A Genetic System for *Clostridium ljungdahlii*: a Chassis for Autotrophic Production of Biocommodities and a Model Homoacetogen

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Methods for genetic manipulation of *Clostridium ljungdahlii* are of interest because of the potential for production of fuels and other biocommodities from carbon dioxide via microbial electrosynthesis or more traditional modes of autotrophy with hydrogen or carbon monoxide as the electron donor. Furthermore, acetogenesis plays an important role in the global carbon cycle. Gene deletion strategies required for physiological studies of *C. ljungdahlii* have not previously been demonstrated. An electro-portion procedure for introducing plasmids was optimized, and four different replicative origins for plasmid propagation in *C. ljungdahlii* were identified. Chromosomal gene deletion via double-crossover homologous recombination with a suicide vector was demonstrated initially with deletion of the gene for FliA, a putative sigma factor involved in flagellar biogenesis and motility in *C. ljungdahlii*. Deletion of *fliA* yielded a strain that lacked flagella and was not motile. To evaluate the potential utility of gene deletions for functional genomic studies and to redirect carbon and electron flow, the genes for the putative bifunctional aldehyde/alcohol dehydrogenases, *adhE1* and *adhE2*, were deleted individually or together. Deletion of *adhE1*, but not *adhE2*, diminished ethanol production with a corresponding carbon recovery in acetate. The double deletion mutant had a phenotype similar to that of the *adhE1*-deficient strain. Expression of *adhE1* in *trans* partially restored the capacity for ethanol production. These results demonstrate the feasibility of genetic investigations of acetogen physiology and the potential for genetic manipulation of *C. ljungdahlii* to optimize autotrophic biocommodity production.

Homocetogenic microorganisms have unique metabolic pathways and energy conservation mechanisms that could substantially enhance microbial strain design options for the production of fuels and other biocommodities. Furthermore, homocetogens play an important role in the carbon cycle of a diversity of anaerobic environments (1, 2). However, the understanding of homocetogenic physiology and the development of a homocetogenic microorganism as a chassis for the production of biocommodities have been limited by a lack of methods for genetic manipulation.

The homocetogen *Clostridium ljungdahlii* has been proposed as a potential chassis for biocommodity production (3). Like other acetogens, *C. ljungdahlii* metabolizes sugars through the Embden-Meyerhof-Parnas pathway, and CO₂ released during glycolysis is fixed via the Wood-Ljungdahl pathway, which makes it possible to recover completely the carbon from sugars in organic end products (4, 5), i.e., C₆H₁₂O₆ + 2H₂O → 2CH₃COOH + 2CO₂ + 8H⁺ + 8e⁻ and 2CO₂ + 8H⁺ + 8e⁻ → CH₃COOH + 2H₂O. Depending on the growth conditions, other organic products such as ethanol and 2,3-butanediol are also generated (3, 6).

*C. ljungdahlii* can grow autotrophically using H₂ and/or CO as the electron donor, reducing CO₂ via the Wood-Ljungdahl pathway to produce organic products (3, 5, 6). The ability of *C. ljungdahlii* to use CO as an electron donor is significant because CO is a waste product of steel manufacturing and a major component of the syngas produced from the gasification of municipal waste and other organic feedstocks (7, 8). Biocommodity production using syngas as an intermediate is an attractive strategy because organic feedstocks, such as lignocellulosic biomass, municipal waste, and plastics, are difficult for microorganisms to degrade directly (9–11).

Furthermore, *C. ljungdahlii* was able to grow with electrons derived directly from an electrode as the electron donor coupled to reduction of CO₂ to produce acetate (12). Electrode-driven reduction of carbon dioxide via acetogenic microorganisms, known as microbial electrosynthesis (13, 14), is a strategy for conversion of CO₂ to organic commodities without a biomass intermediate. Biofilms of acetogenic microorganisms colonize surfaces of cathodes and directly convert CO₂ to organic products that are excreted from the cells. When microbial electrosynthesis is powered with electricity derived from solar technology, it is an artificial form of photosynthesis that converts CO₂ to desired products much more efficiently and in a more environmentally sustainable manner than biomass-based approaches (13, 15).

