Consolidated bioprocessing for biofuel production: recent advances

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Abstract: Consolidated bioprocessing (CBP), the combination of saccharolytic enzyme production and secretion, hydrolysis of polysaccharides, and fermentation of available sugars within a single-unit operation, improves cellulose conversion efficiency and decreases lignocellulosic biomass processing costs for producing biofuels and value-added products. *Clostridium thermocellum*, an anaerobic, thermophilic bacterium is a significant biocatalyst aspirant for CBP, due to its native cellulolytic and ethanologenic capabilities. This review highlights strain development/modification, metabolic engineering, and process improvements associated with CBP in the context of using *C. thermocellum* as a model biocatalyst to reduce operating expenditures and inhibitory effects for enhanced biofuels production. In addition, opportunities in using a microbial consortia and biofilms are discussed. As an overview of recent advances in CBP technologies to convert lignocellulosic biomass to biofuels, this review gives researchers a platform for future development of efficient and sustainable CBP approaches.

Keywords: *Clostridium thermocellum*, cellulosome, anaerobic, cellulolytic, ethanol

Introduction

Expected population growth with corresponding energy usage, limiting resources, and environmental stresses will require development of sustainable technological advances to meet future energy demands that do not compromise available resources.1 Sustainable developments, such as renewable energy systems, equalize energy supply and demand while improving food, economic, energy, and environmental security.2 In 2012, 19% of the global final energy consumption came from renewable forms of energy, with 10.2% (50.3 EJ yr⁻¹) supplied from various forms of biomass.3,4 Lignocellulosic biomass, organic biological matter derived from agricultural, municipal, and forestry operations, is a renewable resource that can be used for the production of reliable forms of energy, such as biofuels.5,6 The attractiveness of using lignocellulosic biomass as raw material in biofuel production processes is attributed to abundance, relatively low expense, and environmentally negligible production and potential for global distribution.7,8 While lignocellulosics possess roughly 40%–50% cellulose, 20%–40% hemicellulose, and 20%–30% lignin by weight, the major challenge is the presence of lignin, effective breakdown of the recalcitrant cellulose structure, and efficient bioconversion to liquid fuels.9,10 The conversion of biomass through biochemical techniques, including pretreatment, hydrolysis, and fermentation, has the potential to produce heat, electricity, fiber, chemicals, and biofuels while improving economic and environmental sustainability.11 To this end, significant research has focused on consolidated bioprocessing (CBP), a conversion approach, though still in its infancy stages of development, that combines...
Lignocellulosic biomass structure

Lignocellulose comprises of three main polymers, cellulose, hemicelluloses, and lignin, linked in a dense complex matrix with varying compositions depending on type, species, and source of biomass, in addition to pectin, extractives, and structural ash. 

Cellulose, the main component of the plant cell wall bestowing structural support, is composed of β-D-glucopyranose moieties linked through β-(1,4) glycosidic bonds. 

While disaccharide cellobiose is the repeating unit of the cellulose chain, the degree of polymerization in nature ranges from 2,000 to 20,000 units, and when combined through covalent and hydrogen bonding as well as Van der Waals forces form microfibrils. 

Hydrogen bonding within a cellulose microfibril determines stability or straightness of the chain, while hydrogen bonds between cellulose units introduce order, such as crystalline structures, or disorder with amorphous structures. 

In addition, due to the intra- and interchain hydrogen bonding, cellulose is insoluble in most solvents, including water, and considered extremely resistant to enzymatic hydrolysis. 

The cellulose microfibril structures are integrated with hemicellulose, various noncrystalline sugars, and other polymers, such as pectin. Hemicellulose is the second most abundant polymer and contrasts with cellulose by lacking chemical homogeneity, possessing a lower molecular weight and short lateral chains that are relatively easily hydrolyzed. 

While differing in composition, hemicelluloses are highly branched, heterogeneous polymers of pentoses, such as xylose and arabinose; hexoses, such as mannose, glucose, and galactose; and acetylated sugars. 

Among the main polymers in lignocellulosic materials, hemicellulose is the most thermochemically susceptible and alleged to cover the cellulose microfibrils; therefore, to significantly increase cellulose digestibility, at least 50% of this polymer must be removed. 

Lignin, the adhesive binding various components of lignocellulosic biomass together, is a highly complex three-dimensional amorphous heteropolymer network of phenyl propane units, such as p-coumaryl, coniferyl, and sinapyl alcohol, which provides strength as well as opposition to microbial attack and oxidative stress for plant cell walls. 

While lignin is a valuable coproduct for the generation of heat, power, and solid fuel, the noncarbohydrate polymer creates a major limitation in enzymatic and microbial hydrolysis of lignocellulosic biomass. 

This review focuses on highlighting process improvements, recombinant microbial catalyst and enzyme development, and metabolic engineering associated with CBP in the context of using C. thermocellum as a model biocatalyst and providing an overview in support of further research in sustainable biofuel production from lignocellulosic biomass. In addition, recent opportunities in using microbial consortia and biofilms are discussed.

Advancements in bioprocessing

During the past decade, technological advances have promoted commercial feasibility of biochemical conversion processing for the production of liquid fuels from lignocellulosic biomass. 

This renewable energy production approach includes such operations as biomass size reduction, pretreatment, hydrolysis, and fermentation to produce value-added products. Size reduction or comminution mechanically lacerates biomass to facilitate enzymatic accessibility to lignocellulosic materials for further pretreatment and digestibility. 

Pretreatment strategies strive to enhance biomass porosity to increase sugar yields during subsequent hydrolysis and degradation failure of pentoses, as well as to improve the breakdown and recovery of lignin- and hemicellulose-derived sugars, while minimizing by-product inhibition of later unit operations. 

Following pretreatment of lignocellulosic biomass, hydrolysis, also known as saccharification, converts complex carbohydrates into simple five- and six-carbon monomers, such as arabinose, fructose, galactose, glucose, mannose, and xylene, by using acids or highly specific external sources of cellulases and hemicellulases. 

In
contrast with acid hydrolysis, enzymatic hydrolysis has advantages in reduced energy requirements and imper- turbable environments without the formation of inhibitory byproducts.\(^{35,42}\) Furthermore, enzymatic hydrolysis has proven to be advantageous, due to nominal toxicity, decreased utility expenditures, and truncated corrosion compared to acid or alkaline hydrolysis.\(^{38-42}\) Subsequent to saccharification, fermentation procedures can be conducted as batch, fed-batch, continuous, and solid-substrate processes depending on the kinetic properties of choice microbes, source of lignocellulosic hydrolyzate, and process economics to generate biofuels.\(^{45,44}\) Extensive understanding of the genomes, physiologies, and metabolisms of *Saccharomyces cerevisiae*, *Zymomonas mobilis*, and *Escherichia coli* has resulted in their industrial utilization in bioconversion operations.\(^{35,46}\) Natively, *S. cerevisiae* is incompetent in the fermentation of pentose sugars, such as xylose and arabinose, nor proficient at functioning at optimal exogenous hydrolytic enzymatic temperatures between 50°C and 60°C.\(^{3,45}\) Therefore, metabolic and evolutionary engineering was required to enhance usability of various hydrolyzed monomers and tolerance to environmental stressors.\(^{47}\) Generally, strain engineering of saccharolytic and fermentative microbes are conducted to express cellulases and hemicellulases, secrete proteins, produce biofuels, and tolerate solvents and lignin byproducts, such as furans, weak organic acids, and phenolics, from fermentation procedures.\(^{48}\)

