

The BioEnergy Science Center

a DOE BioEnergy Research Center

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BESC Director

<http://www.bioenergycenter.org/>



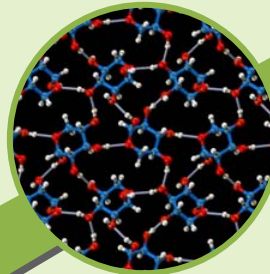
The fundamental science of biomass recalcitrance is poorly understood

Overcoming recalcitrance is the single coherent overarching theme for the BESC

Recalcitrance:
Resistance to
breakdown
into sugars



Fuel(s)



Sugars

Cellulosic
biomass

- A large-scale, integrated, interdisciplinary approach is needed to overcome this problem
 - Current research efforts are limited in scope
 - BESC will launch a broad and comprehensive attack on a scale well beyond any efforts to date
- Without advances, a cellulosic biofuels industry is unlikely to emerge
- Knowledge gained will benefit other biofuels and biofeedstocks

The BESC Team

Joint Institute for Biological Sciences (JIBS)



- Oak Ridge National Laboratory
- University of Georgia
- University of Tennessee
- National Renewable Energy Laboratory
- Georgia Tech
- Samuel Roberts Noble Foundation
- Dartmouth
- ArborGen
- Verenium
- Mascoma
- Individuals from U California-Riverside, Cornell, Washington State, U Minnesota, NCSU, Brookhaven National Laboratory, Virginia Tech