The development of *C. ljungdahlii* as a chassis for production of biocommodities will require strategies for genetic manipulation. Although heterologous gene expression by introduction of a plasmid in *C. ljungdahlii* was reported (3), the efficiency of plasmid transformation by the reported method was low (M. Köpke, personal communication). In general, genetic manipulation of clostridia has been difficult (8, 16–18). Limiting factors have been a strong restriction-modification system, high nuclease activity that can degrade foreign DNA, and the thick outer layers of these Gram-positive organisms. Even when the restriction-modification system barrier has been overcome by protecting DNA with *in*
vivo or in vitro methylation (19, 20), homologous recombination frequencies have been low, with single-crossover recombination as the predominant event (21–23). Consequently, not many Clostridium mutants have been produced in the last 20 years (21, 22, 24–26). However, with renewed interest in biotechnological applications of Clostridium species there have been renewed efforts to develop strategies for genetic modification, leading to such recent developments as the following: replicative plasmids for gene deletion (27); counterselection methods to improve the efficiency of gene deletion and to select for double-crossover events (28–31); the use of a promoterless antibiotic resistance cassette in conjunction with a constitutively expressed promoter to select for double-crossover events (32); the use of the Bacillus subtilis recF gene, which codes for resolvase, to increase homologous recombination (33–36); the use of the bacterial mobile group II intron as an alternative to homologous recombination to disrupt a gene (16, 37–40); and the use of antisense RNA to downregulate a target gene product (41, 42). Here we report on a more efficient gene (16, 37–40); and the use of antisense RNA to downregulate a target gene product (41, 42). Here we report on a more efficient gene (16, 37–40); and the use of antisense RNA to downregulate a target gene product (41, 42). Here we report on a more efficient gene (16, 37–40); and the use of antisense RNA to downregulate a target gene product (41, 42). Here we report on a more efficient gene (16, 37–40); and the use of antisense RNA to downregulate a target gene product (41, 42). Here we report on a more efficient gene (16, 37–40); and the use of antisense RNA to downregulate a target gene product (41, 42). Here we report on a more efficient gene (16, 37–40); and the use of antisense RNA to downregulate a target gene product (41, 42). Here we report on a more efficient gene.
in a secondary container with a petri dish containing palladium pellets in order to eliminate any residual oxygen.

Verification of the presence of plasmids in *C. ljungdahlii* transformants was carried out by either of two methods: (i) restriction analysis of plasmid DNA isolated from an *E. coli* strain transformed with plasmid DNA isolated from *C. ljungdahlii* transformants or (ii) colony PCR analysis of *C. ljungdahlii* transformants to detect the catP gene (primer sequences are listed in Table S1 in the supplemental material).

**Construction of a mutant allele to disrupt the flia gene.** All primers are listed in Table S1 in the supplemental material. The gene *flia* (**CLJU_c10410**) was replaced with the gene *ermC*, such that the coding region from 83 Lys to 220 Val was deleted. DNA fragments containing the upstream (883 bp) and downstream (882 bp) regions of *flia* were amplified by PCR with chromosomal DNA as a template. The *ermC* cassette was amplified by PCR with pCL1 as a template. The PCR products were cloned separately in a plasmid, and their sequences were confirmed. The upstream region of the *flia* gene, the downstream region of the *flia* gene, and the *ermC* gene were prepared by digesting the plasmids with XbaI and EcoRI, HindIII and Xhol, and EcoRI and HindIII, respectively, and were cloned in the XbaI and Xhol sites of pBluescript II KSI (−) (Stratagene). The plasmid (pBuTU-adfIA-ermC) thus constructed was electroporated into the wild-type *C. ljungdahlii* strain as described above. Transformants resistant to clarithromycin were selected as described above. The genotype-primers were examined by PCR amplification with primers *flia*-1 and *flia*-4.