Separate hydrolysis and fermentation and simultaneous saccharification and fermentation are two bioconversion technologies generally commissioned for commercial implementation (Figures 1A and 1B).\(^{16}\) Enzymatic hydrolysis can also be performed simultaneously with the cofermentation of glucose and xylose as separate operations in a process known as simultaneous saccharification and cofermentation (Figure 1C).\(^{47}\) Saccharification and fermentation and saccharification and cofermentation have advantages over traditional separate hydrolysis and fermentation, often supporting increased alcohol yields by eradicating by-product inhibition and improved rates of hydrolysis, as well as reduced cost of operation by jettisoning the need for a secondary reactor, lowering enzyme loadings, and decreasing processing time and risk of contamination.\(^{48,49}\) Technological advancements to improve operating procedures and biomass solubilization effectiveness naturally led to the holistic CBP approach consisting of three biotransformations.\(^{48}\) To achieve CBP benefits, cellulase generation, saccharification of biomass, and fermentation of reducing sugars take place in conjunction by a monoculture or coculture of microorganisms, such as bacteria like *C. thermocellum* and fungi including *Neurospora crassa*, *Fusarium oxysporum*, *S. cerevisiae*, and *Paeilomyces* sp., for the generation of biofuels (eg, ethanol, butanol) and other value-added products.\(^{12,35,50-52}\) Alleviation of production expenditures and reduced chemical usage can be achieved by CBP, as the microbes used reduce the need for a multitude of external enzymes, which are not substrate specific.\(^{16,48}\) Additionally, this approach decreases the need for numerous reactors and offers simplicity in operating procedures by minimizing the compatibility requirements of enzyme and fermentation systems.\(^{53-55}\) In fact, a comparative cost analysis conducted on ethanol production, when considering capital, raw materials, utilities, and yield loss expenditures, resulted in a projection of $0.04 gal\(^{-1}\) for CBP, while a saccharification and cofermentation was projected at $0.19 gal\(^{-1}\).\(^{54}\) Eclectic selections of microorganisms have been recommissioned for CBP (Table 1); however, a microbial consortium that combines optimum substrate use and product formation properties, such as rapid hydrolysis rates and enhanced product concentrations and selectivity is preferable in CBP systems.\(^{56}\) In addition, anaerobic metabolism is imperative to CBP, due to superfluous expenditures associated with aerating large culture volumes, as well as product and lignocellulosic energy inefficiencies, as a result of aerobic respiration.\(^{13}\) Thermophilic microorganisms are also necessary to improve hydrolysis rates, which is a major challenge when conducting CBP at optimum ambient conditions for mesophilic microbes of interest.\(^{48}\) Although, the potential and rationale for CBP of biofuels exists, long fermentation periods and meager biofuel yields resulting from by-product formation (eg, organic acids), sensitivity of microorganisms to alcoholic solvents, and limited growth in hydrolysis supernatant resulted in significant research focused on improving the robustness of microorganisms utilized in CBP by employing recombinant strategies on cellulolytic and solventogenic organisms.\(^{57,58}\) While biochemical conversion systems demonstrate prodigious potentials for producing biofuels with minimal environmental impacts, the present challenge is efficiently converting lignocellulosic material to available sugars and fermenting crude sugars to biofuels with a robust microorganism and relatively high operating costs.\(^{59,60}\)

**Native cellulolytic and ethanologenic microbes**

*C. thermocellum*, an extensively researched strict anaerobic, acetogenic, cellulolytic, and thermophilic bacterium, possesses the ability to degrade cellulose and ferment mixed products from cellulose solubilization, while producing ethanol, acetate,
hydrogen ($H_2$), carbon dioxide ($CO_2$), lactate, and formate under various growth conditions.\textsuperscript{61-67} Cellulose degradation rates approaching 2.5 g L\textsuperscript{-1} h\textsuperscript{-1}, thermally stable biomass degrading enzymes, and proclivity to synthesize value-added products makes \textit{C. thermocellum} of great interest to CBP development.\textsuperscript{61,68,69} In addition, an optimum growth temperature of 60°C precludes that of most contaminating microorganisms, which allows for \textit{C. thermocellum} cultures to be maintained and viable when using nonsterile substrates for pure-culture fermentation processes.\textsuperscript{70} High fermentation temperatures and anaerobic conditions also reduce operational expenditures for ethanol recovery and reactor cooling, which are typically associ-

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**Figure 1** Bioprocessing approaches.

Notes: Bioprocessing approaches for the conversion of lignocellulosic biomass to biofuels and other value-added products with (A) separate hydrolysis and fermentation; (B) simultaneous saccharification and fermentation; (C) simultaneous saccharification and co-fermentation; and (D) consolidated bioprocessing.
Ethanol yield (g/L) for different microorganisms and substrates:

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Substrate</th>
<th>Time (h)</th>
<th>References</th>
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<td></td>
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Table 1. Cellulolytic and hemicellulolytic, ethanologenic (including genetically modified) microorganisms utilized for consolidated bioprocessing.

Fermentation by C. thermocellum

C. thermocellum hydrolyzes cellulosic substrates into shorter chain sugars, primarily cellobiose for conversion to ethanol, acetate, and lactate as primary end products through various metabolic pathways (Figure 2). Decreases in solubility of product gases (H2 and CO2) at higher fermentation temperatures also allow enhanced removal efficiency of product gases to be achieved, based on Henry’s law. The ability to hydrolyze most recalcitrant forms of cellulose as effectively as the commercially significant fungus, Trichoderma reesei, in combination with the robustness of thermotolerant enzymes, limited contamination and continuous distillation of fermentation products at elevated temperatures has resulted in the persistent interest in C. thermocellum as a biocatalyst in CBP for ethanol generation (Table 2). Utilizing the three-branched pathway to metabolize hexoses without genetic manipulation or the addition of external factors, C. thermocellum has been shown to produce 0.6 mol to 1.0 mol of ethanol per mol of hexose with an ethanol tolerance of 5 g L-1, due to a high degree of membrane fluidity based on lipid content. Aside from ethanol, acetate, and lactate, other compounds including pyruvate, malate, uracil, soluble glucan, and free amino acids, which normally are products disassociated with C. thermocellum, have been observed in the liquid fraction of lignocellulosic fermentations.