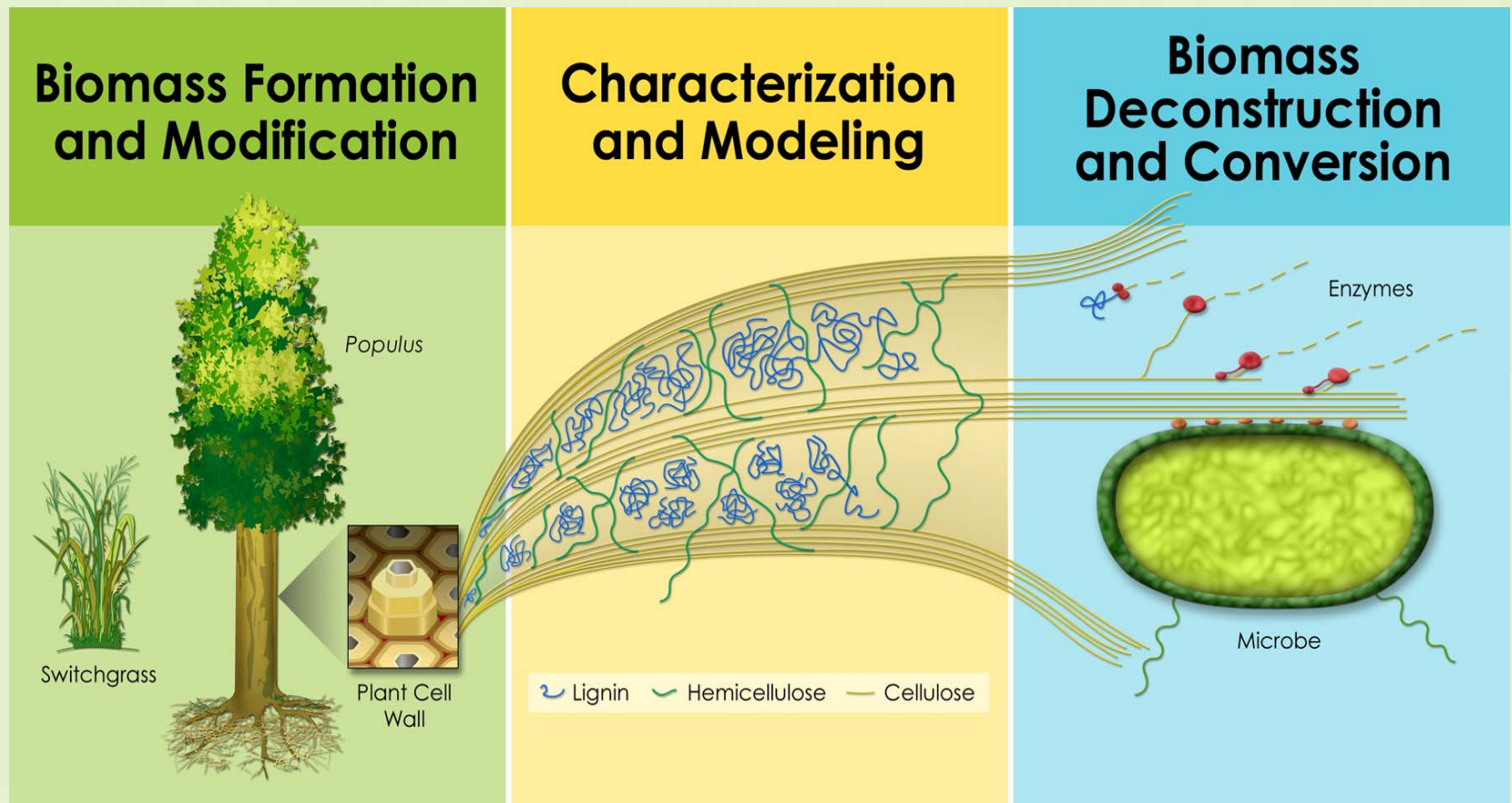
Alternative Fuels User Facility



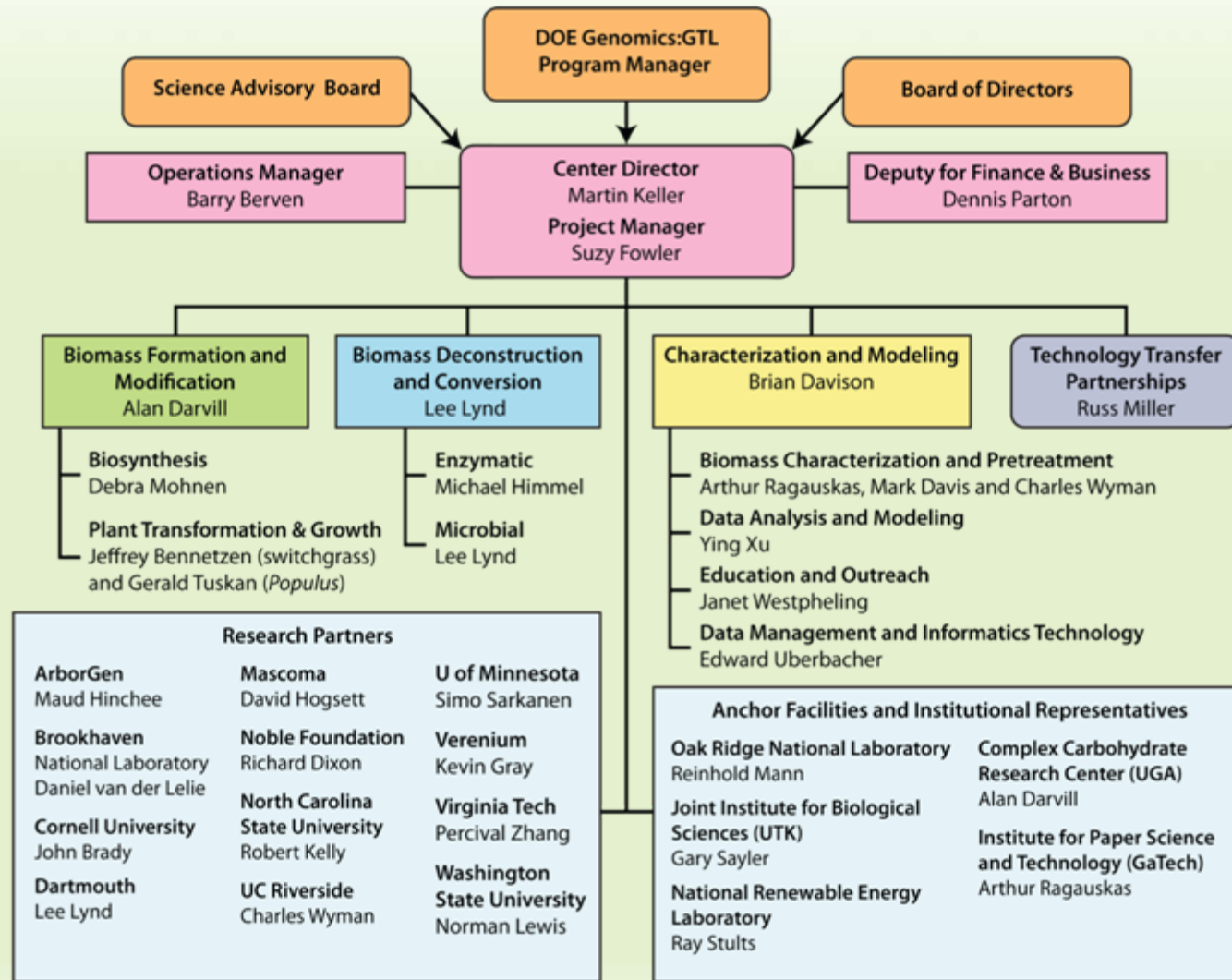
Complex Carbohydrate Research Center



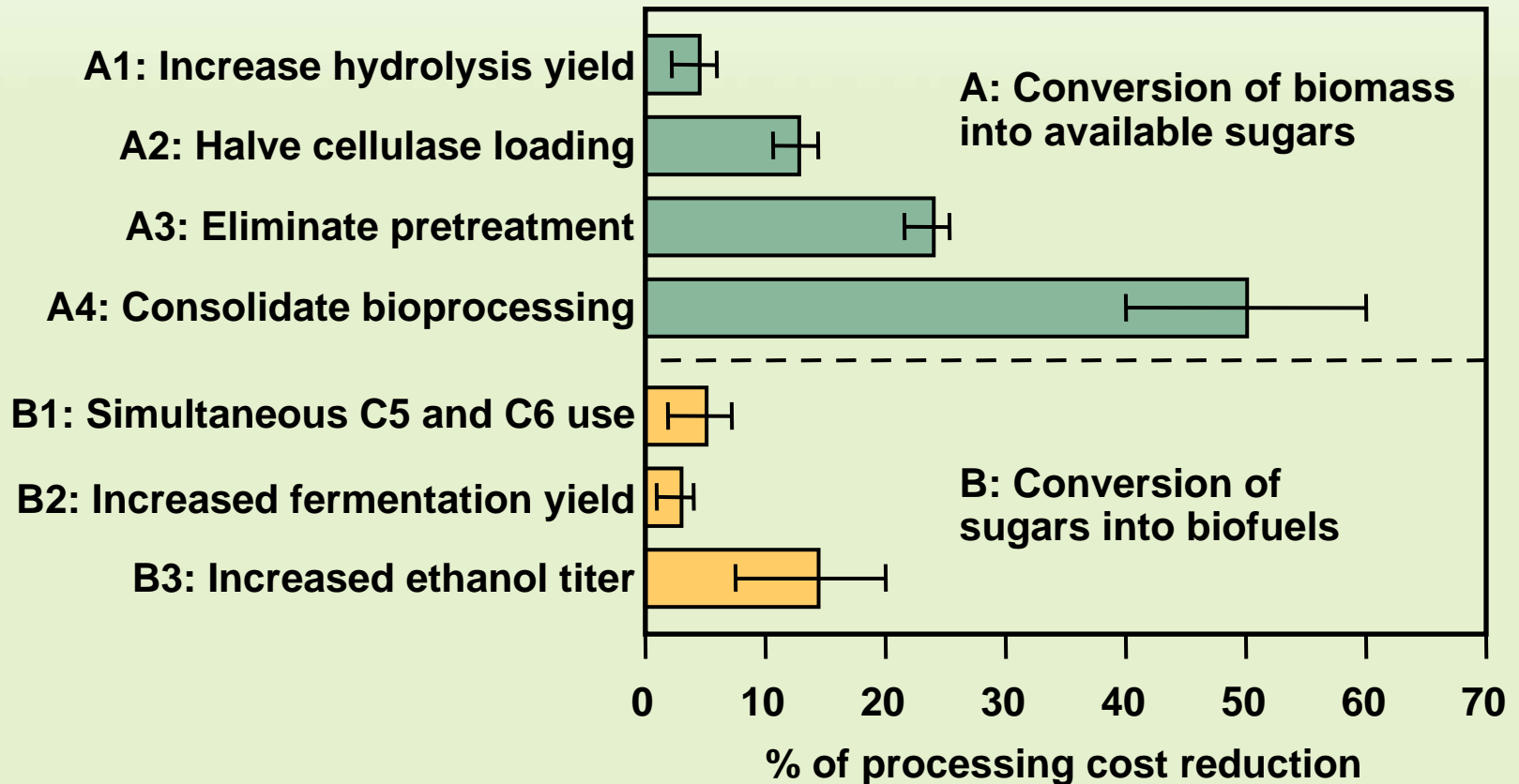
Three linked scientific focus areas will enable BESC to understand and overcome biomass recalcitrance



BESC is organized to provide clear operations and science accountability



Comparative impacts of R&D on biomass processing cost



Without overcoming biomass recalcitrance (A), cellulosic biofuels will be more expensive than corn biofuels. Improved sugar conversion (B) is not enough.

Ref: Lynd, L.R., M.S. Laser, D. Bransby, B.E. Dale, B. Davison, R. Hamilton, M. Himmel, M. Keller, J.D. McMillan, J. Sheehan, C.E. Wyman, 2007. "Energy Biotechnology: Targeting a Revolution" Nature Biotechnology (in press)

BESC has well-defined objectives

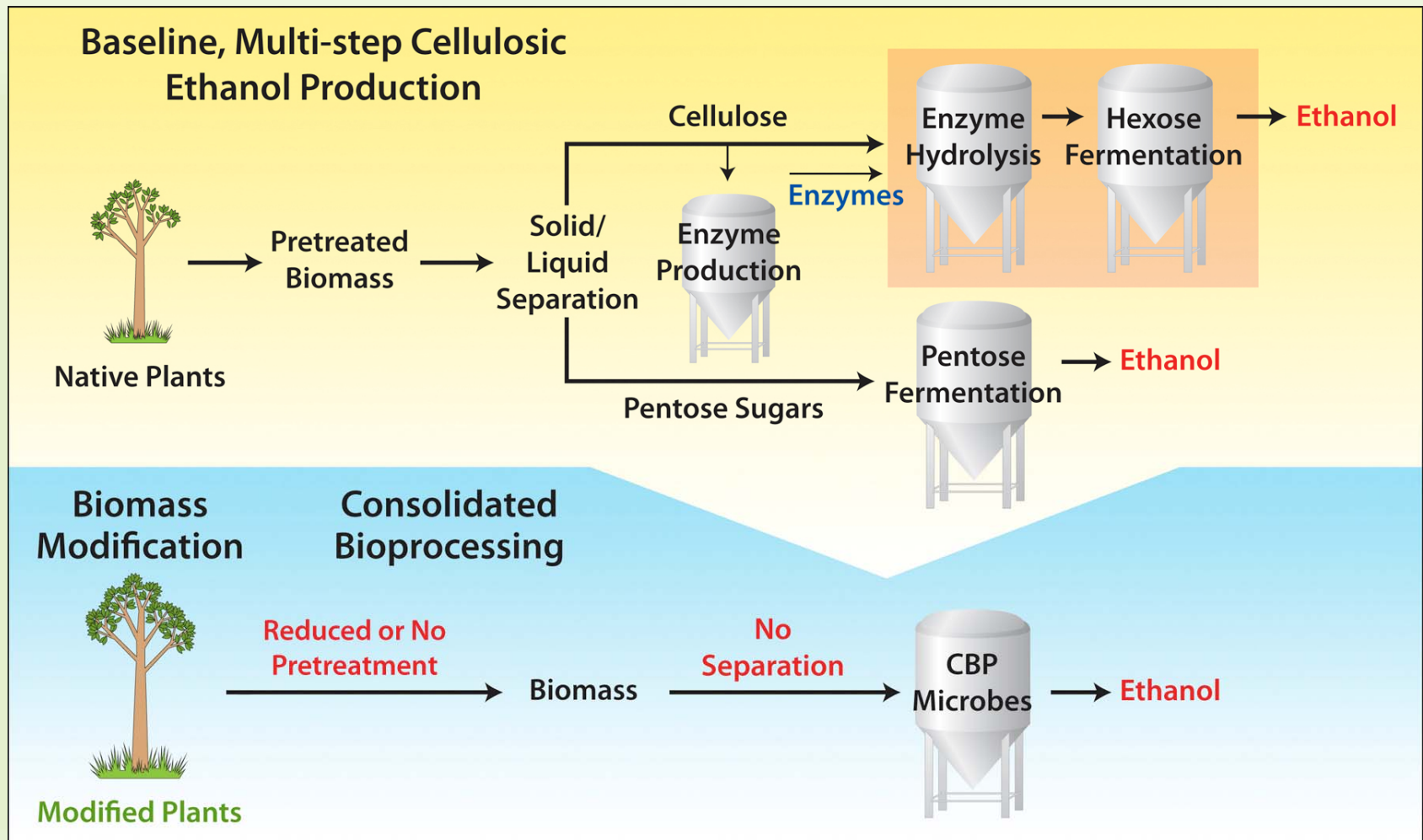
Revolutionize the processing of biomass within 5 years