**Construction of mutant alleles to disrupt adhE1, adhE2, or both.** The coding region from 327 Gln to 685 Pro of the gene *adhE1* (**CLJU_c16510**) was replaced with the gene *ermC*. Upstream (977 bp) and downstream (1,024 bp) regions of *adhE1* were amplified by PCR with wild-type genomic DNA as a template. The coding region of the *ermC* gene was amplified by PCR with pCL1 as a template. The SacI site within the multiple-cloning sites in pBluescript II KSI(−) was deleted by digestion of the vector with SacI, filling in with Klenow fragment, and vector ligation. The resulting vector, designated pBuKsII-SacI, was sequenced to confirm that the SacI site was absent. The upstream and downstream regions and the *ermC* coding region were digested with XbaI and SacI, HindIII and Xhol, and SacI and HindIII, respectively, and were cloned into the XbaI and Xhol sites of pBuKsII-SacI.

The coding region from 34 Val to 775 Arg of *adhE2* (**CLJU_c16520**) was replaced with the gene *ermC*. For construction of a mutant allele to disrupt *adhE2*, the upstream (977 bp) and downstream (997 bp) regions of *adhE2* were amplified by PCR. The *ermC* cassette was amplified with the same primers as for the *flia* mutant allele. The three pieces were digested with the respective restriction enzymes and cloned into pBluescript II KSI(−) as described above.

For disruption of both *adhE1* and *adhE2*, the coding region from 34 Val of *adhE1* to 775 Arg of *adhE2* was replaced with the gene *ermC*. The 904-bp upstream region of *adhE1* and the 997-bp downstream region of *adhE2* were amplified by PCR and the mutant allele was constructed as described above.

**Expression of adhE1 in trans.** The complete coding sequence of *adhE1* was amplified with Phusion DNA polymerase (New England Biolabs). The *adhE1* coding sequence was digested with NdeI and BamHI and inserted into the NdeI and BamHI sites of the expression vector pMTL83152 (45) to generate plasmid pMTL83152-adhE1. The *adhE1* gene was then sequenced to confirm that no mutations were introduced during amplification. The pMTL83152-adhE1 plasmid was then electroporated into either the *adhE1* or the *adhE1 adehE2 deletion mutants. The presence of the plasmid was confirmed by PCR and plasmid preparation.

**Analytical techniques.** Acetate was measured via high-performance liquid chromatography (HPLC) as previously described (12). Ethanol was measured with a gas chromatograph as previously described (46). Cell growth was monitored using a Genesys 2 spectrophotometer (Spectronic Instruments, Rochester, NY) at 600 nm. Cell numbers were determined by epifluorescence microscopy using acidine orange staining (47).

**Transmission electron microscopy.** Both wild-type and *flia* deletion mutant cells grown in PETC medium were placed on 400-mesh carbon-coated copper grids, incubated for 5 min, and then stained with 2% uranyl acetate. Cell appendages were observed using a Tecnai 12 transmission electron microscope at an accelerating voltage of 100 kV. Images were taken digitally with the Teitz TLC camera system.

**RESULTS AND DISCUSSION**

**Growth on solid medium.** Conditions for growth of *C. ljungdahlii* on solidified media were evaluated in order to obtain single colonies of *C. ljungdahlii* with a high plating efficiency for isolation of mutant strains. The PTEC medium (ATCC 1754) that was used routinely for maintenance of *C. ljungdahlii* cultures was unsuitable for sustaining growth on solidified medium. On average, fewer than 5 colonies were obtained when ~100 cells were plated on the PTEC agar medium. The poor plating efficiencies might be due to a shift in pH caused by differences in gas compositions between the culture tube containing the liquid medium (100% CO2) and the anaerobic chamber (10% CO2, 7% H2, and 83% N2), where the plates were incubated. In contrast, the plating efficiency with RCM medium was ~30%. Furthermore, if cells were added to molten agar (~45°C), plating efficiencies were 72% ± 10% (mean ± standard deviation; n = 3). Single colonies were visible within 3 days.