Varying substrate complexity and cultivation systems render a multitude of product ratios for a particular strain (Table 2), in addition to versatile functionality and inherent by-product tolerance. For instance, S14 advantageously possesses the capability to cultivate in an inclusive temperature and pH growth range and produce considerable quantities of cellulosomal enzymes in the medium. Furthermore, cellulosomes of S14 were shown to have an increased activity...
Table 2  *Clostridium thermocellum* strains utilized for consolidated bioprocessing

<table>
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<th>Strain</th>
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<th>Ethanol (mM)</th>
<th>Acetate (mM)</th>
<th>Lactate (mM)</th>
<th>Total products (mM)</th>
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<tr>
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<td>–</td>
<td>–</td>
<td>116</td>
<td>–</td>
<td>83</td>
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<tr>
<td>SmC</td>
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<td>–</td>
<td>–</td>
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<tr>
<td>SSC</td>
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<tr>
<td>SmC</td>
<td>Cellulose</td>
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<td>27</td>
<td>–</td>
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<td>SmC</td>
<td>MN300</td>
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<td>22.5</td>
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<td>Solka flocculant</td>
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<tr>
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<td>16.9</td>
<td>13.6</td>
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<td>–</td>
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<td>Steam-exploded wood</td>
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<td>167</td>
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<tr>
<td>SmC</td>
<td>Untreated wood</td>
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<td>6.4</td>
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<td>–</td>
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<td>M1570</td>
<td>SmC</td>
<td>Avicel</td>
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<td>1.2</td>
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<td>Microcrystalline cellulose</td>
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<td>SmC</td>
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<tr>
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<td>12</td>
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</tbody>
</table>

Abbreviations: Liq, liquid cultivation, soluble carbon; SmC, semi-solid cultivation, liquid insoluble carbon; SSC, solid-substrate cultivation.
Figure 2 Metabolic functionality of Clostridium thermocellum cellulosome for product formation.

Notes: The lone numbers correspond to enzymes. ABC transporter (1); cellulose phosphorylase (2); glucokinase (3); phosphofructokinase (4); phosphoglycerate kinase (5); phosphoenolpyruvate carboxykinase (6); malate dehydrogenase (7); malic enzyme (8); oxaloacetate decarboxylase (9); pyruvate phosphate dikinase (10); phosphoglucomutase (11); membrane-bound pyrophosphatase (12); ATP-energized protein pump (13); ADP-glucose synthase (14); NDP-kinase (15); lactate dehydrogenase (16); pyruvate:formate lyase (17); pyruvate:Fd oxidoreductase (18); ferredoxin hydrogenase (19); NAD(P)H hydrogenase (20); phosphotransacetylase (21); acetate kinase (22); acetaldehyde dehydrogenase (23) and alcohol dehydrogenase (24). The closed circle represents conversion between H$_2$ and H$^+$ by (19 and 20). Broken arrows indicate hypothesized source and point of use of pyrophosphate in glycolysis. The asterisk designates a strain dependent reaction. Figure adapted from: Applied and Environmental Microbiology; Zhou J, Olson DG, Argyros DA, et al. Atypical glycolysis in Clostridium thermocellum; 2013;79(9):3000–3008; doi: 10.1128/AEM.04037-12; and amended with permission from the American Society for Microbiology; Copyright © 2013, American Society for Microbiology. 72 And adapted from Springer; Applied Microbiology and Biotechnology; End-product induced metabolic shifts in Clostridium thermocellum ATCC 27405; 92; 2011;199–209; Rydzak T, Levin D, Cicek N, Sparling R; Copyright © Springer-Verlag 2001; with kind permission of Springer Science+Business Media. 210
on microcrystalline cellulose and lignocellulosics, such as rice straw, with higher resistance to cellobiose inhibition, compared to the cellulosomes of ATCC 27405.82

In addition to substrate utilization, supplemental nutrients, such as salts, vitamins, and reducing agents, are of great importance to product formation when utilizing C. thermocellum and other anaerobes.83,84 Islam et al85 demonstrated enhanced cellulose fermentation and end-product synthesis by C. thermocellum DSM 1237 with varied nutrient compositions of α-cellulose, yeast extract, urea, CaCl₂, 2H₂O, MgCl₂, 6H₂O, FeSO₄·6H₂O, and vitamins under carbon-excess conditions. The researchers also illustrated two major effects, a general growth enhancement effect and a carbon flux shifting effect, which rendered volumetric ethanol and H₂ yields that increased by 2.3-fold and 2.04-fold, respectively, when compared to the basic nutritional blend.

Shifting metabolic product synthesis in C. thermocellum can also be induced with the supplement of acetone, ethanol, formate, or sodium azide or by increasing the hydrostatic bioreactor pressure by incorporating exogenous gases.14,16,86,87 More specifically, the addition of acetate when initiating fermentative procedures increases ethanol and decreases formate production, while the addition of ethanol increases hydrogen and acetate concentrations. Formate proves advantageous not only at increasing hydrogen and ethanol but also at decreasing acetate. Alternatively, the initial incorporation of hydrogen was determined to decrease carbon dioxide and increase formate production, while the addition of headspace carbon monoxide considerably enhanced the production of ethanol and inhibited the generation of H₂, CO₂, and acetate.16 Shifts in end-product formation can also be accomplished through strain modifications, such as with the evolved M1570 (Δhpt, Δldh, Δpta), which produced a 40:1 molar ratio of ethanol to organic acid while making 5.61 g L⁻¹ ethanol.89

**Cellulosome structure and capability**

C. thermocellum expresses a collection of cellulolytic enzymes, which accumulate into large, complex, multi-protein structures on the cell surface, known as cellulosomes.70,88 Cellulosomes with molecular weights ranging from 2.0 to 6.5 × 10⁶ and encompassing 14–26 polypeptide subunits, depending on strain and growth conditions, were first recognized while conducting research on adhesion factors linking bacterium to cellulose.89–99 Specifically, an electron micrograph demonstrated that the cytoplasmic membrane of C. thermocellum was bordered by a thin peptidoglycan layer, a regular S-layer, and an amorphous outer layer formed by the protuberate cellulosome.68,100 By way of the cellulosome, C. thermocellum indeed attaches to cellulose, while over 20 enzymes, including endoglucanases, cellobiohydrolases, and xylanases, within the cellulosome efficiently degrade cellulose to glucose and cellulodextrins, followed by subsequent transportation for cellular metabolism, in earlier stages of cellulolysis.71,101 More specifically, during optimal growth conditions, C. thermocellum forms a monolayer biofilm without an extracellular polymeric matrix, parallel to the carbon fibers of the lignocellulosic substrate, caricaturing the topography to facilitate extracellular hydrolysis.102,103 During the latter stages of a cell culture, it has been reported that the cellulosome detaches from the bacterium cell; however, the possibility exists that the cellulosome remains attached to high-molecular weight cellulose compounds.36 The effectiveness of cellulosomes to catalyze the hydrolysis of cellulose depends significantly on the maintenance of structural integrity, as partially disassociated cellulosome complexes result in major activity loss, especially as it relates to crystalline forms of cellulose.104 Nonetheless, economic production of cellulolytic enzymes and reducing enzyme to biomass ratio required for commercialization of biofuels derived from lignocellulosic biomass could be achieved when utilizing cellulolytic CBP microbes for enzyme production, secretion, and recycling.104,105 While advancements are still required in enzyme recycling, solutions can be found exploiting the tethering capability of the C. thermocellum cellulosome.12,105