- **Improve overall yields**
- **Simplify operations through consolidated bioprocessing (CBP)**
- **Decrease (or eliminate) the need for costly chemical pretreatment**

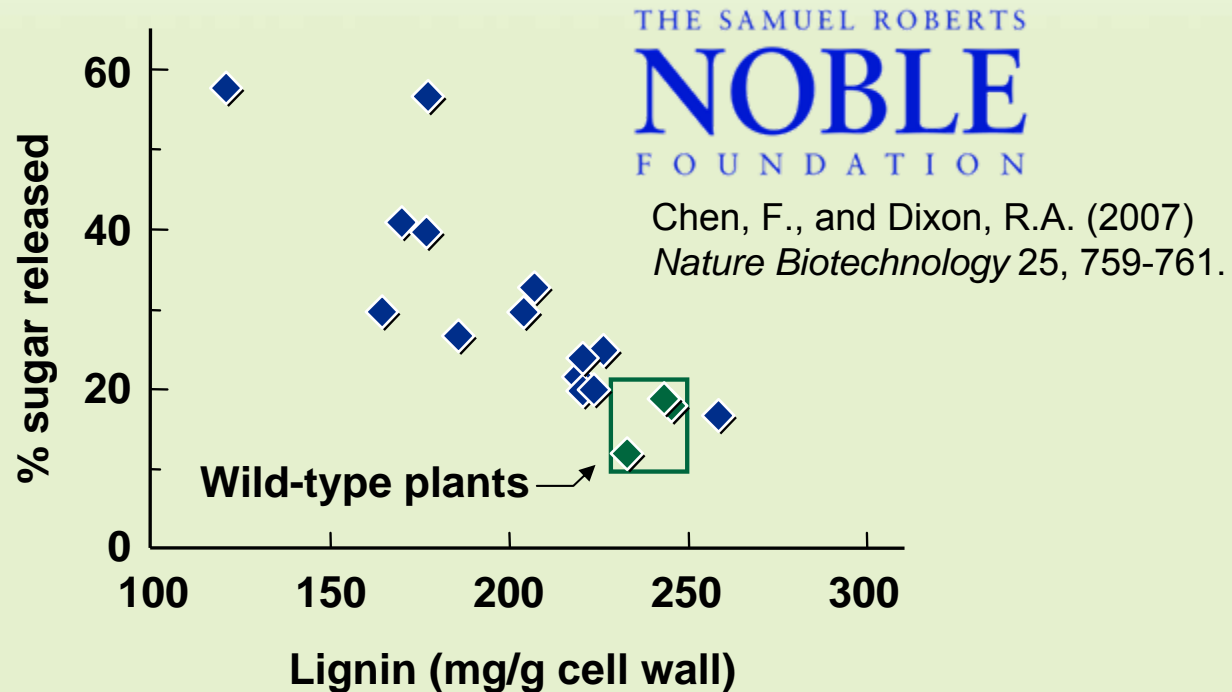
Apply a systems biology approach and new higher-throughput pipelines

- **Reduce recalcitrance by targeted modification of plant cell wall composition and structures**
- **Develop and understand single microbes or microbial consortia and their enzymes to enable CBP for low-cost cellulose hydrolysis and fermentation**
- **Provide a synergistic combination of modified plants and CBP for even more cost-effective biofuel production**

BESC will revolutionize how biomass is processed within five years

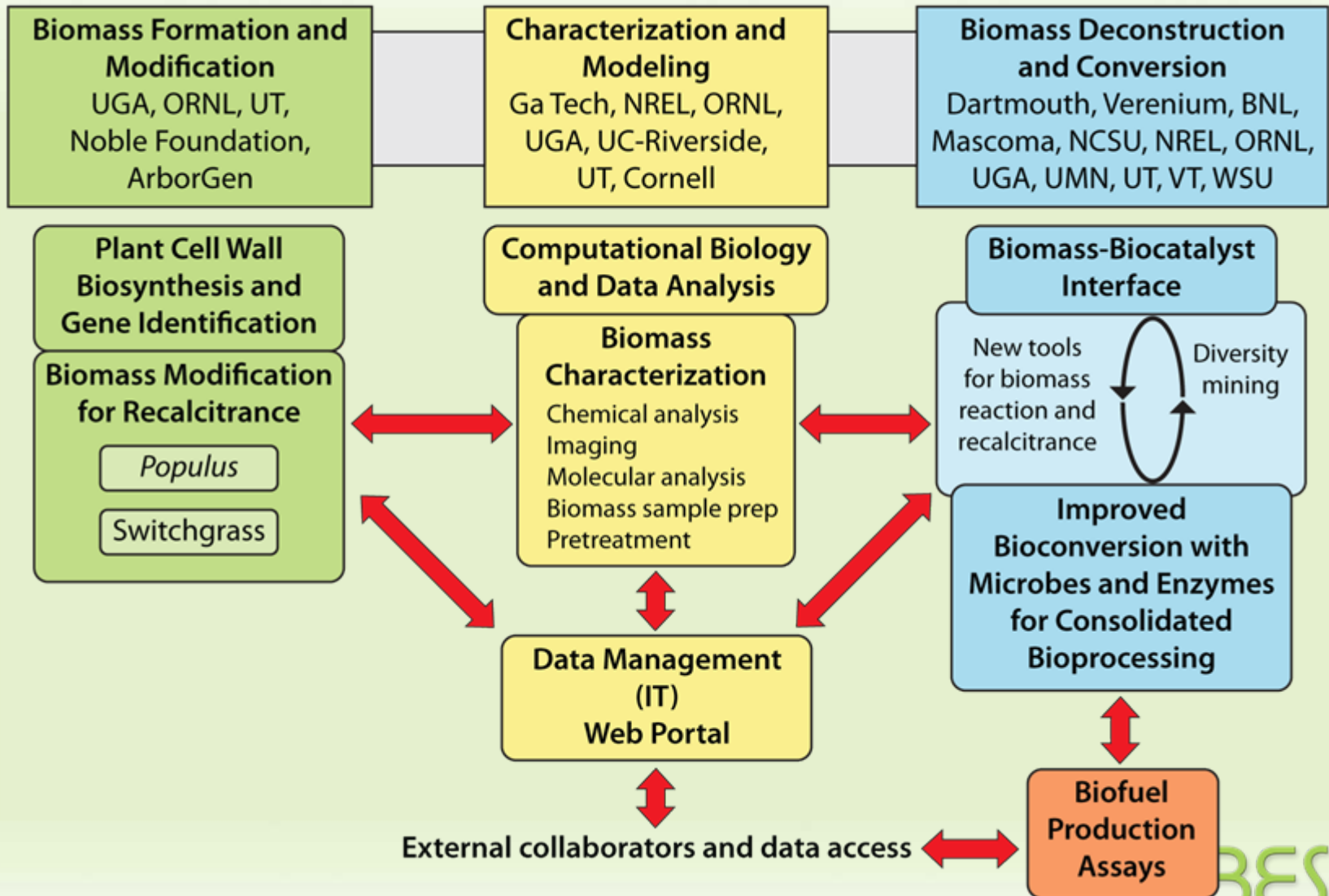


Modifying cell wall composition and structure can reduce recalcitrance



- More sugar is solubilized by cellulase when the lignin content of alfalfa cell walls is reduced
- Strategy is feasible for *Populus* and switchgrass