The MCIs of thiamphenicol and clarithromycin were determined with the molten agar plating method. The growth of ca. 108 cells on solid medium was inhibited by thiamphenicol (5 µg/ml) or clarithromycin (4 µg/ml).

**Development of an electroporation protocol and identification of E. coli-C. ljungdahlii shuttle vectors.** A transformation protocol for *C. ljungdahlii* was recently reported (3, 48). However, the reported protocol did not consistently yield transformants with the *E. coli-Clostridium* shuttle vector pIMP1 (M. Köpke, personal communication). After the evaluation of the protocol, several changes were made, including changes in (i) the pH of the wash buffer, (ii) the density of competent cells, and (iii) the electroporation procedures (Table 1). With this revised protocol, transformants were consistently obtained with plasmid pCL1, a derivative of pIMP1 (0.2 transformants/µg DNA) (Table 2). However, the transformation efficiency was still poor, possibly due to the plasmid not being stably maintained.

In order to determine whether plasmids known to be stably maintained in other *Clostridium* species (49) might be more effectively propagated in *C. ljungdahlii*, plasmids pQexp (40) and pJIR750ai (38), with origins of replication from pAMB1 and pIP404, respectively, were tested. Both plasmids were more efficiently transformed than pIMP1 or pCL1 (Table 2). The transformation efficiencies for pQexp and pJIR750ai were 0.7 and 7 transformants/µg DNA, respectively (Table 2). The presence of these plasmids in *C. ljungdahlii* was confirmed with restriction analysis and/or colony PCR (Fig. 1). These results indicate that replication origins from pQexp and pJIR750ai are functional in *C. ljungdahlii*.

The transformation protocol was further optimized with pCL2, which was constructed from pJIR750ai by deleting the region for the group II intron insertion that is not required for its propagation in *C. ljungdahlii*. One modification in the optimized protocol (Table 1) was to change the growth phase at which cells were harvested to prepare competent cells, because it is known that growth phase can affect competence and the optimal growth
With the optimized conditions, the transformation efficiency of pCL1 using the final optimized conditions was 1.1 \times 10^4 (Table 2). The transformation efficiency of pCL1 was not due to selections with different antibiotics. The poor transformation efficiency of pCL1-catP that has the same origin of replication as pCL1 but carries the same antibiotic resistance gene as pCL2 (data not shown), suggesting that the poor transformation efficiency of pCL1 was not due to selections with different antibiotics. The competence of these frozen competent cells remains consistent for about 1 month (data not shown).

After the optimization of the transformation protocol with pCL2, plasmids from the pMTL80000 modular system (45) with origins of replication other than pAM\beta_1 and pIP404 were made available to us. The pBP1 and pCB102 origins of replication were functional in \textit{C. ljungdahlii}, whereas the pCD6 origin of replication was not. The transformation efficiency for plasmids with either a pBP1 or pCB102 origin of replication was somewhat lower than that of pCL2 (Table 2).

In \textit{in vivo} or \textit{in vitro} methylation of plasmid DNA to be transformed stimulates the transformation efficiency in some \textit{Clostridium} species (19, 20), and this procedure was employed in \textit{C. ljungdahlii} in the previously reported protocol (3). However, \textit{in vivo}

