

COMMENTARY

Open Access



# Progress in understanding and overcoming biomass recalcitrance: a BioEnergy Science Center (BESC) perspective

Paul Gilna<sup>1,2</sup>, Lee R. Lynd<sup>2,3</sup>, Debra Mohnen<sup>2,4</sup>, Mark F. Davis<sup>2,5</sup> and Brian H. Davison<sup>1,2\*</sup>

## Abstract

The DOE BioEnergy Science Center has operated as a virtual center with multiple partners for a decade targeting overcoming biomass recalcitrance. BESC has redefined biomass recalcitrance from an observable phenotype to a better understood and manipulatable fundamental and operational property. These manipulations are the result of deeper biological understanding and can be combined with other advanced biotechnology improvements in biomass conversion to improve bioenergy processes and markets. This article provides an overview of key accomplishments in overcoming recalcitrance via better plants, better microbes, and better tools and combinations. A perspective on the aspects of successful center operation is presented.

**Keywords:** Bioconversion, Bioenergy, Recalcitrance, Center operation, Biomass

## Background

Biomass recalcitrance—the resistance of plants to release their sugars for fermentation or upgrading—is a primary barrier to efficient and economical production of advanced biofuels [1, 2]. Overcoming and understanding recalcitrance was the unifying vision of the US Department of Energy (DOE) BioEnergy Science Center (BESC), now in its final and 10th year of operation. The mission of BESC was “to enable the emergence of a sustainable cellulosic biofuels industry by leading advances in science and science-based innovation resulting in removal of recalcitrance as an economic barrier to cost-effective production of biofuels [3]”. Due to advances in biotechnology, BESC believed that biological solutions were the most promising path by which to achieve these breakthroughs. In response to a DOE challenge [4], Oak Ridge National Laboratory (ORNL) led the formation of BESC by gathering experienced researchers from multiple US institutions, who had been separately interested in separate

aspects of overcoming biomass recalcitrance targeting advanced biofuels and specifically cellulosic ethanol.

Recalcitrance began as an operationally defined phenotype. With both applied and fundamental goals, BESC perceived that we needed to transform the understanding of recalcitrance; this required detailed knowledge of the chemical, structural, and physical properties of biomass and how these properties influenced deconstruction by enzymes and thermophilic microorganisms. This search led to altering plant cell wall properties by manipulating key plant polymer biosynthetic pathways, which led to studies of the interactions of the plant cell walls and the enzymes and microbes during deconstruction and fermentation. The BESC team has redefined recalcitrance so that now recalcitrance is on the path to being an understandable and manipulatable set of properties based on cell wall formation and bioconversion. A key outcome of the BESC team’s approach was to transform understanding in both fundamental and operational impacts to strategies that will eliminate recalcitrance as an economic barrier to commercialization.

This singular focus on recalcitrance science was BESC’s hallmark worldwide. BESC was organized into three areas: Biomass Formation and Modification, Biomass Deconstruction and Conversion, and Enabling

\*Correspondence: [davisonbh@ornl.gov](mailto:davisonbh@ornl.gov)

<sup>2</sup> Biosciences Division, Oak Ridge National Laboratory, 1 Bethel Valley Road, Bldg. 1505, Rm. 100A, Oak Ridge, TN 37831-6037, USA  
Full list of author information is available at the end of the article

Technologies (Fig. 1). All three areas included both fundamental understanding and complementary proof-of-concept components. Our ability to design, conduct, and analyze wide-ranging campaigns, along with our effective communications and capacity to integrate cross-disciplinary teams within the BESC organization, has been key to our success in scientific areas that are critical to overcoming the formidable biological and technological barriers that biomass recalcitrance presents.

**Discussion: major accomplishments to date**

From late 2007 to fall 2017, BESC published more than 945 journal articles, 10% in high-profile journals (impact factor > 9) and advanced the education of more than 230 professionals, who are now productive members of the bioeconomy workforce. More details with respect to the output of BESC and the other two USDOE Bioenergy Research Centers are in Slater et al. [5].

**Biomass formation**

*Populus* and switchgrass (*Panicum virgatum*) were the chosen feedstocks for studies of cell wall-related genetic modifications that could impact recalcitrance and inform understanding. Both are high yield perennials recognized as potential domestic biofeedstocks [4, 6]. *Populus* was the first sequenced woody feedstock [7]. Switchgrass is a native herbaceous perennial that could grow on marginal land. Both were deemed tractable for studies aimed at determining the basis of, and ameliorating, recalcitrance. Key advances in biomass formation led by BESC include:

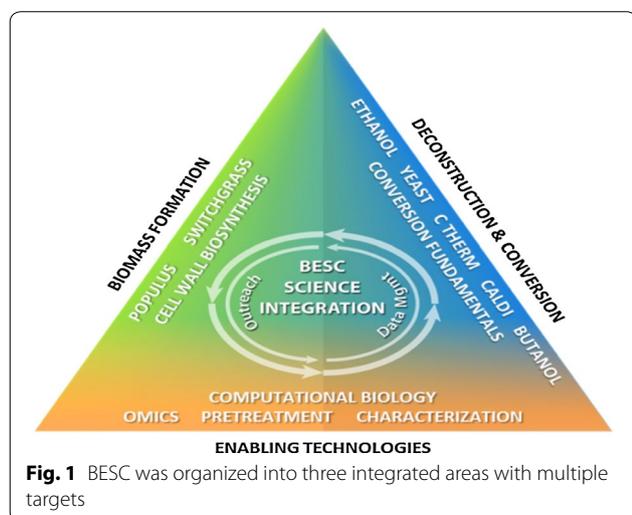
- Significant advances were made in understanding, manipulating, and managing plant cell wall recalcitrance and conversion. We showed that multiple plant genes control cell wall recalcitrance, and that manipulation of these genes can yield lower recal-

citrance perennial biofeedstocks [8]. This included increasing our understanding of the cell wall structure and biosynthetic pathways for lignin, xylan, cellulose, and surprisingly pectin and their resultant effects on recalcitrance [9–25].