Definitively, the primary and largest structural subunit of the multi-functional C. thermocellum cellulosome, known as the cellulosome-integrating protein (CipA), is a glycopolypeptide with a mass of 210–250 kDa and functions as a nonhydrolytic scaffoldin.98,99 The modular protein consists of a carbohydrate-binding module (CBM-3a), also referred to as the cellulose-binding domain, with a comprehensive binding specificity for crystalline cellulose, a hydrophilic module of unknown functionality, termed X, a modified dockerin domain and nine internal repeated sequences or hydrophobic cohesion domains positioned relative to the amino terminus, which bind catalytic subunits.106,107 Specifically, amalgamation of the catalytic subunits into the cellulosome transpires by way of calcium-dependent interactions between the scaffoldin cohesions and Type I dockerin domains of the catalytic subunits.108,109 Furthermore, the cellulosome binds to cellulose via the CBM-3a, as well as through the CBMs of the catalytic subunits. In fact, Kataeva et al106 demonstrated synergism between the catalytic subunit, CelD, and the CBM of the C. thermocellum scaffoldin. Type II dockerin domains
attached to the C-terminus of the bacterium scaffoldin do not bind to the scaffoldin cohesion domains, instead, these dockerin domains bind to specific Type II cohesion domains on the cell surface, known as anchoring proteins.\textsuperscript{111–114} These proteins (SdbA, Orf2p, and OlpB) contain an S-layer homology module for correlating with the cell surface and consequently anchoring the cellulose to the cell.\textsuperscript{115} While 23 celllobiohydrolase (exoglucanases) genes for cellulolysomal components that contain dockerin domains have been recognized, endoglucanases have also been ascertained, as well as lichenase, chitinase, mannanase, and five xylanases, with two containing xylan esterase modules that remove feruloyl residues.\textsuperscript{104,116–120} Although \textit{C. thermocellum} is incapable of fermenting xylan, xylose, and other five-carbon sugars, the latter enzymes are believed to breakdown glycans encasing cellulose microfibrils to improve accessibility of the cellulose to be degraded by celluloses.\textsuperscript{115}

The efficient degradation of lignocellulosic biomass is due to the juxtaposition of directing the enzymatic complex to the substrate, known as the targeting effect, and the spatial propinquity of the different types of cellolysomes to one another, known as the proximity effect.\textsuperscript{121} While the cellulose assembles in a temperately selective manner, this multi-enzyme system is one of the most efficient natural biocatalyst for degrading lignocellulosic biomass, therefore research groups have attempted to capture its function physically, incorporate it into other microorganisms, and mimic its behavior in synthesized enzyme complexes.\textsuperscript{109,122–124}

### Recombinant cellulolytic approach

Microbial strain engineering to facilitate high cellulolytic activity, the ability to use numerous carbon sources, and resistance to toxic compounds released during the pretreatment of lignocellulosic biomass are important for the development of cost-effective fermentation of lignocellulosics for the directed generation of biofuels and value-added chemicals.\textsuperscript{125} To this end, recombinant cellulolytic approaches originating from natural anaerobic mesophilic and thermophilic bacteria and fungi possessing cellulosomes (Table 3) have been investigated.\textsuperscript{117,126,127}

In fact, natural cellulosomes detectible on the cell surface increases the localized concentration of enzymes allowing for enhanced consumption of cellobiose and cellodextrins by a microorganism, which minimizes inhibition related to product formation.\textsuperscript{88} Through the use of electron microscopy, Fourier-transform infrared spectroscopy, and X-ray diffraction analysis, synergistic enzymatic activity of the cellulosomes are considered advantageous over aerobic bacteria and fungi, which exhibit fluctuating enzymatic functionality and

### Table 3 Studied bacteria and fungi with cellulosomal structures

<table>
<thead>
<tr>
<th>Microorganisms</th>
<th>Temperance</th>
<th>Cellulose structures</th>
<th>Domain</th>
<th>Source</th>
<th>References</th>
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<td>\textit{Vibrio vulnificus}</td>
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<td>Scaffoldin</td>
<td>Fungal-type dockerin</td>
<td>Ala Wai Canal</td>
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<td></td>
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<td>\textit{Acetivibrio cellulolyticus}</td>
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<td>Scaffoldin</td>
<td>CBM, Type I cohesion and Type II dockerin</td>
<td>Sewage</td>
<td>218,219</td>
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<td>Surface-anchoring proteins</td>
<td>CBM and Type II cohesion</td>
<td>Sewage</td>
<td>219–221</td>
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<td>Multi-enzyme complexes</td>
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<td>Rumen/feces</td>
<td>236–238</td>
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**Abbreviation:** CBM, carbohydrate-binding module.
specificity associated with external enzyme secretion.16,128

*C. thermocellum* is the most cellulolytic thermophile and
distinctively possesses exceptionality with regard to size,
complexity, and genomic arrangement of its cellulosome,
vindicating one of the highest rates of cellulose degradation
and utilization.14,38,117,129,130 As a result, the recombination
of cellulosomal components of *C. thermocellum* into
minicellulosomes has been engineered onto the surface of
*Aspergillus niger*, *Bacillus subtilis*, *Clostridium acetobutylicum*,
*E. coli*, *Lactococcus lactis*, *Thermoanaerobacterium saccharolyticum*, and *S. cerevisiae* by way of anchoring proteins or cohesion–dockerin interactions.5,131–137

**Engineering of bacteria**

With regard to bacteria, fragments of the scaffoldin protein
CipA from *C. thermocellum* containing a single cohesin
binding module, two cohesin modules, one cohesin and a cellulose-
binding module, or only a cellulose-binding module were
functionally displayed on the cell surface of *L. lactis*.134,135
To alleviate challenges associated with cell toxicity from
protein overexpression, a *nisA* inducible promoter was
used as well as the C-terminal-anchoring streptococcal M6 motif.135
While significant variation in efficiencies were exhibited among the designed minicellulosomes, accredited to structural characteristics in protein conformation, scaffold size, and presence of noncohesion modules, the surface display of functional scaffold proteins proved imperative for developing recombinant microorganisms capable of using multiple metabolic pathways to directly convert carbonaceous biomass into biofuels and other value-added chemicals.135 Similarly, *B. subtilis* was engineered to display multiple thermophilic cellulase enzymes (Cel8A) from *C. thermocellum* on the cell surface by way of proteins containing a *staphylococcus aureus* cell wall sorting signal covalently anchored to peptidoglycan by coexpression with the *Bacillus anthracis* sortase A (SrtA) transpeptidase.136
Additionally, a Cel8A–dockerin fusion protein was stably
anchored onto *B. subtilis* utilizing noncovalent cohesion–dockerin interactions to increase lignocellulosic degradation potential during CBP.136

The capability of *T. saccharolyticum* to unhisitatingly
solubilize hemicellulose with the heterologous expression of
a functional cellulosome makes this Gram-positive anaero-
bic thermophile of interest in CBP. In fact, expression and
localization of a full-length CipA from *C. thermocellum* was
observed by developing an inducible system based on the
native *xynA* *T. saccharolyticum* promoter, regulated by xylan
and xylose.131 As part of the study, an exorbitant quantity of
xylose and SigmaCell 101, a microcrystalline cellulose, was
hydrolyzed when the ΔcipA mutant *C. thermocellum* was
cocultured with the CipA-expressing *T. saccharolyticum*
strain.131

In addition to native ethanologenic species, other solven-
togenic microbes, such as *C. acetobutylicum*, that proficiently
convert sugars to ethanol and butanol are of interest in CBP;
however, these species are known to inefficiently grow on
and metabolize crystalline cellulose, which has prompted
the engineering of secretion and assemblage of cellulosomes
by allele-coupled exchange technology.133 Specifically,
BioBrick2-standarized fragments were used to assemble
a range of synthetic genes encoding *C. thermocellum* cel-
lusomal scaffoldin proteins (CipA variants) and glycoside
hydrolases (GHs, Cel8A, Cel9B, Cel48S, and Cel9K) as well
as synthetic cellulosomal operons that direct the synthesis
of Cel8A, Cel9B, and a truncated form of CipA. Successful
heterologous protein expression, secretion, and self-assembly
of cellulosomal subunits by recombinant *C. acetobutylicum*
was demonstrated by utilizing supported allele-coupled
exchange technology as a platform for synthesizing novel
cellulosomes for CBP.