### TABLE 1 Changes in the optimized transformation protocol for \textit{C. ljungdahlii}

<table>
<thead>
<tr>
<th>Step or parameter</th>
<th>Original procedure (3, 48)</th>
<th>Optimized procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Preparation of competent cells</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Growth phase for harvesting (OD_{600})</td>
<td>0.3–0.7</td>
<td>0.2–0.3</td>
</tr>
<tr>
<td>pH of wash buffer</td>
<td>7.4</td>
<td>6</td>
</tr>
<tr>
<td>Resuspension buffer</td>
<td>SMP(^a) (pH 7.4)</td>
<td>SMP(^a) (pH 6) with 10% DMSO(^b)</td>
</tr>
<tr>
<td>Cell density of competent cells</td>
<td>~80(\times) concentrated from the original cultures</td>
<td>10(^{10}-10^{15}) cells/ml (~1,000(\times) concentrated)</td>
</tr>
<tr>
<td>Freeze-thaw</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Thawing of cells</td>
<td>No</td>
<td>1 min on ice</td>
</tr>
</tbody>
</table>

**Preparation of plasmids**

- *E. coli* strain for plasmid preparation: Yes (20) / No

**Electroporation procedures**

<table>
<thead>
<tr>
<th>Step or parameter</th>
<th>Original procedure (3, 48)</th>
<th>Optimized procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell vol ((\mu)l)</td>
<td>600</td>
<td>25</td>
</tr>
<tr>
<td>Preincubation with plasmid</td>
<td>5 min on ice</td>
<td>No</td>
</tr>
<tr>
<td>Amount of plasmid DNA ((\mu)g)</td>
<td>0.1–1.5</td>
<td>1–5</td>
</tr>
<tr>
<td>Electroporation cuvette gap (cm)</td>
<td>0.4</td>
<td>0.1</td>
</tr>
<tr>
<td>Electric pulse</td>
<td>2.5 kV, 600 (\Omega), 25 (\mu)F</td>
<td>0.625 kV, 600 (\Omega), 25 (\mu)F</td>
</tr>
<tr>
<td>Recovery</td>
<td>5 ml PETC; 37°C, until clear growth occurs</td>
<td>10 ml PETC; 37°C, 9–12 h</td>
</tr>
<tr>
<td>Plating</td>
<td>Liquid cultures on a solid agar plate</td>
<td>Liquid cultures mixed with molten agar</td>
</tr>
<tr>
<td>Antibiotic concn ((\mu)g/ml)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Clarithromycin (5), thiamphenicol (20)</td>
<td>Clarithromycin (4), thiamphenicol (5)</td>
<td></td>
</tr>
</tbody>
</table>

\(^a\) SMP, 270 mM sucrose, 1 mM MgCl\(_2\), and 7 mM phosphate buffer.

\(^b\) DMSO, dimethyl sulfoxide.

**TABLE 2 Transformation of \textit{C. ljungdahlii} with different plasmids**

<table>
<thead>
<tr>
<th>Plasmid</th>
<th>Origins of replication (\textit{E. coli}, \textit{Clostridium})(^a)</th>
<th>Antibiotic resistance gene(s)(^b)</th>
<th>Transformation efficiency (transformants/(\mu)g DNA), mean (\pm) SD ((n))</th>
</tr>
</thead>
<tbody>
<tr>
<td>pCL1</td>
<td>pMB1, pLM13</td>
<td>bla, ermC</td>
<td>First optimization(^c) Final protocol</td>
</tr>
<tr>
<td>pQexp</td>
<td>pMB1, pAM\beta_1</td>
<td>ermB</td>
<td>0.2 (\pm) 0 (5) 1.1 (\pm) 0.1 (3)</td>
</tr>
<tr>
<td>pIR750ai</td>
<td>pMB1, pIP404</td>
<td>catP</td>
<td>0.7 (\pm) 0.5 (3) 14.9 (\pm) 4.9 (6)</td>
</tr>
<tr>
<td>pCL2</td>
<td>pMB1, pIP404</td>
<td>catP</td>
<td>0.9 (1) ND(^d)</td>
</tr>
<tr>
<td>pMTL82151(^e)</td>
<td>CoEl1, pBP1</td>
<td>catP</td>
<td>(1.7 (\pm) 0.6) (\times) 10(^4) (5)</td>
</tr>
<tr>
<td>pMTL83151(^e)</td>
<td>CoEl1, pCB102</td>
<td>catP</td>
<td>(3.8 (\pm) 0.2) (\times) 10(^3) (3)</td>
</tr>
</tbody>
</table>