- BESC led large-scale campaigns to understand natural variation in both switchgrass and *Populus*. This included both high-throughput (HTP) recalcitrance phenotyping and sequencing along with other omics for these natural variants (as well as the generated transgenics). These resulted in advances in genome-wide association studies (GWAS) [26–28].
- BESC conducted greenhouse and field trials for a limited number of *Populus* and switchgrass lines with reduced recalcitrance arising from both directed transgenics and natural variants. We utilized a collective “TOP Line” experimental design protocol [29] with multiple phenotypic characterization assays developed by the Enabling Technology groups. These included sugar release, sugar and lignin composition, ethanol production, crystallinity, etc. A key discovery was the ability to achieve both lower recalcitrance and higher biomass simultaneously in certain lines [25, 30–32].
- One goal of BESC was to understand the molecular basis of recalcitrance. The reduced recalcitrance feedstock biomass generated in BESC was analyzed by a series of chemical, biochemical, molecular, and systems biology approaches. The outcome was the identification of multiple wall polymers whose modified abundance or structure could be engineered to reduce feedstock recalcitrance [8]. The results begin to provide mechanistic understanding of the molecular bases of recalcitrance.
- From this research, we can see a path for improving feedstocks by cisgenic manipulations, by selecting the best natural variants, or by genetically assisted breeding [33].

**Biomass conversion**

One-step Consolidated Bioprocessing (CBP) without added enzymes [34] was the central focus of BESC’s work in the conversion area, which featured both fundamental and applied components. BESC initially focused on two approaches (a) improving product formation in thermophilic cellulolytic bacteria (primarily *Clostridium thermocellum* and *Caldicellulosiruptor bescii*), and (b) conferring to yeasts the ability to ferment cellulose by virtue of heterologous expression of glycosyl hydrolases. We came to regard the former approach as more promising and by the end of BESC were focused exclusively on this path. Key conversion advances led by BESC included:



**Fig. 1** BESC was organized into three integrated areas with multiple targets

- Large differences were found among the biocatalysts in the most comprehensive comparative evaluation to date of biomass deconstruction under controlled conditions. Among the biocatalysts tested, thermophilic anaerobes and specifically *C. thermocellum* achieved the highest carbohydrate solubilization yields which were several-fold higher yields than industry-standard fungal cellulase [35–37].
- We developed and improved the genetic tools for thermophiles, most notably *C. thermocellum* and *Caldicellulosiruptor* spp., and use of these tools to initiate metabolic engineering of these non-model microbes [38–41].
- Substantial advances were made in understanding and manipulating the metabolism of target CBP microbes. Zhou et al. [42], described non-standard glycolysis in *C. thermocellum*. *Thermoanaerobacter saccharolyticum* was improved to produce economically recoverable ethanol concentrations at near-theoretical yield in the hemicellulose-fermenting [43]. Iso-butanol was produced by adding key pathway enzymes in modified *C. thermocellum* at unprecedented yields and titers [44]. Ethanol titer and yield were increased in *C. thermocellum* by elimination of side-products [45–47].
- BESC identified the specific deconstruction enzymes which target the major biopolymers of lignocellulosic biomass. Work on enzyme fundamentals emphasized multifunctional cellulases based on the enzymes found in *Caldicellulosiruptor* species and *C. thermocellum* [48]. CelA, a multifunctional glycosyl hydrolase from *C. bescii*, was shown to be a particularly powerful hydrolytic enzyme despite being inhibited by the presence of lignin [49, 50].
- BESC demonstrated that *C. thermocellum* is capable of active fermentation in the presence of mechanical milling—an approach referred to as co-treatment [35, 51, 52]. With co-treatment, *C. thermocellum* was able to achieve greater than 85% carbohydrate solubilization for *Populus* and switchgrass in the absence of added enzymes and thermochemical pretreatment implying that *C. thermocellum* can attack all the major chemical linkages in representative woody and herbaceous lignocellulose crops given sufficient physical access.

### Enabling technology

Enabling technologies were organized to develop and apply cutting-edge analytical methodologies to characterize biomass as well as its conversion. There was also significant omics and computational biology of the modified plants and microbes to help improve metabolic models. The resulting data were used to create new

insights into how biomass structure and chemistry affect recalcitrance during CBP or pretreatment. These efforts included analyses of partially digested solid residues from CBP.