**Engineering of fungi**

*A. niger* was utilized in CBP, as a direct result of its inherent
ability to secrete feruloyl esterases that hydrolyze diferulate
cross-links in lignocellulose and enhance overall hydrolysis
performance.137 In an effort to facilitate a stronger syner-
gism between catalytic domains, a minicellulosome was
incorporated into *A. niger* to prevent large-scale diffusion of
enzymes and lower protein requirements for hydrolysis. In
detail, a chimeric protein composed of the feruloyl esterase
A from *A. niger* was associated with the Cel48S dockerin
from *C. thermocellum* and produced in *A. niger*. Analyz-
ing the chimeric enzyme for its binding capacity indicated
that translational fusion to glucoamylase improved the
secretion efficiency of the protein and allowed production
of the first functional fungal enzyme joined to a bacterial
dockerin.137

For *S. cerevisiae*, most cell surface display methods
developed have been based on agglutinin and flocculin model
systems, which incorporate cell wall proteins (α-agglutinin,
Aga1, Cwp1, Cwp2, Tip1p, Srp1, FIo1p, Sed1p, Tir1p, and
YCR89W) containing a glycosylphosphatidylinositol (GPI)
signal motif covalently cross-linked to β-1,6-glucan.138 More
specifically, *S. cerevisiae* was genetically modified to assem-
bly a cell surface designer cellulosome by heterologously
expressing a chimeric scaffoldin protein (Scaf3p) regulated
by a phosphoglycerate kinase 1 promoter, β-xylanase 2 secretion signal, cell wall protein 2 (Cwp2), and termination sequences, for GPI-mediated anchoring to the cell wall.\textsuperscript{138} While fluorescent microscopy confirmed that Scaf3p targeted the yeast cell surface, Far Western blot analysis demonstrated functionality of the \textit{C. thermocellum} dockerin domain binding the Scaf3 protein. Phenotypic evidence for cohesion–dockerin interaction was also established with the detection of a two-fold increase in tethered endoglucanase enzyme activity in \textit{S. cerevisiae} cells compared to the wild type. This work highlighted the feasibility of designing cellulosolytic strains of \textit{S. cerevisiae} through emulation of the cellulosome concept.

Tsai et al\textsuperscript{139} functionally displayed a cell surface mini-cellulosome exhibiting three divergent cohesin domains (CelE, CelA, and CelG) from \textit{C. thermocellum}, \textit{Clostridium cellulolyticum}, and \textit{Ruminococcus flavefaciens} on \textit{S. cerevisiae}. The recombinant cellulosome maintained synergistically significant glucose liberation and produced ethanol when utilizing a β-glucosidase (BglA) from \textit{C. thermocellum} tagged with dockerin from \textit{R. flavefaciens}.\textsuperscript{139} As a result, \textit{S. cerevisiae} was engineered to display a succession of uni-, bi-, and trifunctional minicellulosomes consisting of a miniscaffoldin containing a CBM and three cohesin modules tethered to the cell surface through the yeast α-agglutinin adhesion receptor.\textsuperscript{140} While the cell surface assembly of the minicellulosome was dependent on high-affinity interactions between cohesion–dockerin binding domains, the triplicating enzymatic functionality of the surface-displayed minicellulosome enhanced the capabilities of \textit{S. cerevisiae} at hydrolyzing lignocellulosic material for ethanol production during CBP by improving enzyme–enzyme and enzyme proximity synergies, as well as conceptually explicating cellulosome synthesis and anatomical modality. Subsequently, a cellulosolytic four-strain \textit{S. cerevisiae} consortium capable of either displaying a CipA scaffoldin derived from \textit{C. thermocellum} or secreting one of three types of cellulases, CelA from \textit{C. thermocellum}, CBHII from \textit{T. reesei}, or BGLI from \textit{Aspergillus aculeatus}, was developed for CBP.\textsuperscript{141} A 20% increase in ethanol production was observed by regulating the combination and concentration of the four \textit{S. cerevisiae} strains, with a CipA:CelA:CBHII:BGLI ratio of 2:3:3:0:53 producing 1.80 g L\textsuperscript{-1} ethanol after 94 hours. Advantageously, this system allows for the optimization of ethanol production as well as limitless implementation of enzymes into the minicellulosome construct, such as hemicellulases and pectinases adhered through fusion domains.

### Artificial cellulosomes

In an effort to understand the relationship between the cellulosome structure and enzyme activity, reduce enzyme loadings and related costs, and improve compatibility of multi-protein complexes with biorefinery applications for biofuel production, truncated designer cellulosomes were constructed with cohesion modules and proven highly active compared to free cellulases during lignocellulosic degradation.\textsuperscript{142–144} One such example is the robust 18-subunit, self-assembled synthetic multi-enzymatic complex, known as the rosettazyme, which consists of a CipA cohesion module and four dockerin-containing cellulases (Cel9B, Cel9K, Cel9R, and Cel48S) from \textit{C. thermocellum}.\textsuperscript{122,144} More specifically, rosettazymes are thermostable, group II chaperonins (scaffold-base) from the hyperthermo-acidophilic archaeon \textit{Sulfolobus shibatae}, which in the presence of ATP/Mg\textsuperscript{2+} assemble into double-ringed structures that truss dockerin-containing endo- and exo-glucanases and enhance the cellulose degradation activity of bound enzymes.\textsuperscript{144} The versatility of the rosettazymes cohesion–dockerin interaction on the cellulosomal scaffoldin provides a limitless number of arrays for the utilization of fabricating defined enzymatic nanostructures for the production of biofuels.\textsuperscript{142} A chimeric cohesion-fused β-glucosidase (BglA-CohII) that binds directly to the cellulosome of \textit{C. thermocellum} through an unoccupied dockerin module of the CBM was designed to direct enzymatic activity to substrate location.\textsuperscript{145} BglA was proven to increase microcrystalline cellulose and pretreated switchgrass degradation, maintain cellulobiose activity, and integrate with the native cellulosome, permitting the \textit{C. thermocellum} cellulosome to subsist as a homo-oligomer. These findings demonstrate the significance of enzyme targeting to enhance lignocellulosic biomass degradation.