\(^a\) All plasmids are \textit{E. coli}-\textit{Clostridium} shuttle vectors. \textit{E. coli} origins of replication, pMB1 and CoEl1; \textit{Clostridium} origins of replication, pLM13, pAM\beta_1, pIP404, pBP1, and pCB102.

\(^b\) bla, ampicillin resistance; erm\(\beta\) or erm\(\beta\), clarithromycin/erythromycin resistance; catP, thiamphenicol/chloramphenicol resistance.

\(^c\) The first optimization included the changes of wash buffer pH, cell density of the competent cells, and electroporation procedures (details are listed in Table 1).

\(^d\) ND, not determined.

\(^e\) The plasmid became available after the optimized protocol was developed.
methyltransferase that contributed to ethanol production in C. ljungdahlii. Gene replacement via homologous recombination. In order to expand the available genetic tools for C. ljungdahlii, genetic modification of the C. ljungdahlii chromosome was examined with the improved transformation protocol described above. Homologous recombination was evaluated with the fliA gene (CLJU_c10410), which encodes a putative sigma factor of RNA polymerase known to control the expression of genes involved in flagellar biosynthesis and motility in other bacteria (53, 54). Deletion of fliA was expected to result in the loss of flagella and motility in C. ljungdahlii.

Initial attempts to obtain a fliA deletion mutant with introduction of a linear DNA fragment prepared by digesting the plasmid pBuTU-ΔfliA-ermC with XhoI were not successful. No transformants were obtained. Transformants were obtained only with the introduction of the intact plasmid pBuTU-ΔfliA-ermC into C. ljungdahlii competent cells. PCR analysis demonstrated both single- and double-crossover homologous recombination (Fig. 2B). The frequencies of the double-crossover events were ca. 30%. This result demonstrated that a strategy for mutagenesis via homologous recombination with a suicide vector was possible.

Transmission electron microscopy revealed that wild-type cells produced multiple flagella, whereas the mutant did not (Fig. 3A). Deletion of the fliA gene did not affect cell growth in the PETC liquid medium with fructose. However, when the wild-type and the mutant cells were spotted onto YTF soft agar plates, the mutant cells were nonmotile, whereas the wild-type cells were motile and formed a larger growth zone than the mutant cells (Fig. 3B). These results demonstrated that it was possible to create a deletion mutant of C. ljungdahlii by double-crossover homologous recombination.

Identification of a bifunctional aldehyde/alcohol dehydrogenase that contributes to ethanol production in C. ljungdahlii. In order to determine whether carbon and electron flow could be altered by gene deletion, the possibility of diminishing ethanol production was evaluated for proof of concept. CLJU_c16510 and CLJU_c16520, designated adhE1 and adhE2, respectively, have
been annotated to code for bifunctional aldehyde/alcohol dehydrogenases (3) and thus have the potential to promote ethanol production. These genes are located next to each other and possibly are transcribed from the same promoter. Therefore, care was taken when designing the mutagenesis cassette to avoid polar effects. The mutagenesis cassette for deletion of \textit{adhE1} was designed to introduce two stop codons (TAA and TAA) after the sequence for amino acid 326 (Leu), followed by a promoterless \textit{ermC} and then the downstream homologous region. This ensured that \textit{adhE2} was transcribed from the original promoter sequence. The mutagenesis cassettes for deletion of either \textit{adhE2} or both \textit{adhE1} and \textit{adhE2} were designed as described above for deletion of \textit{fliA} because polar effects were not a concern. All three mutants were isolated from agar plates supplemented with fructose and clari-thromycin. Double-crossover events for all three mutants were confirmed by PCR analysis (data not shown).