- The development of high-throughput methods for rapid analysis of pretreatment and enzymatic hydrolysis allowed for rapid identification of low recalcitrant plant lines from thousands of natural and transgenic variants. These low recalcitrant plant lines then could be characterized using multiple analytical and omic approaches which rapidly advanced BESC's deeper understanding of the recalcitrance phenotype [53–55].
- Increased understanding of recalcitrance was supported by developing techniques such as glycome profiling [56], and improving the use of nuclear magnetic resonance spectroscopy (NMR) for biomass [12, 57–60].
- BESC also supported the development of new ways to image the chemical components comprising the cell wall. Raman spectroscopy was used to image hemicellulose for the first time [61]. Modified AFM techniques were used to chemically image the cell wall at the submicron level [62]. Quantitative fluorescence CLSM and surface spectroscopy by ToF-SIMS showed, following microbial digestion, the decrease in surface cellulose while surface lignin increased. This indicates that biomass recalcitrance may be controlled by surface characteristics [63].
- Co-solvent enhanced lignocellulosic fractionation was developed as a new pretreatment that removes significant amounts of lignin and increases enzymatic digestibility of biomass [64].
- The center was able to provide integrated omics data for key processes. Integrated omics of microbial growth on complex lignocellulosic biomass over time provided a detailed view of the molecular machinery (metabolites and enzymes) and revealed temporal adaptation to a complex, lignocellulose substrate [65]. Profiling genotype-specific proteomes derived from RNA sequencing data better defined the link between genotypes and phenotypes in *Populus* [66].
- Lignin has been shown to play a key role in biomass recalcitrance [67–69]. The potential removal or recovery of lignin would allow its valorization [70] whether into fiber [71] or into value-added intermediates [72].

### Structures and management

As a thematically rather than institutionally defined center, BESC recognized early on the need to develop a shared organizing vision, a sense of priority, and strong

mechanisms for shared samples and data as well as strong management. This structure allowed us to recruit many of the nation's experts in recalcitrance and to draw on the intellectual cultures and strengths of different institutions. BESC successfully implemented a flexible management approach, modeled after successful biotech startup companies that have relied on academic research to strengthen their science base and industrial partnerships to translate discoveries into commercial products.

Over the decade, BESC established a distinctive, high functioning collaborative team with participants from 22 institutions and a broad range of disciplines. As needs and research progressed, six partners left the center and five new partners joined. BESC included researchers from universities, national laboratories, and private companies. These partners included major efforts at ORNL, University of Georgia, Athens, and the National Renewable Energy Laboratory. Specialized expertise was provided by Dartmouth College, Georgia Tech, University of Tennessee, Knoxville, Cornell University, West Virginia University, University of California-Riverside, University of California-Los Angeles, North Carolina State University, University of North Texas along with The Samuel Roberts Noble Foundation (Noble). Earlier partners included Brookhaven National Laboratory, University of Minnesota, Washington State University, and Virginia Polytechnic Institute. Our industrial partners included DuPont, Mascoma Corporation, Diversa Corporation, ArborGen, Inc., Ceres, Inc., and Greenwood Resources, Inc.

BESC brought together individuals, institutions, and disciplines to focus on understanding and ameliorating biomass recalcitrance. As a result of discussions at our retreats and other fora, ideas emerged that would not have happened without a center so designed. As a result of common management, resources, and non-disclosure agreements, barriers to collaboration were substantially lowered as compared to individual investigators acting on their own. Students and postdoctoral staff were among the greatest beneficiaries. Upon hiring BESC-supported students, companies observed that they had extraordinary experience functioning as part of interdisciplinary teams. As an indication of the extent of collaboration, about half of our publications in year 9 had co-authors from more than one BESC institution.

Top-down structures and bottom-up networking were useful and complementary in fostering integration. Weekly calls were held by the science and operational management team. Twice-monthly calls were held with a larger group (roughly 15) consisting of the science management and activity leads, with topics alternating between science and management calls. BESC refreshed its management, all but two of the original

eight management team members being replaced by year 10; this included hiring a new Director. Keeping leadership fresh was also accomplished as early and mid-career staff—some of them graduate students at the start of BESC—were promoted and given added responsibility such that by the end of BESC they comprised over half of BESC activity and project leads. Task- and organism-specific points of contact were designated to facilitate interactions among teams and individuals.

### Technology transfer and outreach

Technology transfer, managed by a Commercialization Council chaired by ORNL, and consisting of the COO and technology transfer leads from each partner institution operated as a community of best practice to strategically and effectively engage with industrial partners. A “storefront” on the BESC website provided a centralized online portal for industry to view available technologies for licensing and partnering. The IP management plan was built on a common Inter-Institutional Agreement template that allows a designated lead institution to offer jointly owned IP from multiple BESC members [73]. Another assessment of the value of the advances is shown by technoeconomic evaluation of several advanced disruptive improvements; CBP with co-treatment was projected to have a potential eight-fold improved return-on-investment [51].

Tech transfer metrics at the time of writing featured more than 190 invention disclosures resulting in 60 patent applications and 21 executed licenses. For example, in 2016, two companies licensed a gene discovered using GWAS in *Populus trichocarpa* [74]. Greenwood Resources plans to utilize the gene to select low lignin poplar variants for further breeding resulting in lower-cost improvements in either conversion processes or pulping. Forage Genetics Intl. will commercialize this genetic mechanism to reduce lignin and increase desirable flavonoids. This will increase digestibility and the nutritional value of animal feedstocks such as alfalfa, corn, and sorghum.