BESC – a highly integrated cutting-edge research team



The challenges (part 1): Lignocellulosic biomass is complex and heterogeneous

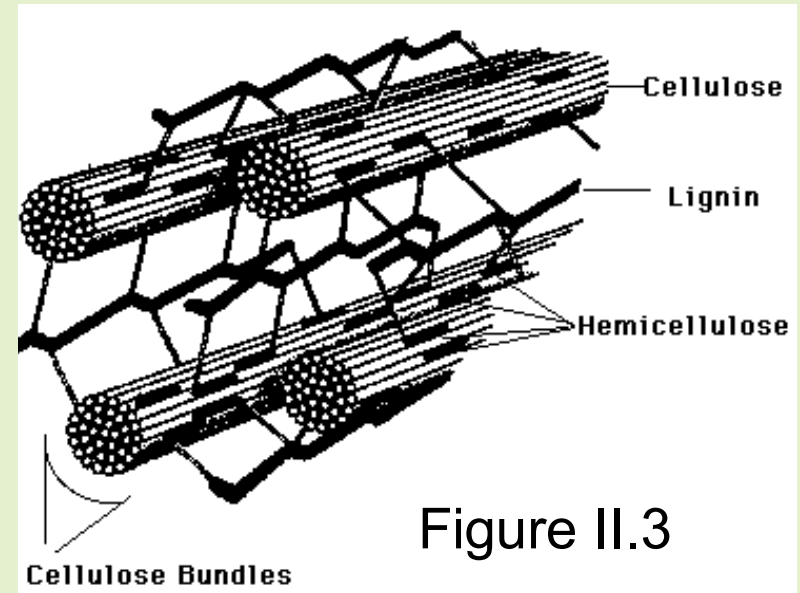
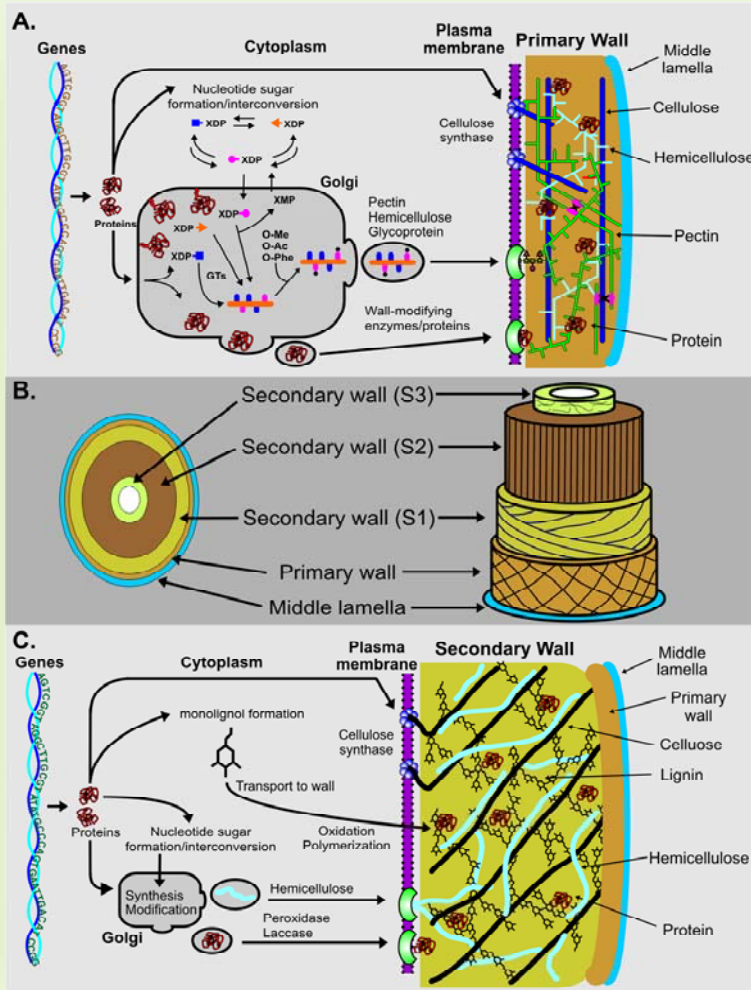
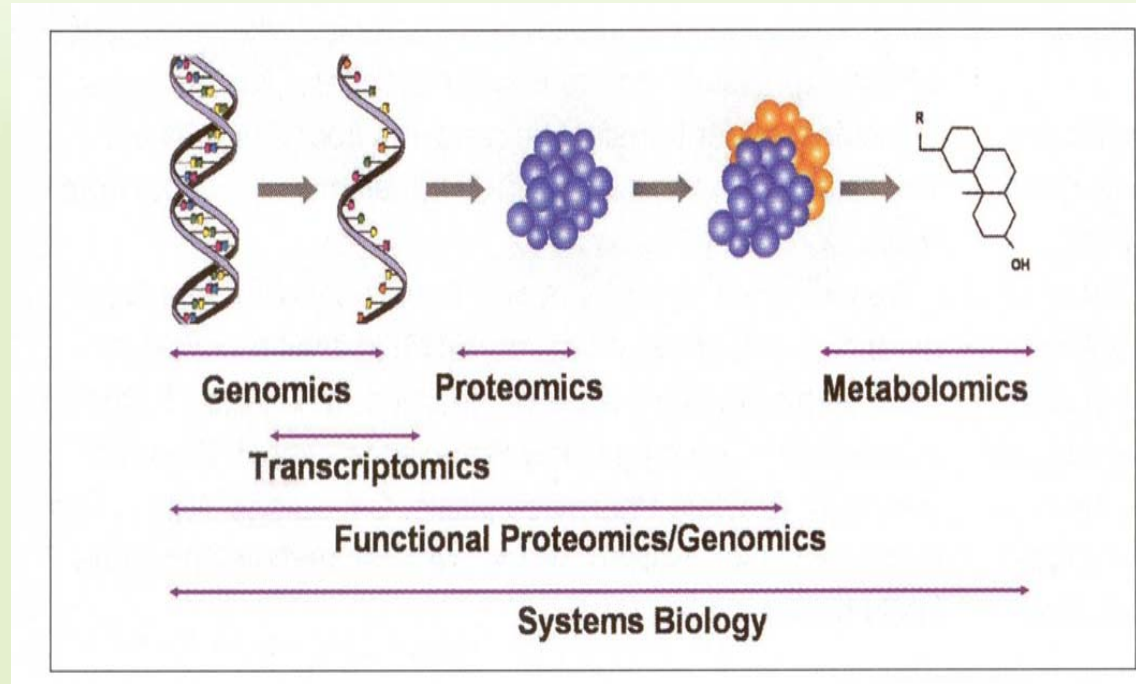


Figure II.3

Fig. II.2. Biosynthesis of primary and secondary walls: from genes to polymers. **A.** Primary wall polysaccharides are synthesized at the plasmamembrane (cellulose) and in the Golgi (pectin and hemicellulose) by the action of glycosyltransferases that use nucleotide-sugar substrates. **B.** Some cells (e.g. xylem) form secondary walls internal to the primary wall. **C.** Secondary wall synthesis includes cellulose, hemicellulose and lignin deposition.

“Omic” capabilities for systems biology

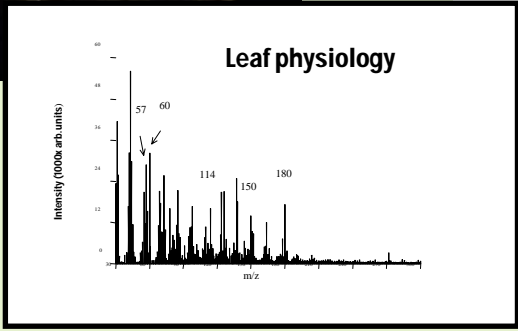
- Genomics
- Transcriptomics
- Proteomics
- Interactomics
- Metabolomics



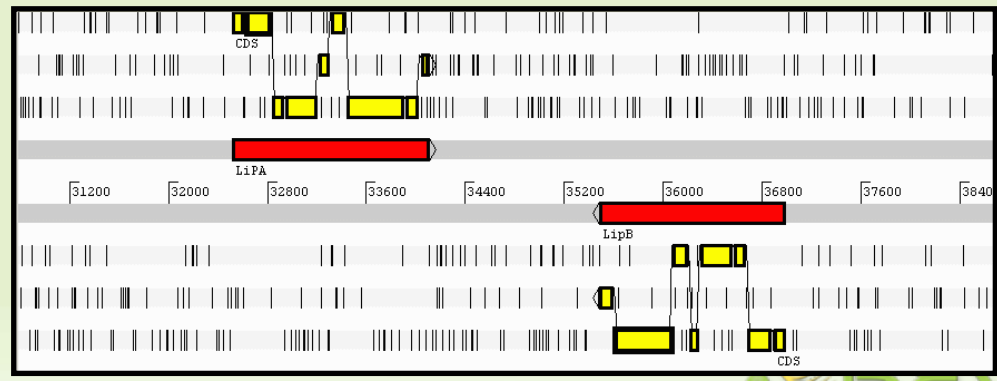
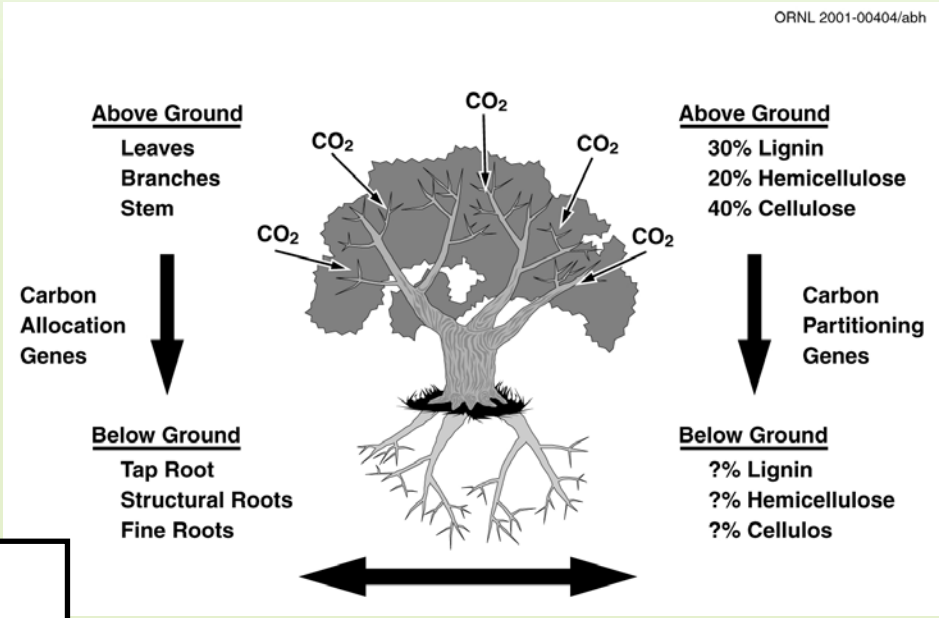
- Together these can provide a deeper picture of how a microbe or plant is functioning
- This can help identify where improvements need to be made