In addition to cohesion–dockerin interaction, conjugation techniques dependent on scaffold material and enzyme type, such as metal affinity between polyhistidine tag and core-shell quantum dots, protein fusion, and zinc-finger protein (ZFP)-guided assembly, have been investigated to improve stability, storage properties, and enzymatic synergies of synthetic multi-protein complexes.\textsuperscript{122,144} In contrast with rosettazymes, cellulose–protein fusions are single polypeptide chains with cellulose domains internal to the scaffolding protein designed to increase cellulase thermostability and activity.\textsuperscript{146} Purposefully, CelA from \textit{C. thermocellum} was inserted into a hyperstable α-helical consensus ankyrin protein domain scaffoldin, which gave rise to an arrangement of multiple cellulose domains at a predetermined spacing within a single polypeptide to optimize reactivity of a repetitive
cellulose lattice.\textsuperscript{146} Nanoparticles can be model supports for cellulose immobilization to enhance enzymatic activity.\textsuperscript{147} In a study to evaluate the effects of nanoparticles on catalytic performance of artificial cellulosomes, it was found that size was moderately significant and enzyme proximity was extremely important to enhancing enzymatic activity.\textsuperscript{147} Proteins can also be site-specifically localized onto a double-strand DNA scaffold using DNA-binding proteins, such as ZFPs composed of three subunits recognizing specific 3-bp sequences to create artificial bifunctional cellulosomes for improving the hydrolysis of cellulose.\textsuperscript{148} By taking advantage of ZFP modality, site-specific docking of CelA and CBM of \textit{C. thermocellum} onto a single DNA template was achieved.\textsuperscript{148} As a result of advancements in protein engineering and conjugation technology, artificial cellulosomes have shown great promise by mimicking the enzymatic synergism observed in native cellulosome systems; however, these complexes are still less active than naturally occurring cellulosytic microorganisms.\textsuperscript{136} While synergistic interactions between CBMs and catalytic domains impact the efficient degradation of lignocellulosic biomass by native, recombinant, and artificial cellulosomal possessing microbes, investigation of molecular mechanisms by way of metabolic fluxes are also required to improve growth potential, uptake and utilization of monosaccharides, alcoholic yields, and resiliency to inhibitory byproducts.\textsuperscript{149}

\textbf{Genomics, transcriptomics, proteomics, and metabolic fluxes}

To understand the complex reactions required to degrade and ferment lignocellulosic biomass to biofuels, significant research has focused on the genomic, transcriptomic, proteomic, and metabolic profiles of \textit{C. thermocellum}.\textsuperscript{150} To expand on the knowledge base for clostridial species, such as \textit{C. thermocellum}, relevant to current biofuel production efforts, the genome was sequenced and shown to include a 3.8-Mb DNA, single-chromosome arrangement consisting of a 39.8\% guanine/cytosine content and 3,173 protein-encoding genes.\textsuperscript{150,151}

Microarray transcriptomic analysis on \textit{C. thermocellum} demonstrated deviations in gene expression levels resulting from modifications in carbon source and structure, nutrient availability, and microbial density, which validates the microbe’s ability to sense and respond to external factors by signaling peptides or transcriptional regulators to transport and metabolize nutrients.\textsuperscript{152} When altering the fermentative substrate from cellobiose to crystalline cellulose, expression profiles of genes corresponding to energy generation, translation, glycolysis and amino acid, nucleotide, and coenzyme metabolism increased.\textsuperscript{153} Moreover, expression profiles for cellulosomal genes, inorganic ion transport and metabolism, signal transduction, amino acid transport, phosphate transport, and resistance—nodulation—division transport increased when utilizing pretreated yellow poplar, diluted acid-pretreated \textit{Populus}, and switchgrass as lignocellulosic carbon sources.\textsuperscript{154,155} These discoveries highlight the importance of carbon source on the metabolic functionality and performance of \textit{C. thermocellum} in CBP.

Supporting proteomic studies expressing core metabolism proteins demonstrated growth-phase dependency for positioning of \textit{C. thermocellum} to efficiently utilize cellulosic substrates and corresponding nutrients, which facilitates specific and consistent protein expression.\textsuperscript{156} More specifically, metabolic proteins associated with pyruvate synthesis exhibited a decrease in expression, while proteins associated with glycolgen metabolism, pyruvate catabolism, and end-product synthesis pathways increased when the microbe transitioned from exponential to stationary phase. Relative expression profiles demonstrated specific proteins utilized in carbohydrate consumption and end-product synthesis, which reinforced previous findings that hydrogen synthesis occurs by way of bifurcating hydrogenases, while ethanol synthesis is principally catalyzed by a bifunctional aldehyde/alcohol dehydrogenase. The differences in expression profiles of core metabolic proteins in response to growth phase may dictate the carbon and electron flux toward energy storage compounds and fermentation products. Cellulosome proteins also illustrate a change in expression as it relates to carbon availability. For instance, hemicellulases, such as XynA, XynC, XynZ, and XghA, are upregulated, in addition to endoglucanases CelA, CelB, CelE, CelG, and GH5, when \textit{C. thermocellum} is grown on cellobiose; however, when grown on cellulose, GH9 are superiorly expressed with the corresponding surface-anchoring protein OlPB and endoglucanases CelS and CelK.\textsuperscript{157} The results support the existing theory that expression of scaffoldin-related proteins is coordinately regulated by a catabolite repression mechanism, xylanase expression is prone to a growth rate-independent regulation, and transcriptional control of cellulases, such as endoglucanases, is conditional on catabolite repression. Similar results were demonstrated with pretreated switchgrass with the exception of an increased expression of GH9 and CelK as well as the decrease in xylanases due to the pretreatment-induced reduction in hemicellulose and xylan composition.\textsuperscript{158}
A major challenge in using *C. thermocellum* for CBP biofuel production is the need to modify the organism for increased production efficiency; however, the process of properly engineering an organism is typically onerous. To this end, a genome-scale model of *C. thermocellum* metabolism, iSR432, was developed by incorporating genomic sequence data, network topology, and experimental measurements of enzyme activities and metabolite fluxes for the generation of a computational apparatus for evaluating the metabolic network of *C. thermocellum* and facilitating enhanced biofuel production by way of strain engineering. In fact, utilization of this model emphasized the correlation among reduction and oxidation states, as well as ethanol secretion, which permitted the prediction of gene deletions and environmental conditions that would potentially increase ethanol production.

**Recombinant solventogenic approach**

Engineering to prolong existing metabolic pathways for the production of novel products, accelerating a rate-determining step, engineering enzymatic activities that synthesize unique biocatalytic nanostructures, and shifting metabolic fluxes toward the generation of value-added products, such as biofuels, is of extreme interest for aiding in the commercial viability of *C. thermocellum*, as a CBP biocatalysts. In an effort to improve *C. thermocellum* ethanol yields by redirecting the carbon flux, a genetic system for making targeted gene knockouts was developed utilizing a toxic uracil analog, 5-fluoroorotic acid to select for deletion of the *pyrF* gene involved in organic acid production, namely *pta*, which encodes the enzyme phosphotransacetylase. While the *C. thermocellum Δpta* strain failed to produce acetate, the deletion marginally affected ethanol production. Enzymes associated with organic acid formation were also deleted by creating a counter-selection system based on endogenous *hpt* and *T. saccharolyticum tdk* genes. By combining these selection markers, the use of replicating plasmids to insert and remove markers from the host chromosome was realized. Following the deletion of the *l-lactate dehydrogenase* (*ldh*) and *pta* genes from *C. thermocellum* M1570 with the counter-selection system and 2,000 hours of adaption, the ethanol yield of the mutant increased by 4.2-fold compared to the wild-type strain; however, ethanol yields failed to increase with decreasing acetate and lactate formation. Conversely, when using the engineered *C. thermocellum* M1570 strain, CBP of downregulated caffeic acid 3-O-methyltransferase transgenic switchgrass was realized with a 20% increase in lignocellulosic conversion, followed by the primary production of ethanol, indicating the importance of substrate utilization when developing strains for enhanced biofuel yields. In addition, Deng et al examined the impact of targeted modification of enzymes associated with the malate shunt pathway in wild-type *C. thermocellum* DSM1313, including expression of pyruvate kinase gene from *T. saccharolyticum*, mutation of the phosphoenolpyruvate carboxykinase and deletion of malic enzyme gene to increase ethanol production. The researchers concluded that *C. thermocellum* with exogenous pyruvate kinase exhibited a 3.25-fold increase in ethanol yield when compared to the wild-type strain. Similarly, when the gene for malic enzyme and part of malate dehydrogenase were deleted, the anaerobic bacterium demonstrated ethanol yields more than three fold higher than that of the wild-type strain.