The ability to freely share materials and protect potential IP that belong to the BESC partners is an essential function for expeditious collaboration within the Center. A laboratory information management system (LIMS) served as the main mechanism for documenting the transfer of materials among BESC partners as allowed under the innovative BESC Master Material Transfer Agreement. The LIMS also represented the primary system for tracking large experimental campaigns, protocols, data, and metadata and for data quality assurance. LIMS is a relatively mature system developed during BESC using a commercial LIMS software package, Nautilus (<http://www.thermo.com>), which was specifically

designed to manage flexible laboratory processes. This system has an Oracle relational database engine as its back end and generated numerous customized workflows and web interfaces to view results from laboratory processes and experimental campaigns, which has successfully been used to track more than 100,000 samples during the BESC project.

The nationwide BESC Outreach program targeted science enrichment and educational standards in 4th–6th grades. In collaboration with the Creative Discovery Museum in Chattanooga, Tennessee, we developed a hub-and-spoke model using hubs at 18 national museums and science centers in 14 states (Utah, Idaho, Montana, New Mexico, Kansas, Oregon, Washington, Georgia, Tennessee, Alabama, Texas, Michigan, Illinois, Florida, and Oklahoma) [75]. The “Farming for Fuels” Program is available on our websites. Over 225,000 students, parents, and teachers have participated in hands-on activities. These are not hits on a website, they are person-to-person contacts and educational activities. The enhanced Biofuels website (<http://www.learnbiofuels.org>) with information and downloadable biofuels-related lesson plans has received more than 45,000 page views. A Biofuels/Alternative Energy iPad software app “Road Trip Challenge” is available through the iTunes App Store with eight “trips” between hub museums. Importantly, the program is moving closer to becoming self-sustaining. Of the over 50,000 students, teachers, and parents reached during 2016, 81% were served with no direct program-support cost to BESC.

## Summary

BESC has redefined biomass recalcitrance from an observable phenotype to a better understood and manipulatable fundamental and operational property. These manipulations are the result of deeper biological understanding and can be combined with other advanced biotechnology improvements in biomass conversion [76, 77] to improve bioenergy processes and markets.

## Authors' contributions

BHD and PG prepared the manuscript draft. LRL, MFD, and DM edited and provided pertinent references. BHD compiled the final version. All authors read and approved the final manuscript.

## Author details

<sup>1</sup> BioEnergy Science Center, Oak Ridge National Laboratory, Oak Ridge, TN 37831, USA. <sup>2</sup> Biosciences Division, Oak Ridge National Laboratory, 1 Bethel Valley Road, Bldg. 1505, Rm. 100A, Oak Ridge, TN 37831-6037, USA. <sup>3</sup> Thayer School of Engineering, Dartmouth College, Hanover, NH 03755, USA. <sup>4</sup> Complex Carbohydrate Research Center and Department of Biochemistry and Molecular Biology, University of Georgia, Athens, GA 30602, USA. <sup>5</sup> National Bioenergy Center, National Renewable Energy Laboratory, Golden, CO 80401, USA.

## Acknowledgements

We acknowledge Martin Keller, the first BESC director, and Alan Darvill for contributions to the initial science vision and management.

This manuscript has been authored by UT-Battelle, LLC under Contract No. DE-AC05-00OR22725 with the US Department of Energy. The publisher, by accepting the article for publication, acknowledges that the United States Government retains a non-exclusive, paid-up, irrevocable, world-wide license to publish or reproduce the published form of this manuscript, or allow others to do so, for United States Government purposes. The Department of Energy will provide public access to these results of federally sponsored research in accordance with the DOE Public Access Plan (<http://energy.gov/downloads/doe-public-access-plan>).

## Competing interests

The authors declare that they have no competing interests.

## Ethical approval and consent to participate

Not applicable.

## Funding

This research was funded by the BioEnergy Science Center (BESC) which is a US Department of Energy Bioenergy Research Center supported by the Office of Biological and Environmental Research in the DOE Office of Science. ORNL is managed by UT-Battelle, LLC, Oak Ridge, TN, USA, for the DOE under contract DE-AC05-00OR22725.

## Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Received: 19 June 2017 Accepted: 15 November 2017