Woody plant genomics – *designing crops for energy & C sequestration*

ORNL 2001-00404/abh



High-throughput Phenotyping

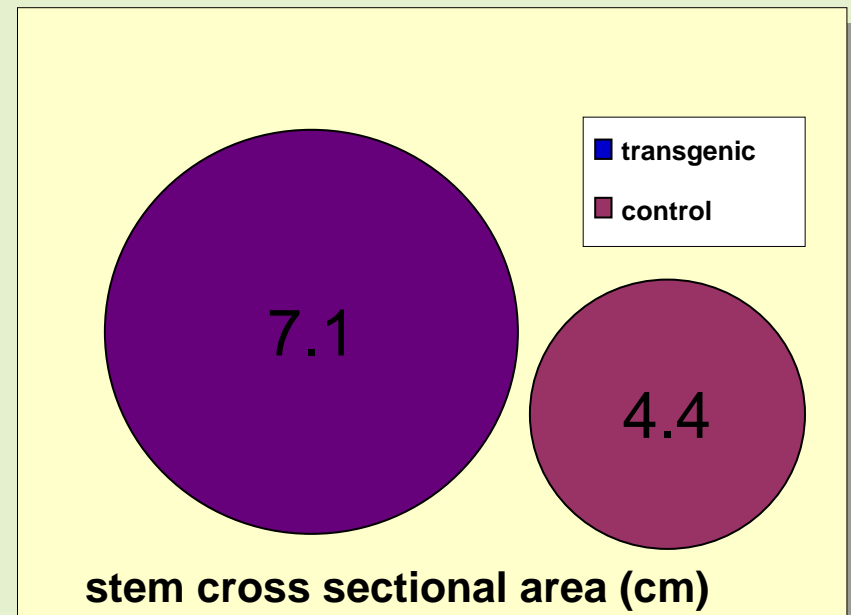


Populus - early results from genome sequence availability (Jerry Tuskan, ORNL)

90-day-old *Populus* cuttings



Using Poplar tree genome, the expression of one gene (IAA16.3) was altered. This resulted in enhanced radial growth of IAA16.3 transgenics vs. controls



Activation tagging to identify Poplar genes: Some mutants can be detected using infrared aerial photography



Provided by:
Dr. Peggy Payne,
Boise Cascade

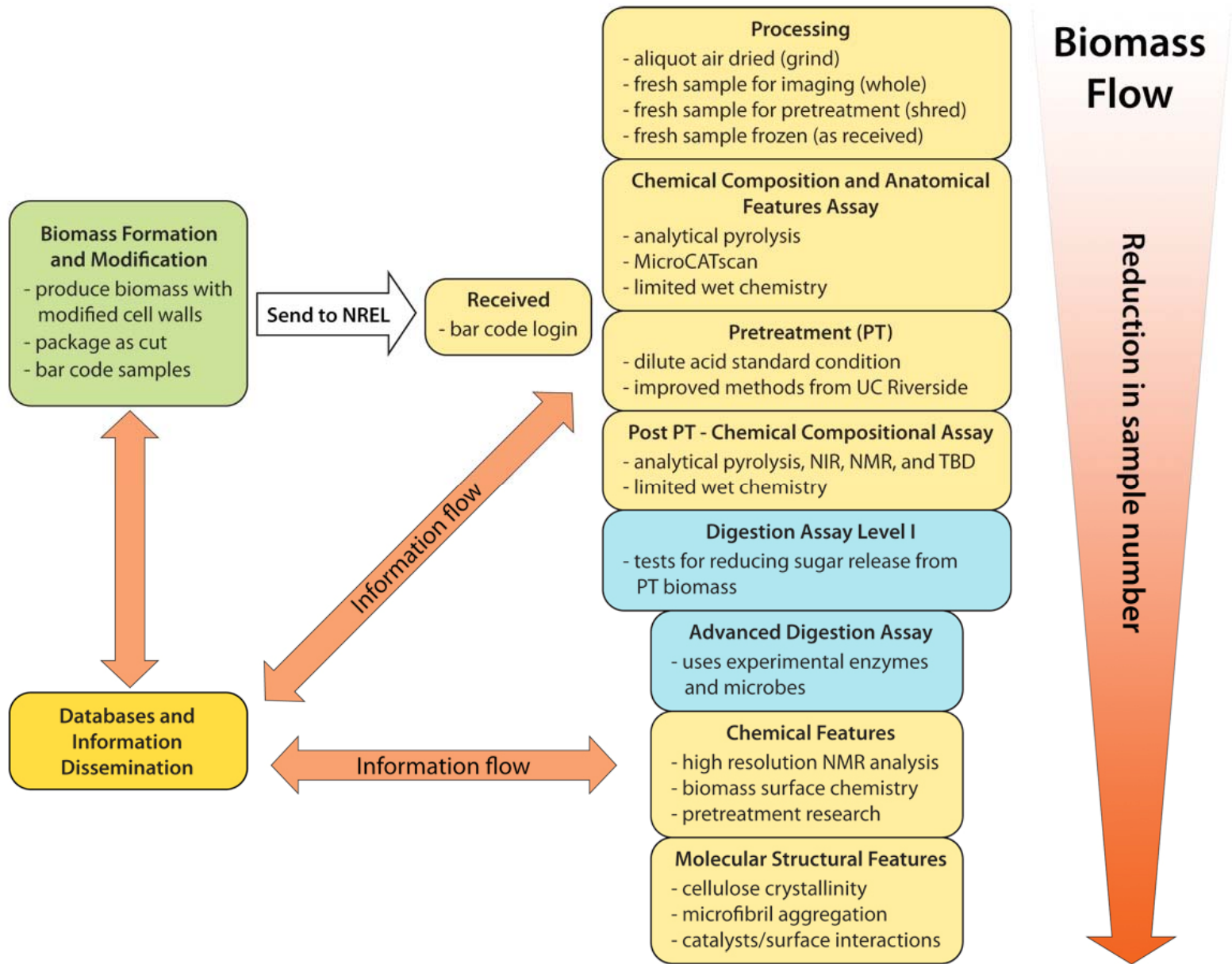
**Populus trichocarpa x deltoides
clone block**

**P. trichocarpa x nigra
clone block**

Others are evident at the whole-tree level

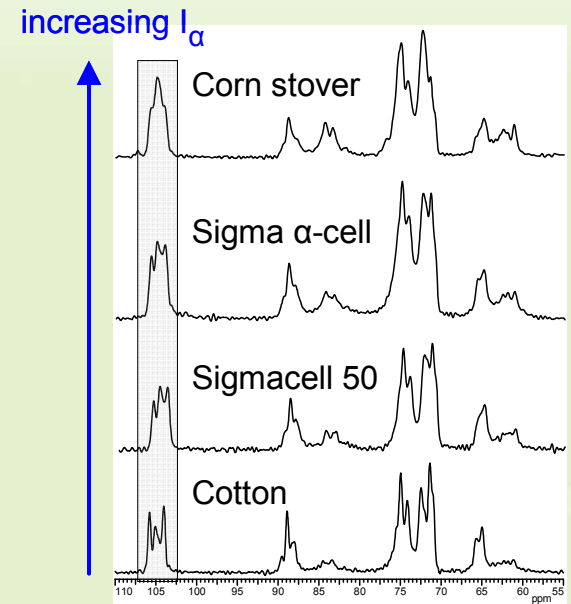


Schematic of sample flow in BESC



Identify structural and chemical features of recalcitrance

- **High throughput analysis**
 - Compositional analysis of 1000's of samples
 - NREL pbMS is being adapted to *Populus* and switchgrass
 - Pretreatment screens
 - Biomass enzyme digestibility (recalcitrance phenotype)
- **High resolution analysis of plant cell walls**
 - Monoclonal antibodies
 - AFM mapping of surface chemistry
 - Imaging MS
 - MicroCat for plant anatomy
- **Biomass surface chemistry**
- **Baseline samples of biomass provided across BESC for methods testing, control, and shared insights**
- **Pretreatment insights to understanding recalcitrance**



Comparison of ^{13}C CPMAS NMR spectra of different celluloses show increasing crystallinity (I_{α}).