As a result of solvent toxicity being attributed to chaperonic effects on biological membranes, such as increased fluidity, degraded proteins and RNA, decreased energy generation and nutrient transportation, and damaged DNA and lipids, the development of strains with superior tolerance is imperative for the sustainable production of biofuels with increased yields. Using an innovative engineering approach to increase ethanol tolerance, which typically ranges from 10 g L^{-1} to 20 g L^{-1} in wild-type strains, as a means of lowering production costs, Shao et al isolated ethanol-tolerant strains of *C. thermocellum* that were capable of growing in medium containing up to 50 g L^{-1} ethanol. Genomic analysis of the isolated ethanol-tolerant strains revealed six common mutations, which originated in genes associated with ethanol, arginine, and pyrimidine biosynthesis pathways. Celloextrin synthesis was also shown to be active as well as metabolically balanced. Furthermore, Brown et al demonstrated that a shift of cofactor specificity from NADH to NADPH for the bifunctional acetaldehyde-CoA/alcohol dehydrogenase enzyme profiles ethanol tolerance to *C. thermocellum*, resulting from an interference with electron flow. These studies provide knowledge on the mechanisms of ethanol tolerance to further metabolically engineer *C. thermocellum* aimed at higher ethanol yields to complement increased tolerance; however, the extensive realization necessitates targeted development and optimization of specific characteristics that will assist in the synergistic functionality.

**Microbial consortia**

Thus far, recent advances regarding engineered microorganisms to produce a plethora of enzymes and biofuels from a
variety of lignocellulosic substrates are associated with low titers and consequently not commercially viable organisms.\textsuperscript{56} Conversely, CBP conducted utilizing a microbial consortium, which is similar to natural conversion systems, is of interest due to synergies that result in extremely efficient substrate utilization and increased product yields.\textsuperscript{56} For instance, \textit{C. thermocellum} demonstrates a high growth rate on crystalline cellulose; nonetheless, limited ethanol yields, failure to effectively metabolize xylan, and exhibiting insufficient growth on xylose or other pentoses have resulted in hemicellulolytic thermophiles being used in conjunction with \textit{C. thermocellum} to hydrolyze hemicellulose and ferment all sugars present in biomass.\textsuperscript{125,166}

Cocultures with \textit{C. thermocellum} have been reported with \textit{Methanobacterium thermoautotrophicum} for methane and acetate as well as \textit{Clostridium thermosaccharolyticum} for ethanol, butyrate, and acetate, which kinetically illustrated cellulose and cellobiose fermentation with enhanced ethanol yields from corn stover.\textsuperscript{167} Once \textit{Clostridium thermohydrosulfuricum} was isolated and discovered to ferment cellobiose, hexoses, and pentoses to ethanol, this too was coupled with \textit{C. thermocellum} as part of a CBP study.\textsuperscript{168} Unlike \textit{C. thermosaccharolyticum}, \textit{C. thermohydrosulfuricum} fails to produce butyrate and functions at thermophilic temperatures. More specifically, the microbial consortia, \textit{C. thermocellum} and \textit{C. thermohydrosulfuricum}, increased ethanol yields by two fold when compared to monocultures, due to the metabolic capability of \textit{C. thermocellum}'s cellulases to hydrolyze \(\alpha\)-cellulose and hemicellulose, enhanced utilization of mono- and disaccharides by \textit{C. thermohydrosulfuricum}, improved cellulose consumption, increased ethanol production, and decreased acetate production.\textsuperscript{167} This coculture was also shown to actively ferment MN300 cellulose, Avicel, Solka Floc, \(\text{SO}_2\)-treated wood, and steam-exploded wood.

More recently, Argyros et al\textsuperscript{69} cocultured \textit{C. thermocellum} and engineered \textit{T. saccharolyticum} for 146 hours, which yielded 38.1 g L\(^{-1}\) ethanol from 92.2 g L\(^{-1}\) Avicel, with concentrations of acetic and lactic acids falling below detectable limits. Due to saccharification being crucial in producing lignocellulosic-derived bioethanol during CBP, extreme pH and ethanol concentrations inhibit production efficiency; therefore, several saccharides derived from lignocellulosics were investigated utilizing \textit{C. thermocellum} and \textit{Clostridium thermolacticum}.\textsuperscript{169} The coculture actively fermented glucose, xylose, cellulose, and microcrystallized cellulose; in addition, the alkali environments proved conducive for ethanol production. While fermentation inhibition was observed when conditions exhibited high ethanol concentrations and extreme pH, initially low levels of ethanol resulted in an unforeseen stimulatory influence on ethanol production.\textsuperscript{169} Conversely, a novel coculture of \textit{C. thermocellum} and \textit{Thermoanaerobacterium aetereoense} with pretreated sugarcane bagasse (SCB) under mild alkali conditions for bio-hydrogen production was established, which demonstrated an economically viable and synergetic advantage in bio-hydrogen production over monocultures with untreated SCB.\textsuperscript{170} This successful microbial consortium is of interest as ethanol is another main product.

In addition to hemicellulolytic thermophiles, mesophiles, such as \textit{C. acetobutylicum} and \textit{Clostridium beijerinckii}, have enormous potential in coculturing CBP applications in conjunction with \textit{C. thermocellum} for \(n\)-butanol and ethanol production from lignocellulosics. In fact, alcoholic solvents with more than two carbons, such as butanol, are ideal candidates for alternative fuels, due to compatibility with existing infrastructure, low hygroscopicity, flexible blending ratios and comparable octane value, energy density, and Reid vapor pressure similar to that of gasoline and diesel.\textsuperscript{48,54,125,171–173} Currently, butanol is utilized for solvent extraction of fats, dye, nitro enamel, plastificator, butyl acetate, phenol formaldehyde resin, and oil-additive manufacturing.\textsuperscript{174} With these benefits, a sequential coculture approach with \textit{C. acetobutylicum} and \textit{C. thermocellum} grown on solka floc or a combination of solka floc and aspen wood xylan was implemented. The results indicated an efficient utilization of all hydrolysis products derived, which produced a 1.7- to 2.6-fold increase in total fermentation products.\textsuperscript{175} The majority of the fermentation products were acids; however, induction of solventogenesis by butyric acid was suggested as a solution. In regards to \textit{C. beijerinckii}, a novel strategy for sequential coculturing with \textit{C. thermocellum} was conducted to increase the production of alcoholic solvents from alkali-extracted corncobs.\textsuperscript{176} Under combinatory optimal culture conditions for sugar and solvent production, this CBP consortium degraded 88.9 g L\(^{-1}\) of carbonaceous material and produced 19.9 g L\(^{-1}\) of total products, with 10.9 g L\(^{-1}\) ethanol in 200 hours without the addition of butyrate.\textsuperscript{176} Nonetheless, the application of coculture CBP is vaguely understood with potential challenges of sole acid production and low product titers arising when symbiotically optimizing processing conditions, such as temperature, pH, and nutrient loads, through quorum sensing and biofilm formation for all strains as it relates to control, stability, and productivity.\textsuperscript{176–178}
Biofilms