Published online: 30 November 2017

## References

- Lynd LR, Wyman CE, Gerngross TU. Biocommodity bioengineering. *Biotechnol Prog*. 1999;15:777–93.
- Himmel ME, Ding SY, Johnson DK, Adney WS, Nimlos MR, Brady JW, et al. Biomass recalcitrance: engineering plants and enzymes for biofuels production. *Science*. 2007;315:804–7.
- BioEnergy Science Center (BESC), Oak Ridge. 2017. <http://www.bioenergycenter.org>. Accessed June 2017.
- USDOE. Breaking the barriers to cellulosic ethanol: a joint research agenda. US Department of Energy Office of Science and Office of Energy Efficiency and Renewable Energy. 2006;DOE/SC-0095.
- Slater SC, Simmons BA, Rogers TS, Phillips ME, Nordahl K, Davison BH. The DOE bioenergy research centers: history, operations and scientific output. *BioEnergy Res*. 2015;8(3):881–96.
- U.S. Department of Energy. U.S. billion-ton update: biomass supply for a bioenergy and bioproducts industry. Perlack RD, Stokes BJ (Leads), ORNL/TM-2011/224. Oak Ridge, TN: Oak Ridge National Laboratory; 2011. p. 227
- Tuskan GA, Difazio S, Jansson S, Bohlmann J, Grigoriev I, Hellsten U, et al. The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science*. 2006;313(5793):1596–604. <https://doi.org/10.1126/science.1128691>.
- Mohnen D, Nelson RS, Tuskan GA, Dixon RA, Stewart CN, Chen J. Genetic determinants and mechanisms that control plant biomass recalcitrance. *Biotechnol Biofuels*. 2017; (**this issue**).
- Shen H, Mazarei M, Hisano H, Escamilla-Trevino L, Fu C, Pu Y, et al. A genomics approach to deciphering lignin biosynthesis in switchgrass. *Plant Cell*. 2013;25(11):4342–61. <https://doi.org/10.1105/tpc.113.118828>.
- Zhao Q, Nakashima J, Chen F, Yin Y, Fu C, Yun J, et al. Laccase is necessary and nonredundant with peroxidase for lignin polymerization during vascular development in Arabidopsis. *Plant Cell*. 2013;25(10):3976–87. <https://doi.org/10.1105/tpc.113.117770>.
- Barros J, Serrani-Yarce JC, Chen F, Baxter D, Venables BJ, Dixon RA. Role of bifunctional ammonia-lyase in grass cell wall biosynthesis. *Nat Plants*. 2016;2(6):16050. <https://doi.org/10.1038/nplants.2016.50>.
- Peña MJ, Kulkarni AR, Backe J, Boyd M, O'Neill MA, York WS. Structural diversity of xylans in the cell walls of monocots. *Planta*. 2016;244(3):589–606. <https://doi.org/10.1007/s00425-016-2527-1> (**Epub 2016 Apr 22**).