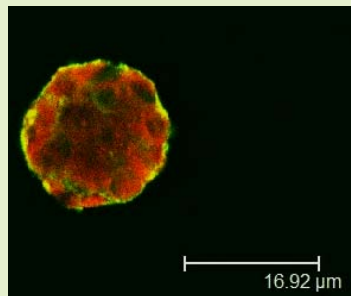
New combined imaging tools to elucidate cell wall formation

- utilizing polysaccharide antibodies to visualize layers in the cell wall



Green fluorescence from positive antibody reaction

Red autofluorescence from Chloroplasts (intracellular)



Positive signal in cell walls of 2-day old spheroplasts (*Populus* protoplasts growing in wall formation culture condition) obtained using CCRC monoclonal antibodies *.

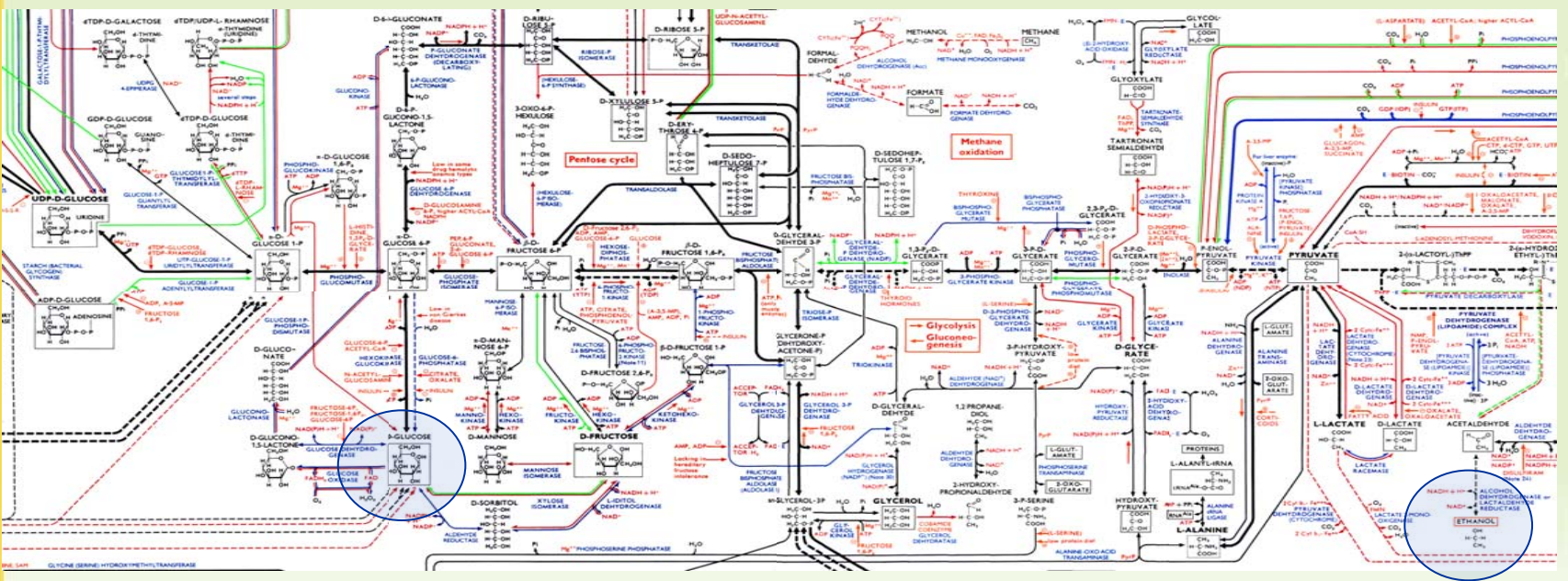
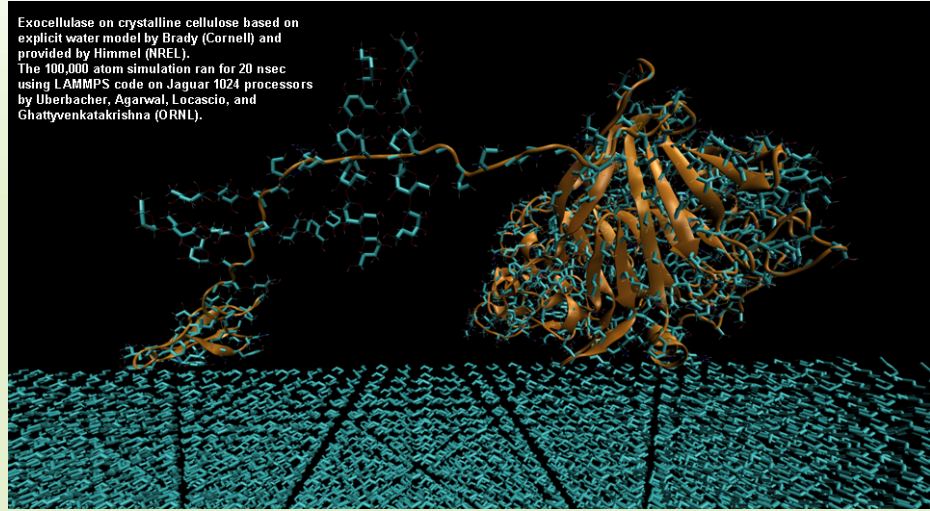
*Antibody mix composition: CCRC-M1, M13, M38, M48, M56. This mixture of antibodies targets wall polysaccharides such as pectin (Rhamnogalacturonan I) and hemicellulose (Xyloglucan).

Kalluri, Hahn: unpublished results

In the near term, the study will involve the use of ~140 antibodies to track spatiotemporal developments during wall formation around a single cell.

The challenge (part 2): Lignocellulosic biomass is difficult to breakdown and ferment

Exocellulase on crystalline cellulose based on explicit water model by Brady (Cornell) and provided by Himmel (NREL). The 100,000 atom simulation ran for 20 nsec using LAMMPS code on Jaguar 1024 processors by Uberbacher, Agarwal, Locascio, and Ghattyenkatakrishna (ORNL).

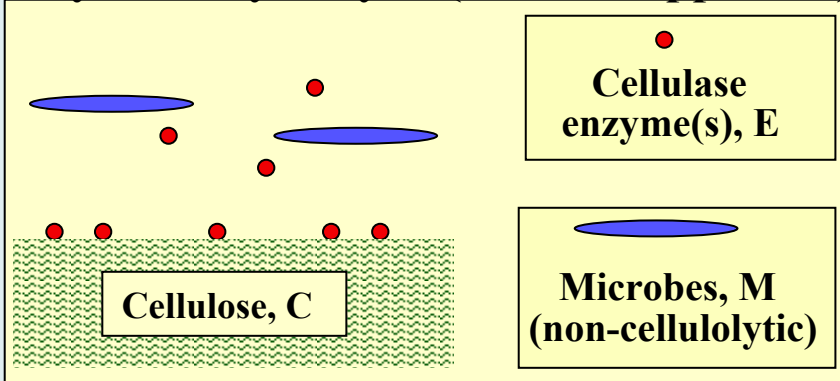


GLUCOSE

ETHANOL

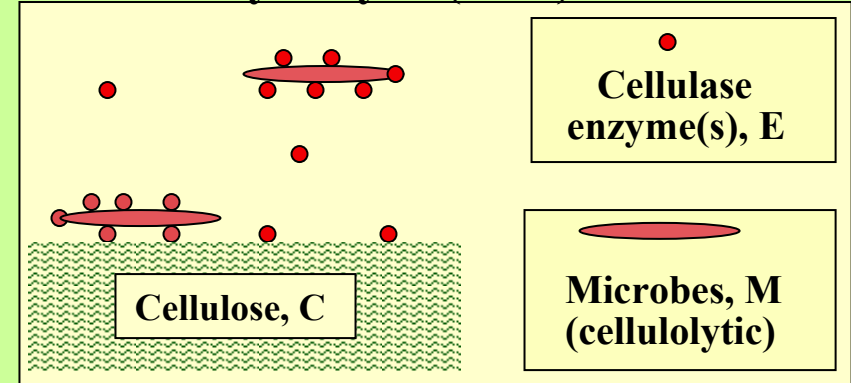
Microbial hydrolysis and enzymatic hydrolysis: A fundamentally different relationship between microbes and cellulose