Comprehensive implementation of microbial biofilms, structured communities immobilized in a matrix of extracellular polymers, has been expansively applied to bioremediation; however, the potential beneficial application of biofilms in CBP for the production of biofuels has not yet been extensively investigated. 179-185 Biofilms have the potential to improve lignocellulosic biomass conversion efficiency, due to the concentration of cell-associated hydrolytic enzymes at the biofilm–substrate interface leading to increased reaction rates, a layered microbial structure allowing sequential conversion of complex substrates, and cofermentation of hemicelluloses and pentoses with corresponding secretion and fungal–bacterial symbioses. 183 More impactful is the confined microenvironment within a biofilm selectively remunerating microbes with superior phenotypes deliberated from intercellular gene or signaling convergence, a process which is deficient in suspended cultures, by altering diffusion rates. 183,184 In addition, the immobilized property of biofilms, particularly when membrane attached, simplifies the separation of biofuels from microbial producer and liquid media as well as promotes retention of biomass for continued processing. With these benefits and importance of bacterial adherence in microbial lignocellulose conversion, the organization, dynamic formation, and carbon flow associated with biofilms of C. thermocellum was examined using noninvasive, in situ fluorescence imaging. 185 Investigation of the biofilm demonstrated the ability to extensively convert lignocellulosic substrates with a characteristic monolayered cell structure without an extracellular polymeric matrix, typically seen in biofilms. Moreover, cell division at the interface and terminal endospores appeared throughout all stages of biofilm growth. While utilizing continuous-flow reactors with an excessively high rate of dilution (2 h⁻¹), biofilm activity under low (44 g L⁻¹) and high (202 g L⁻¹) initial cellulose loadings resulted in fermentative catabolism being comparable, with 4% of metabolized sugar being utilized for cell production. 185 The study also observed 75.4% and 66.7% of the low and high cellulose loadings, respectively, being converted to primary carbon metabolites, including ethanol, acetic acid, lactic acid, and carbon dioxide. 185 Differences were also observed in ethanol/acetic acid ratios (g/g), suggesting that substrate availability for cell attachment rather than biofilm colonization rates govern the efficiency of cellulose conversion.

The importance of cellulose surface exposure to microbial hydrolysis has received little attention regardless of implied influence on conversion kinetics; however, spatial heterogeneity of fiber distribution in pure cellulose sheets made direct measurements of biofilm colonization and surface penetration unattainable. 102 This was circumvented by utilizing online measurements of carbon dioxide (CO₂) production in continuous-flow reactors, in conjunction with confocal imaging. 102 Results illustrated that the specific biofilm development rate of C. thermocellum has a significant effect on overall reactor kinetics during the period of microbial limitation. Due to biomass recalcitrance and the need to simplify enzymatic conversion, a single multi-species biofilm silicone membrane-attached reactor was designed for CBP that featured both aerobic and anaerobic conditions. 56 Concept feasibility was successfully validated by producing ethanol with a 67% yield from un-detoxified whole-slurry dilute acid-pretreated wheat straw by the combined action of T. reesei, S. cerevisiae, and Scheffersomyces stipitis. The results achieved accentuates the potential of the process as a versatile inexpensive sugar platform for holistically producing biofuels and value-added chemicals from lignocellulosic biomass by specifically compiled consortia of industrially proven robust microorganisms in a CBP system. 56 Concisely, immobilized biofilms address solvent productivity, inhibitor tolerance, scalability, electron flux, and excessive fermentation periods.

Industries with interest in CBP

While academic advancements have proven beneficial in the promotion of CBP, so have the industrial advancements of Mascoma and Qteros as they relate to a holistic approach for producing biofuels and value-added products from a microbial consortium with C. thermocellum for the economic sustainability of transportation and rural- and agricultural-based sectors. Mascoma Corporation, an innovative renewable-fuels company, was first to report the targeted metabolic engineering of cellulose-fermenting thermophile, C. thermocellum, to reduce the production of unwanted organic acid byproducts and rapidly degrade and metabolize cellulose with high conversion efficiency and tolerance to commercially relevant levels of ethanol. 156 To produce high rates, titers, and yields of biofuels and biochemicals from the conversion of starch, sugars, and cellulosics, Mascoma utilizes CBP, the novel breakthrough technology, and high-performing industrial biocatalysts. 187 Mascoma has engineered yeast, TransFerm, and TransFerm Yield* for improved hydrolysis and enhanced xylose fermentation capabilities to increase yields from CBP processes. 188 In 2011, Mascoma was awarded $80 million from the Department of Energy to assist in the design, construction,
and operation of a commercial-scale hardwood cellulosic ethanol facility in Kinross, MI, USA.\textsuperscript{199}

Qteros, a startup based in Marlborough, MA, USA, is also pursuing CBP with patented \textit{Clostridium phytofermentans}, an anaerobic microbe with the ability to both convert recalcitrant polysaccharides into available sugars and ferment hydrolyzate into fuel-grade ethanol as the primary fermentation product.\textsuperscript{190,191} This Q Microbe\textsuperscript{®} genome has been fully sequenced, which revealed characteristics directly relevant to the efficient and cost-effective production of ethanol, such as over 105 different genes responsible for producing lignocellulosic-degrading enzymes regulated by the type of growth substrate utilized. With $100,000 awarded from the Department of Energy, the Q Microbe\textsuperscript{®} has shown consistent saccharification efficiency across a broad range of feedstocks, including wheat straw, sugarcane bagasse, energy crops, such as switchgrass, and agricultural residues, such as corn stover, cob, and fiber.\textsuperscript{192,193}

**Conclusion**

Biofuel production from lignocellulosic biomass is extremely attractive because of its substantial and renewable availability, relative low cost, and minimal environmental impact. Conventional sugar and starch sources exhibit high theoretical biofuel yields; however, these resources are inadequate for global utilization and impacts on food security. A potential solution lies in agricultural waste and dedicated energy crops that lack human nutritional value and require less land, water, and energy. Furthermore, biofuel production can significantly reduce greenhouse gas emissions. While biochemical conversion systems demonstrate great promise for producing biofuels, challenges of efficiently converting lignocellulosic biomass to available monomers and subsequent fermentation to biofuels with a robust microbe at low operating costs still exist. To resolve limitations in industrial implementation, CBP systems have been explored, with configurations involving \textit{C. thermocellum} being most widely investigated. CBP has the potential to improve hydrolysis and fermentation efficiencies, eradicate contribution of exogenous saccharolytic enzymes, and eliminate inhibition effects, while requiring low energy with minimal environmental degradation to biologically convert lignocellulosic biomass to biofuels and other value-added chemicals. Hindrance of the overall ability and robustness of biocatalysts observed when incorporating genes from cellulolytic microbes for hydrolytic enzyme functionality has prompted the use of microbial consortia to achieve the advantages of a CBP operation, providing synergies that improve substrate use and increase biofuel yields. Ultimately, the economic production of sufficient quantities of biofuels will require advancements in feedstock development, conversion processes, system integration, marketing, and public policy as it relates to CBP.

**Disclosure**

The authors report no conflicts of interest in this work.

**References**


Recent advances in CBP for biofuel production