13. Urbanowicz BR, Peña MJ, Moniz HA, Moremen KW, York WS. Two *Arabidopsis* proteins synthesize acetylated xylan in vitro. *Plant J*. 2014;80(2):197–206. <https://doi.org/10.1111/tpj.12643>.
14. Mazumder K, Peña MJ, O'Neill MA, York WS. Structural characterization of the heteroxylans from poplar and switchgrass. *Methods Mol Biol*. 2012;908:215–28. [https://doi.org/10.1007/978-1-61779-956-3\\_19](https://doi.org/10.1007/978-1-61779-956-3_19).
15. Kulkarni AR, Peña MJ, Avci U, Mazumder K, Urbanowicz BR, Pattathil S, et al. The ability of land plants to synthesize glucuronoxylans predates the evolution of tracheophytes. *Glycobiology*. 2012;22(3):439–51. <https://doi.org/10.1093/glycob/cwr117>.
16. Mazumder K, York WS. Structural analysis of arabinoxylans isolated from ball-milled switchgrass biomass. *Carbohydr Res*. 2010;345(15):2183–93. <https://doi.org/10.1016/j.carres.2010.07.034> (Epub 2010 Jul 30).
17. Pattathil S, Avci U, Baldwin D, Swennes AG, McGill JA, Popper Z, et al. A comprehensive toolkit of plant cell wall glycan-directed monoclonal antibodies. *Plant Physiol*. 2010;153(2):514–25. <https://doi.org/10.1104/pp.109.151985> (Epub 2010 Apr 2).
18. Bar-Peled M, Urbanowicz BR, O'Neill MA. The synthesis and origin of the pectic polysaccharide rhamnogalacturonan II—insights from nucleotide sugar formation and diversity. *Front Plant Sci*. 2012;3:92. <https://doi.org/10.3389/fpls.2012.00092> (eCollection 2012).
19. Urbanowicz BR, Peña MJ, Ratnaparkhe S, Avci U, Backe J, Steet HF, et al. 4-O-methylation of glucuronic acid in *Arabidopsis glucuronoxylan* is catalyzed by a domain of unknown function family 579 protein. *Proc Natl Acad Sci USA*. 2012;109(35):14253–8. <https://doi.org/10.1073/pnas.1208097109> (Epub 2012 Aug 14).
20. Bali G, Khunsupat R, Akinoshio H, Payyavula RS, Samuel R, Tuskan GA, Kalluri UC, Ragauskas AJ. Characterization of cellulose structure of *Populus* plants modified in candidate cellulose biosynthesis genes. *Biomass Bioenergy*. 2016;94:146–54. <https://doi.org/10.1016/j.biombioe.2016.08.013>.
21. Vandavasi VG, Putnam DK, Zhang Q, Petridis L, Heller WT, Nixon BT, et al. A structural study of CESA21 catalytic domain of *Arabidopsis* cellulose synthesis complex: evidence for CESA trimers. *Plant Physiol*. 2015;170(1):123–35. <https://doi.org/10.1104/pp.15.01356>.
22. Payyavula RS, Tschaplinski TJ, Jawdy SS, Sykes RW, Tuskan GA, Kalluri UC. Metabolic profiling reveals altered sugar and secondary metabolism in response to UGPase overexpression in *Populus*. *BMC Plant Biol*. 2014;14:265. <https://doi.org/10.1186/s12870-014-0265-8>.
23. Tan L, Eberhard S, Pattathil S, Warder C, Glushka J, Yuan C, et al. An *Arabidopsis* cell wall proteoglycan consists of pectin and arabinoxylan covalently linked to an arabinogalactan protein. *Plant Cell*. 2013;25(1):270–87.
24. Atmodjo MA, Hao Z, Mohnen D. Evolving views of pectin biosynthesis. *Annu Rev Plant Biol*. 2013;64:747–79.
25. Biswal AK, Yang X, Gunter L, Winkler K, Collins C, Mohanty SS, et al. Down-regulation of GAUT12 in *Populus deltoides* by RNA silencing results in reduced recalcitrance and increased growth of biofuel feedstock. *Biotechnol Biofuels*. 2015;8:41. <https://doi.org/10.1186/s13068-015-0218-y>.
26. Serba DD, Daverdin G, Bouton JH, Devos KM, Brummer EC, Saha MC. Quantitative trait loci (QTL) underlying biomass yield and plant height in switchgrass. *BioEnergy Res*. 2015;8(1):307–24.
27. Muchero W, Guo J, DiFazio SP, Chen JG, Ranjan P, Slavov GT, Gunter LE, et al. High-resolution genetic mapping of allelic variants associated with cell wall chemistry in *Populus*. *BMC Genom*. 2015;16:24. <https://doi.org/10.1186/s12864-015-1215-z>.
28. Evans LM, Slavov GT, Rodgers-Melnick E, Martin J, Ranjan P, Muchero W, et al. Population genomics of *Populus trichocarpa* identifies signatures of selection and adaptive trait associations. *Nat Genet*. 2014;46(10):1089–96. <https://doi.org/10.1038/ng.3075>.
29. Nelson RS, Stewart CN, Holladay S, Xiao X, Mason A, Wang Z-Y, et al. Development and use of a switchgrass (*Panicum virgatum* L.) transformation pipeline by the BioEnergy Science Center to evaluate plants for reduced cell wall recalcitrance: transgenes and cell wall targets studied (2007–2012). *Biotechnol Biofuels*. 2017; (this issue).
30. Baxter HL, Poovaiah CR, Yee K, Mazarei M, Rodriguez M Jr, Thompson OA, et al. Field evaluation of transgenic switchgrass plants overexpressing PvMYB4 for reduced biomass recalcitrance. *BioEnergy Res*. 2015;8(3):910–21.
31. Baxter HL, Mazarei M, Labbe N, Kline LM, Cheng Q, Windham MT, et al. Two-year field analysis of reduced recalcitrance transgenic switchgrass. *Plant Biotechnol J*. 2014;12(7):914–24.