The \textit{adhE2} deletion mutant grew on fructose as well as the wild type and produced similar amounts of ethanol and acetate (Fig. 4; Table 3). Deleting \textit{adhE1}, either alone or in combination with \textit{adhE2}, slightly diminished the growth yield, increased the doubling time, and significantly inhibited ethanol production while increasing acetate production (Fig. 4; Table 3). The amounts of ethanol produced by the \textit{adhE1} deletion strain and the \textit{adhE1 adhE2} double deletion strain were similar. In both strains, ethanol production was decreased to ca. 15% of that in the wild type (Table 3). Within the error of the measurements, the decreased carbon recovery in ethanol in the \textit{adhE1} deletion or the \textit{adhE1 adhE2} double deletion strain could be accounted for by an increase in carbon recovery in acetate over that produced by the wild type (Table 3). The slightly decreased cell yields and increased doubling times in the absence of AdhE1 or both AdhE1 and AdhE2 may suggest that these mutants were not able to dispose of reducing equivalents as efficiently as the wild type.

![FIG 3](image-url)  
**FIG 3** Characterization of the \textit{fliA} deletion mutant. (A) Production of flagella. Transmission electron micrographs of negatively stained \textit{C. ljungdahlii} wild-type cells (left panel) and the \textit{fliA} deletion mutant (right panel) showed that the mutant did not produce any flagella, whereas the wild-type cells produced flagella as indicated by arrows. Scale bars in both panels represent 2,000 nm. (B) Motility assay. The \textit{fliA} deletion mutant was not motile when spotted on a YTF soft agar plate on which the wild-type cells were motile and thus exhibited a larger growth zone. The scale bar represents 3 cm.

![FIG 4](image-url)  
**FIG 4** Cell growth and production of ethanol and acetate by the \textit{C. ljungdahlii} wild-type strain, bifunctional aldehyde/alcohol dehydrogenase deletion mutants (\textit{\Delta adhE1}, \textit{\Delta adhE2}, and \textit{\Delta adhE1 \Delta adhE2}), and the complemented strains (\textit{\Delta adhE1/adhE1} and \textit{\Delta adhE1 \Delta adhE2/adhE1}). (A) Cell growth (\textit{A}_{600}). (B) Ethanol production (mM). (C) Acetate production (mM). Symbols: filled squares, wild type; green triangles, \textit{\Delta adhE1}; orange circles, \textit{\Delta adhE2}; red diamonds, \textit{\Delta adhE1 \Delta adhE2}; purple crosses, \textit{\Delta adhE1/adhE1}; and maroon crosses, \textit{\Delta adhE1 \Delta adhE2/adhE1}. Data are the means ± standard deviations of quadruplicates.
TABLE 3 Production of acetate, ethanol, and biomass by the wild type, bifunctional aldehyde/alcohol dehydrogenase gene deletion mutants, and complemented strains

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value for strain*:</th>
<th>WT</th>
<th>ΔadhE1</th>
<th>ΔadhE2</th>
<th>ΔadhE1/ΔadhE2</th>
<th>ΔadhE1</th>
<th>ΔadhE2</th>
<th>ΔadhE1/ΔadhE2</th>
<th>ΔadhE1 ΔadhE2 /ΔadhE1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ethanol production (mM)</td>
<td>28.9 ± 3.4</td>
<td>4.7 ± 2.3</td>
<td>27.1 ± 0.5</td>
<td>4.4 ± 0.6</td>
<td>14.7 ± 0.4</td>
<td>11.5 ± 1.3</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Acetate production (mM)</td>
<td>38.5 ± 2.3</td>
<td>64.1 ± 1.5</td>
<td>41.9 ± 3.9</td>
<td>63.0 ± 1.8</td>
<td>53.4 ± 3.1</td>
<td>60.8 ± 1.7</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cell yield (A&lt;sub&gt;600&lt;/sub&gt;)</td>
<td>1.4 ± 0.1</td>
<td>1.3 ± 0.2</td>
<td>1.5 ± 0.1</td>
<td>1.1 ± 0.0</td>
<td>1.2 ± 0.1</td>
<td>1.2 ± 0.1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Doubling time (h)</td>
<td>5.8 ± 0.2</td>
<td>8.4 ± 0.4</td>
<td>5.7 ± 0.1</td>
<td>7.3 ± 0.2</td>
<td>8.7 ± 0.5</td>
<td>9.5 ± 1.0</td>
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</tbody>
</table>