Enzymatic hydrolysis (classical approach)

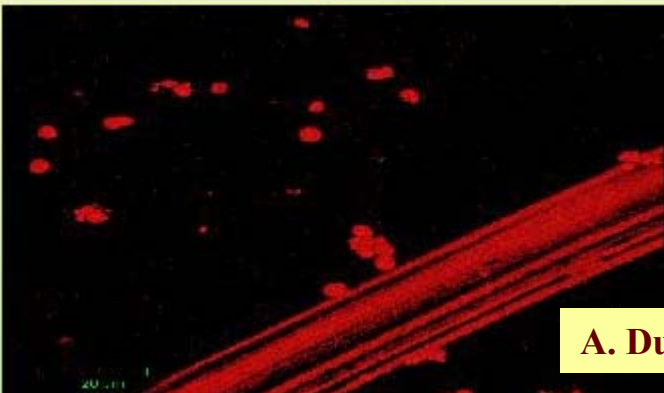


- Hydrolysis mediated by CE complexes
- Enzymes (several) both bound & free
- Cells may or may not be present

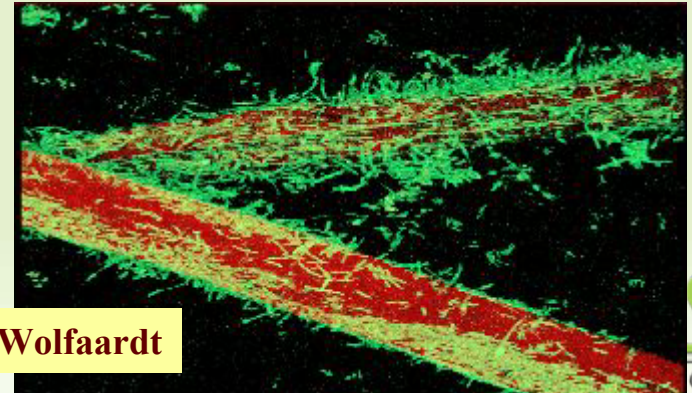
Microbial hydrolysis (CBP)



- Hydrolysis mediated mainly by CEM complexes
- Enzymes both bound & free
- Cells both bound & free

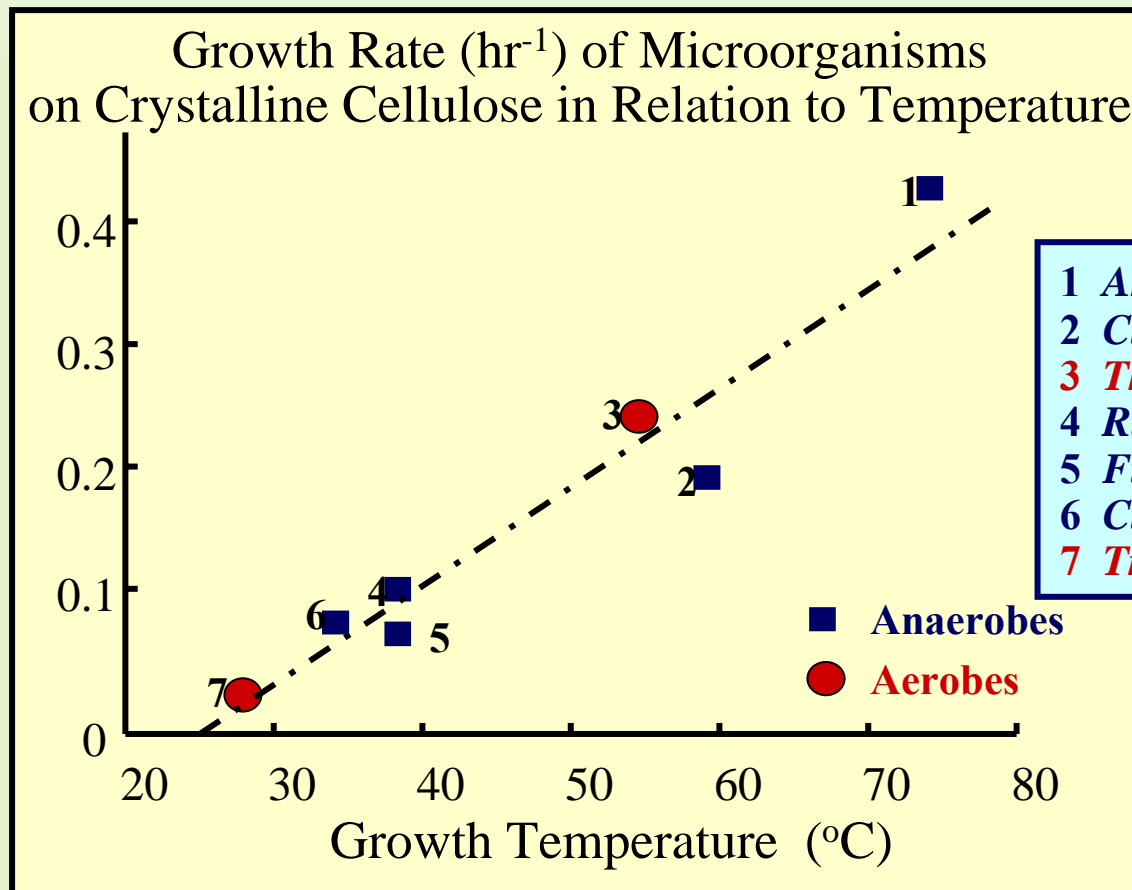


A. Dumitrache & G. Wolfaardt



Search for new biocatalysts

- Hypothesis: will higher temperature microbes be more effective?



- 1 *Anaerocellum thermophilum*
- 2 *Clostridium thermocellum*
- 3 *Thermomonospora sp N-35*
- 4 *Ruminococcus flavefaciens*
- 5 *Fibrobacter succinogenes*
- 6 *Clostridium cellulolyticum*
- 7 *Trichoderma reesei*

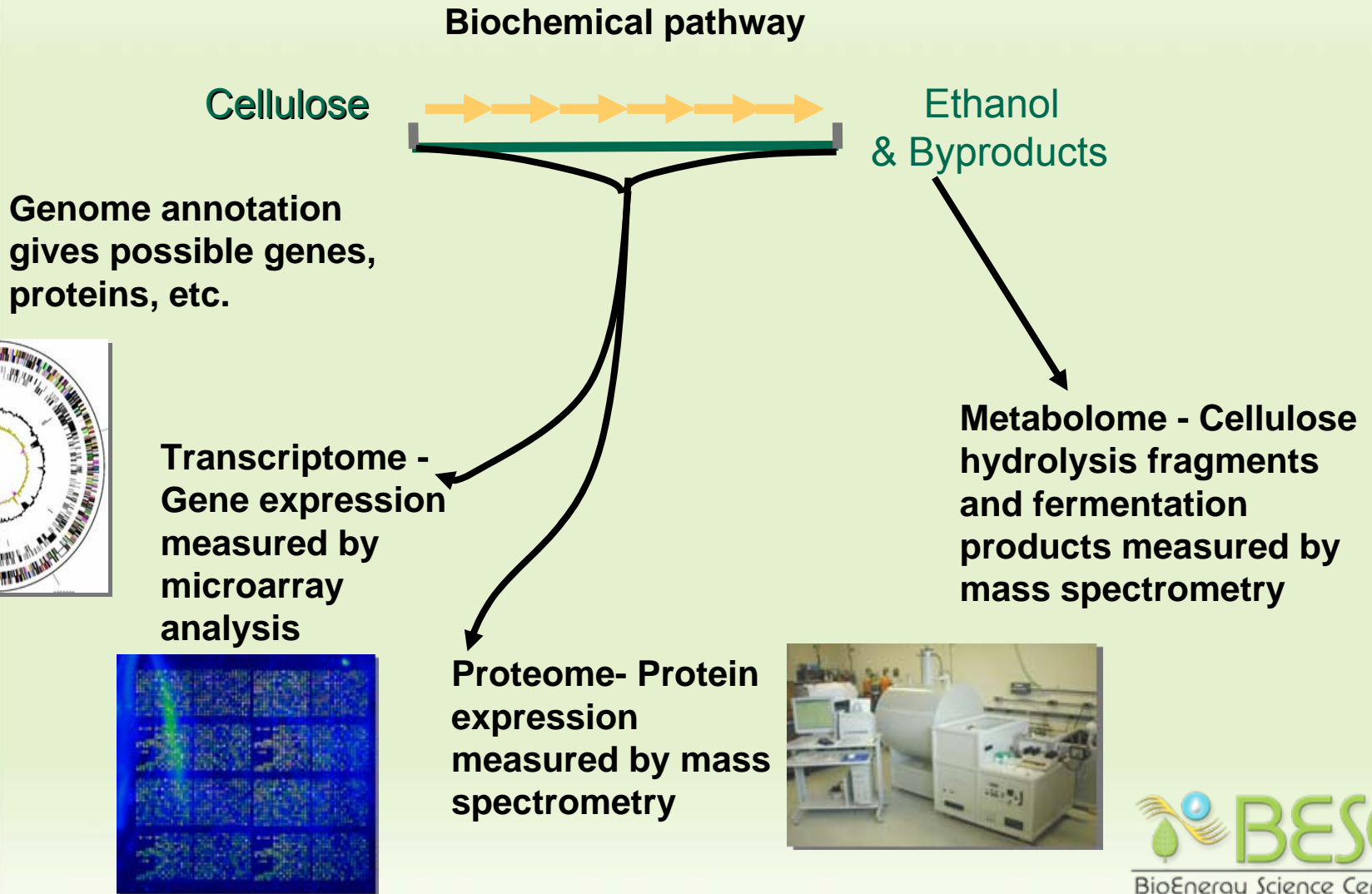
The growth of microbes on cellulose increases linearly with temperature. Lynd, et al., *Microb. Molec. Biol. Rev.* 66: 506 (2002).