32. Dumitrache A, Natzke J, Rodriguez M, Yee K, Thompson O, Poovaiah C, et al. Transgenic switchgrass (*Panicum virgatum* L.) targeted for reduced recalcitrance to bioconversion: a 2-year comparative analysis of field-grown lines modified for target gene or genetic element expression. *Plant Biotechnol J*. 2017;15:688–97. <https://doi.org/10.1111/pbi.12666>.
33. Kalluri UC, Yin H, Davison BH. Systems and synthetic biology approaches to alter plant cell walls and reduce biomass recalcitrance. *Plant Biotechnol J*. 2014;12(9):1207–16.
34. Lynd LR. Overview and evaluation of fuel ethanol production from cellulosic biomass: technology, economics, the environment, and policy. *Ann Rev Energy Environ*. 1996;21:403–65.
35. Paye JMD, Lynd L, Guseva A, Hammer SK, Gjersing E, Davis MF, et al. Biological lignocellulose solubilization: comparative evaluation of biocatalysts and enhancement via cotreatment. *Biotechnol Biofuels*. 2016;9:8.
36. Lynd LR, Guss AM, Himmel ME, Beri D, Herring C, Holwerda EK, et al. Advances in consolidated bioprocessing using *Clostridium thermocellum* and *Thermoanaerobacter saccharolyticum*. *Indus Biotechnol Microorg*. 2016;10:365–94.
37. Chung D, Cha M, Guss AM, Westpheling J. Direct conversion of plant biomass to ethanol by engineered *Caldicellulosiruptor bescii*. *Proc Natl Acad Sci*. 2014;111:8931–6. <https://doi.org/10.1073/pnas.1402210111>.
38. Cha M, Chung D, Elkins JG, Guss AM, Westpheling J. Metabolic engineering of *Caldicellulosiruptor bescii* yields increased hydrogen production from lignocellulosic biomass. *Biotechnol Biofuels*. 2013;6:85.
39. Guss AM, Olson DG, Caiazza NC, Lynd LR. Dcm methylation is detrimental to plasmid transformation in *Clostridium thermocellum*. *Biotechnol Biofuels*. 2012;5:30. <https://doi.org/10.1186/1754-6834-5-30>.
40. Olson D, Lynd LR. Computational design and characterization of a temperature-sensitive plasmid replicon for gram positive thermophiles. *J Biol Eng*. 2012;2012(6):5. <https://doi.org/10.1186/1754-1611-6-5>.
41. Lipscomb GL, Conway JM, Blumer-Schuetz SE, Kelly RM, Adams MWW. Highly thermostable kanamycin resistance marker expands the toolkit for genetic manipulation of *Caldicellulosiruptor bescii*. *Appl Environ Microbiol*. 2016;82:4421–8. <https://doi.org/10.1128/AEM.00570-16>.
42. Zhou J, Olson DG, Argyros DA, Deng Y, van Gulik WM, van Dijken JP, Lynd LR. An atypical glycolysis in *Clostridium thermocellum*. *Appl Environ Microbiol*. 2013;79:3000–8. <https://doi.org/10.1128/AEM.04037-12>.
43. Herring CD, Kenealy W, Shaw J, Corvalla S, Olson D, Zhang J, et al. Strain and bioprocess improvement of a thermophilic anaerobe for the production of ethanol from wood. *Biotechnol Biofuels*. 2016;9:125. <https://doi.org/10.1186/s13068-016-0536-8>.
44. Lin PP, Mi L, Morioka AH, Yoshino KM, Konishi S, Xu SC, et al. Consolidated bioprocessing of cellulose to isobutanol using *Clostridium thermocellum*. *Metab Eng*. 2015;31:44–52.
45. Papanek B, Biswas R, Rydzak T, Guss AM. Elimination of metabolic pathways to all traditional fermentation products increases ethanol yields in *Clostridium thermocellum*. *Metab Eng*. 2015;32:49–54.
46. Tian L, Lo J, Shao X, Zheng T, Olson DG, Lynd LR. Ferredoxin: NAD oxidoreductase of *thermoanaerobacterium saccharolyticum* and its role in ethanol formation. *Appl Environ Microbiol*. 2016;82(24):7134–41. <https://doi.org/10.1128/AEM.02130-16>.
47. Biswas R, Wilson CW, Giannone RJ, Klingeman DM, Hettich RL, Brown SD, Guss AM. Improved growth rate in *Clostridium thermocellum* hydrogenase mutant via perturbed sulfur metabolism. *Biotechnol Biofuels*. 2016;10:6. <https://doi.org/10.1186/s13068-016-0684-4>.
48. Xu Q, Resch MG, Podkaminer K, Yang S-H, Baker JO, Donohoe BS, et al. Dramatic performance of *Clostridium thermocellum* explained by its wide range of cellulase modalities. *Sci Adv*. 2016;2(2):e1501254. <https://doi.org/10.1126/sciadv.1501254> (Epub 2016 Feb 5).
49. Brunecky R, Alahuhta M, Xu Q, Donohoe BS, Crowley MF, Kataeva IA, et al. Revealing nature's cellulase diversity: the digestion mechanism of *Caldicellulosiruptor bescii* celA. *Science*. 2013;342(6165):1513–6. <https://doi.org/10.1126/science.1244273>.
50. Kim SK, Chung D, Himmel ME, Bomble YJ, Westpheling J. Engineering the N-terminal end of CelA results in improved performance and growth of *Caldicellulosiruptor bescii* on crystalline cellulose. *Biotechnol Bioeng*. 2016;114(5):945–50.
51. Lynd LR, Liang X, Biddy MJ, Allee A, Cai H, Foust T, et al. Cellulosic ethanol: status innovation. *Curr Opin Biotechnol*. 2017;45:202–11. <https://doi.org/10.1016/j.copbio.2017.03.008>.
52. Holwerda E, Lynd LR, et al. Evaluation of multiple levers for overcoming the recalcitrance of cellulosic biomass. (personal communication).

