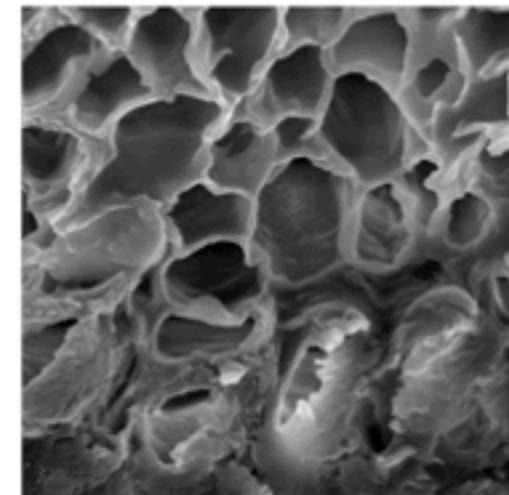
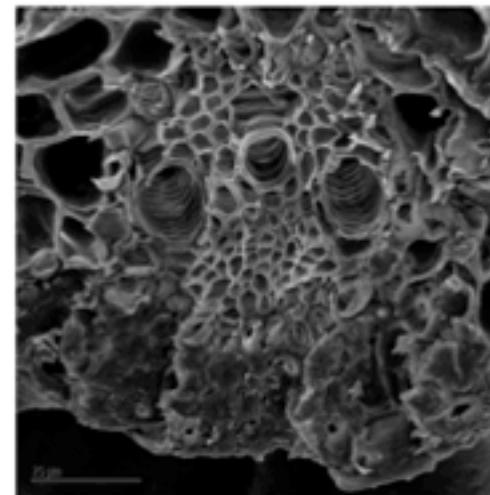
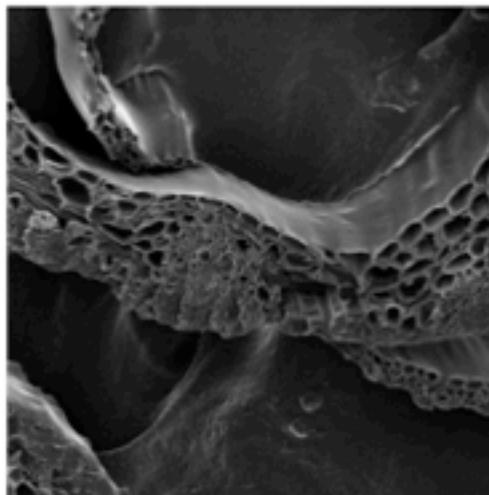


Cel A in Brachypodium after Pretreatment

Wild Type



Cel A



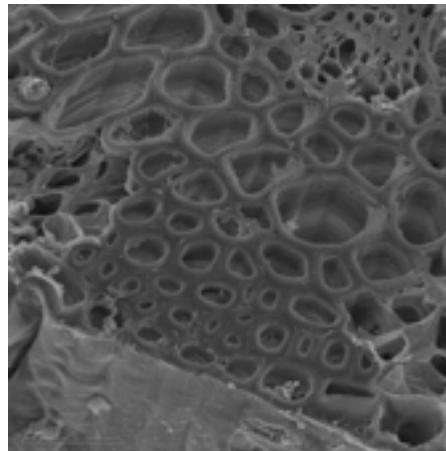
Brachypodium Cel A construct were incubated under hydrothermolysis conditions for 2 hours



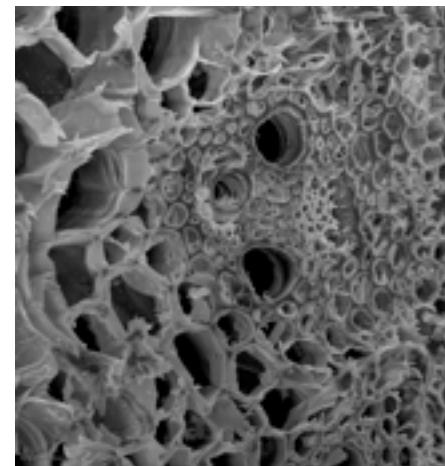
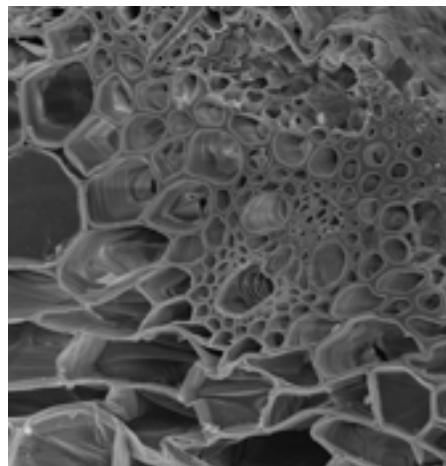
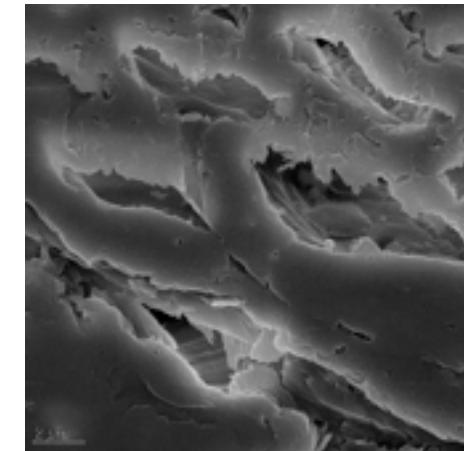
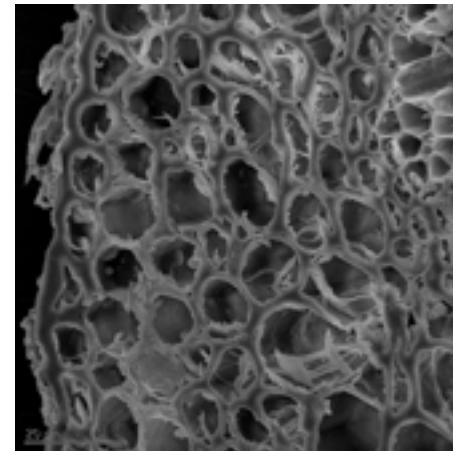
SSO 1949 in Brachypodium

after in situ Enzyme Activation

Wild Type



SSO 1949



Cellular integrity is diminished in recombinant plants after mild pretreatment (T= 60 min)

Brachypodium stem tissue was examined under SEM after 1 hour of dilute acid pretreatment



Summary

- Large Scale purification is the major bottleneck
- "You get what you screen for" remains the dominant truth in the high-throughput screening (HTS) arena
- Biomass substrate source effects results
- Rescreen libraries using these real world substrates
- Evaluate engineered biomass for simultaneous saccharification and fermentation
- Expand genetic toolbox for incorporation into relevant biomass feedstocks (e.g., *Panicum virgatum*)



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- Mary Tran-Gyamfi
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- Harvey Blanch
- Jay Keasling
- Paul Adams



The stone age ended not for a lack of stones, and the
oil age will end, but not for the lack of oil
Founding architect of OPEC