* Data are the means ± standard deviations of quadruplicates. WT, wild-type C. ljungdahlii strain; ΔadhE1, ΔadhE1 deletion mutant; ΔadhE2, ΔadhE2 deletion mutant; ΔadhE1/ΔadhE2, ΔadhE1 and ΔadhE2 double deletion mutant; ΔadhE1 trans ΔadhE1 ΔadhE2, ΔadhE1 and ΔadhE2 double deletion mutant; ΔadhE1 ΔadhE1/ΔadhE2, ΔadhE1 deletion mutant with the ΔadhE1 gene expressed in trans; ΔadhE1 ΔadhE2/ΔadhE1, ΔadhE1 and ΔadhE2 double deletion mutant with the ΔadhE1 gene expressed in trans.

When ΔadhE1 was expressed in trans under the control of a C. acetobutylicum thiolase gene promoter on a plasmid, ethanol production in the ΔadhE1-deficient strain was tripled, with a corresponding decrease in acetate production, maintaining the carbon balance in ethanol and acetate comparable to that for the wild type and the uncomplemented ΔadhE1-deficient strain (Table 3; Fig. 4). In a similar manner, expressing ΔadhE1 in trans in the strain deficient in both ΔadhE1 and ΔadhE2 increased ethanol production and decreased acetate production, with an overall carbon recovery in acetate and ethanol comparable to that for the wild type (Fig. 4; Table 3). The longer doubling time of the complemented strain may be due to the addition of thiamphenicol to the medium, Table 3). The longer doubling time of the complemented strain

These results suggest that AdhE1 is an important bifunctional aldehyde/alcohol dehydrogenase in C. ljungdahlii. This finding demonstrates that it is now possible to elucidate gene function in C. ljungdahlii via genetic manipulations. The results suggest that AdhE2 does not play a role in ethanol production, at least under the conditions evaluated, even though AdhE2 shares 88% identity with AdhE1. This finding emphasizes the importance of functional genomic studies in order to understand cellular metabolism. The results also demonstrate that it is possible to redirect carbon and electron flow in C. ljungdahlii with a gene deletion without significantly impairing overall growth. This indicates that the metabolic engineering of C. ljungdahlii is now feasible.

Conclusions. The ability to effectively express foreign genes in C. ljungdahlii and to delete genes via homologous recombination is expected to substantially promote the development of this organism as a chassis for the production of biocommodities. For example, the wild-type C. ljungdahlii can produce multiple organic products from acetyl coenzyme A (acytL-CoA), the central intermediate in the Wood-Ljungdhal pathway. Efficient production of desired commodities from acetyl-CoA will require disabling these competing pathways. As demonstrated in this study, deletion of the ethanol production pathway led to increased production of acetate in C. ljungdahlii. The homologous recombination method described here should also be applicable for introducing desired metabolic genes or reporters into the chromosome.

Furthermore, the ability to genetically manipulate C. ljungdahlii should aid in basic studies of homoacetogen physiology. Although important aspects of the physiology of acetogens have been elucidated with elegant biochemical investigations, much is still unknown about mechanisms for energy conservation and regulation of gene expression in these organisms (1, 55, 56). Tools for facile genetic manipulation of C. ljungdahlii should enhance further investigation of homoacetogenesis.

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