Biodiversity access

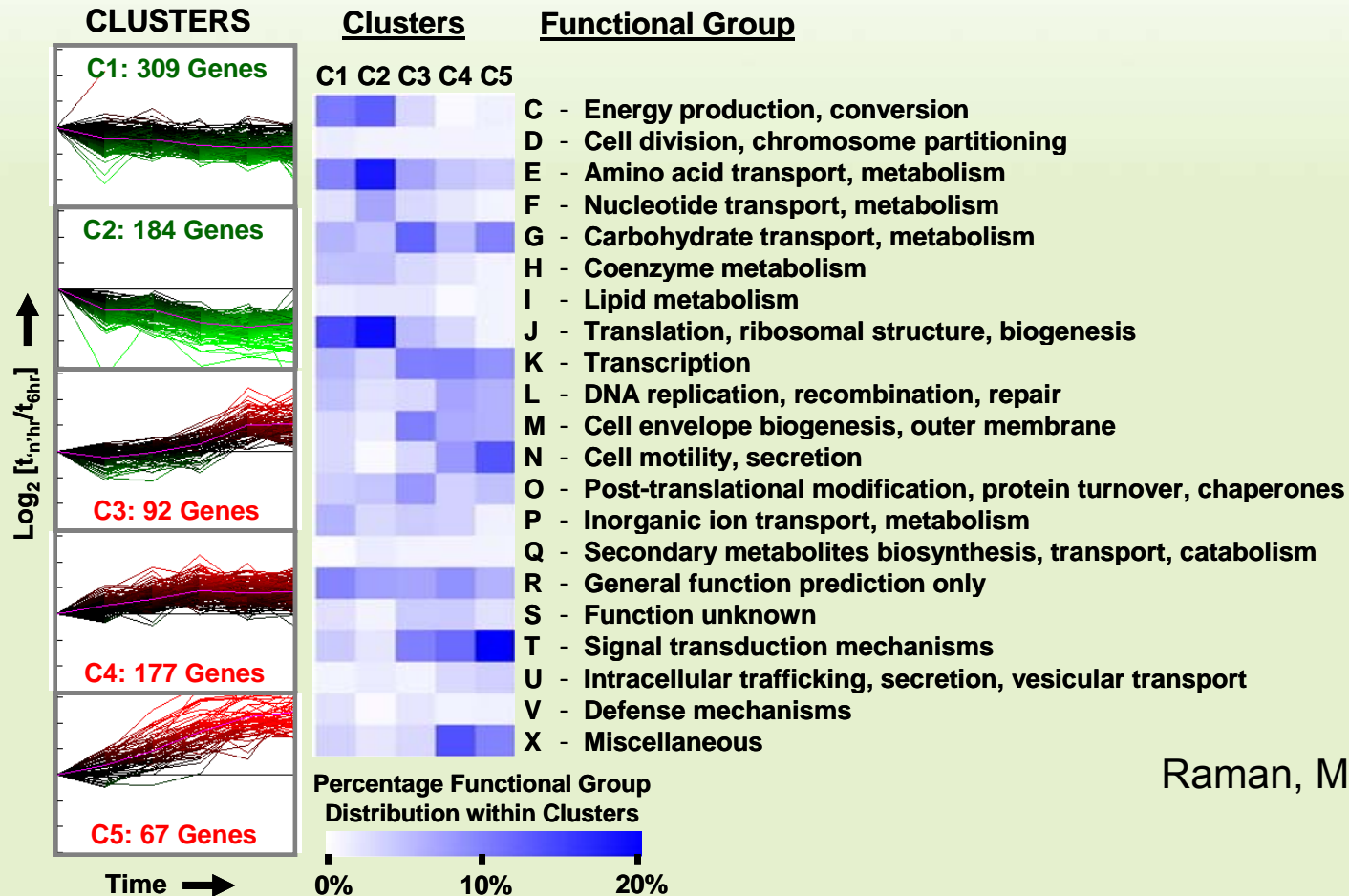
- **Sampling trip to Yellowstone in October**
- **Enrichments are growing at different temperatures**



“Omics” technologies applied to help design better CBP microbes



Gene expression changes during *C. thermocellum* fermentation

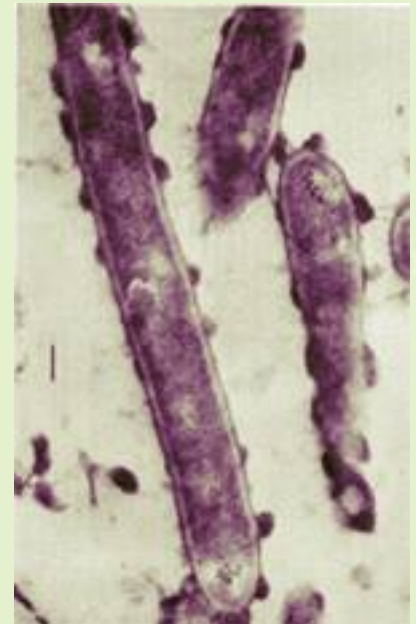
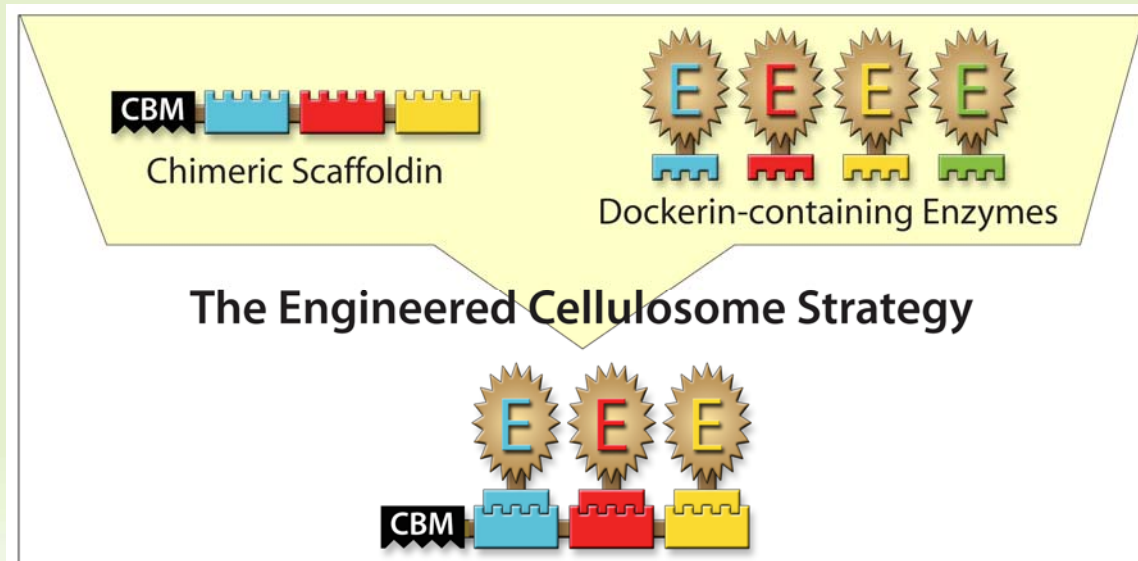


Raman, Mielenz 2007

During cellulose fermentation, the capacity of *C. thermocellum* to sense and respond to its environment increases and cells become more motile over time; however the metabolic capacity decreases progressively with time during batch growth.

Goal: Understanding leading to an improved cellulosome

- A deep proteome analysis of the cellulosome of *C. thermocellum* identified more than 20 'new' cellulosomal components



C. thermocellum image courtesy of Bayer and Lamed, The Weizmann Institute of Science.

Thank you

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