53. Studer ME, DeMartini JD, Davis MF, Sykes RW, Davison BH, Keller M, et al. Lignin content in natural *Populus* variants affects sugar release. *Proc Natl Acad Sci*. 2011;108:6300–5. <https://doi.org/10.1073/pnas.100925210>.
54. Decker SR, Sykes RW, Turner GB, Lupoi JS, Doepcke C, Tucker MP, et al. High-throughput screening of recalcitrance variations in lignocellulosic biomass: total lignin, lignin monomers, and enzymatic sugar release. *J Vis Exp*. 2015;15(103):e53163. <https://doi.org/10.3791/53163>.
55. Selig MJ, Tucker MP, Law C, Doepcke C, Himmel ME, Decker SR. High throughput determination of glucan and xylan fractions in lignocelluloses. *Biotechnol Lett*. 2011;33(5):961–75.
56. Pattathil S, Avci U, Miller JS, Hahn MG. Immunological approaches to plant cell wall and biomass characterization: glycome profiling. In: Himmel ME, editor. *Methods in molecular biology*. New York: Humana Press. 2012; p. 61–72. [https://doi.org/10.1007/978-1-61779-956-3\\_6](https://doi.org/10.1007/978-1-61779-956-3_6).
57. Foston M, Ragauskas AJ. Biomass characterization: recent progress in understanding biomass recalcitrance. *Ind Biotechnol*. 2012;8(4):191–208. <https://doi.org/10.1089/ind.2012.0015>.
58. Pu Y, Meng X, Yoo CG, Li M, Ragauskas AJ. Analytical methods for biomass characterization during pretreatment and bioconversion. In: Kumar R, Singh S, Balan V, editors. *Valorization of lignocellulosic biomass in a biorefinery: from logistics to environmental and performance impact*. New York: Nova Science Publishers; 2016. p. 37–78.
59. Pu Y, Hallac B, Ragauskas AJ. 2013. Plant biomass characterization: application of solution- and solid-state NMR spectroscopy. In: Wyman CE, editor. *Aqueous pretreatment of plant biomass for biological and chemical conversion to fuels and chemicals*. Hoboken: Wiley; 2013. p. 369–387. <https://doi.org/10.1002/9780470975831.ch18>.
60. Kataeva I, Foston MB, Yang S, Pattathil S, Biswal AK, Poole FL, et al. Carbohydrate and lignin are simultaneously solubilized from unpretreated switchgrass by microbial action at high temperature. *Energy Environ Sci*. 2013;6(7):2186–95. <https://doi.org/10.1039/C3EE40932E>.
61. Zeng Y, Yarbrough JM, Mittal A, Tucker MP, Vinzant TB, Decker SR, et al. In situ label-free imaging of hemicellulose in plant cell walls using stimulated Raman scattering microscopy. *Biotechnol Biofuels*. 2016;9:256.
62. Tetard L, Passian A, Farahi RH, Davison BH, Jung S, Ragauskas AJ, et al. Nanometrology of delignified *Populus* using mode synthesizing atomic force microscopy. *Nanotechnology*. 2011;2011(22):465702. <https://doi.org/10.1088/0957-4484/22/46/465702>.
63. Dumitrache A, Tolbert A, Natzke J, Brown SD, Davison BH, Ragauskas A. Cellulose and lignin colocalization at the plant cell wall surface limits microbial hydrolysis of *Populus* biomass. *Green Chem*. 2017;19:2275–85. <https://doi.org/10.1039/C7GC00346C>.
64. Nguyen TY, Cai CM, Kumar R, Wyman CE. Co-solvent pretreatment reduces costly enzyme requirements for high sugar and ethanol yields from lignocellulosic biomass. *Chemsuschem*. 2015;8(10):1716–25.
65. Poudel S, Giannone RJ, Rodriguez M Jr, Raman B, Martin MZ, Engle NL, et al. Integrated omics analyses reveal the details of metabolic adaptation of *Clostridium thermocellum* to lignocellulose-derived growth inhibitors released during the deconstruction of switchgrass. *Biotechnol Biofuels*. 2017;10:14. <https://doi.org/10.1186/s13068-016-0697-5>.
66. Abraham PE, Wang X, Ranjan P, Nookaew I, Zhang B, Tuskan GA, Hettich RL. Integrating mRNA and protein sequencing enables the detection and quantitative profiling of natural protein sequence variants of *Populus trichocarpa*. *J Proteome Res*. 2015;14(12):5318–26. <https://doi.org/10.1021/acs.jproteome.5b00823>.
67. Ziebell A, Gjersing E, Hinchee M, Katahira R, Sykes RW, Johnson DK, Davis MF. Downregulation of p-Coumaroyl quinate/Shikimate 3'-hydroxylase (C3'H) or Cinnamate-4-hydroxylase (C4H) in *Eucalyptus urophylla* × *Eucalyptus grandis* leads to increased extractability. *Bioenergy Res*. 2016;9(2):691–9.
68. Ziebell A, Gracom K, Katahira R, Chen F, Pu YQ, Ragauskas A, et al. Increase in 4-coumaroyl alcohol units during lignification in alfalfa (*Medicago sativa*) alters the extractability and molecular weight of lignin. *J Biol Chem*. 2010;285(50):38961–8.
69. Li M, Pu Y, Ragauskas AJ. Current understanding of the correlation of lignin structure with biomass recalcitrance. *Front Chem*. 2016;4:45.
70. Ragauskas AJ, Beckham GT, Biddy MJ, Chandra R, Chen F, Davis MF, et al. Lignin valorization: improving lignin processing in the biorefinery. *Science*. 2014;344(6185):1246843. <https://doi.org/10.1126/science.1246843>.
71. Sun Q, Khunsupat R, Akato K, Tao J, Labbe N, Gallego NC. A study of poplar organosolv lignin after melt rheology treatment as carbon fiber precursors. *Green Chem*. 2016;18(18):5015–24.
72. Beckham GT, Johnson CW, Karp EM, Salvachua D, Vardon DR. Opportunities and challenges in biological lignin valorization. *Curr Opin Biotechnol*. 2016;42:40–53.
73. Keller M, Miller R. The DOE BioEnergy Science Center—a US Department of Energy bioenergy research center. *In Vitro Cell Dev Biol*. 2009;45(3):193–8.
74. Muchero W, Chen J, Gunter LE, Jawdy S, Tuskan GA, Bryan AC, et al. Transcription factor which regulates flavonoid, phenylpropanoid, tyrosine and tryptophan pathways. US Patent 20,150,353,948. 2015.
75. Robinson W. Farming for fuels. *Dimensions*. 2014;16(2):46–8.
76. Lynd LR, Laser MS, Brandsby D, Dale BE, Davison B, Hamilton R. How biotech can transform biofuels. *Nat Biotechnol*. 2008;26(2):169–72.
77. Davison BH, Brandt CC, Guss AM, Kaluri UC, Palumbo AV, Stouder RL, et al. The impact of biotechnological advances on the future of U.S. bioenergy. *Biofuels Bioprod Biorefin*. 2015;9:454–67.

Submit your next manuscript to BioMed Central and we will help you at every step:

- We accept pre-submission inquiries
- Our selector tool helps you to find the most relevant journal
- We provide round the clock customer support
- Convenient online submission
- Thorough peer review
- Inclusion in PubMed and all major indexing services
- Maximum visibility for your research

Submit your manuscript at  
[www.biomedcentral.com/submit](http://www.biomedcentral.com/submit)

