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Title: Induction of the *celC* operon of *Clostridium thermocellum* by laminaribiose

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Abstract

Clostridium thermocellum, an anaerobic, thermophilic, cellulolytic, and ethanogenic bacterium, produces an extracellular cellulase complex with more than 70 subunits (the cellulosome). It also produces many free glycosyl hydrolases. How the organism commands such a large number of genes and proteins for biomass degradation is an intriguing yet unresolved question. We identified *glyR3*, which is co-transcribed with the cellulase/hemicellulase genes *celC* and *licA*, as a cellulase transcription regulator. The gel shift assay (EMSA) revealed that the recombinant GlyR3 bound specifically to the *celC* promoter region. GlyR3 was also identified from the lysate of the lichenan-grown cells, which bound to the same sequence. DNase I footprinting and competitive EMSA showed the binding site to be an 18 bp palindromic sequence with one mismatch. The DNA-binding activity was specifically inhibited by laminaribiose, a β-1-3 linked glucose dimer, in a dose-dependent manner. In *in vitro* transcription analysis, *celC* expression was repressed by rGlyR3 in a dose-dependent manner. The repression was relieved by laminaribiose, also in a dose-dependent manner. These results indicate that GlyR3 is a negative regulator of the *celC* operon consisting of *celC*, *glyR3*, and *licA*, and inducible by laminaribiose. Thus the bacterium may modulate the biosynthesis of its enzyme components to optimize its activity on an available biomass substrate, in this case, β-1-3 glucan since both CelC and LicA are active on the substrate. The results further indicate that regulation of the degradative enzymes can be accomplished through soluble sugars generated from the insoluble substrate by the action of the enzymes.

Introduction

C. thermocellum is an anaerobic, thermophilic, cellulolytic, and ethanogenic bacterium. It produces a cellulase system highly active on crystalline cellulose (1). The extracellular cellulase components form an ordered protein complex termed the cellulosome (2). In addition, many free glycosyl hydrolases are produced. The core of the cellulosome is CipA, a 250-kDa non-catalytic, scaffold protein (2-5). CipA contains nine cohesin domains. Binding to the cohesin is mediated by the dockerin domain borne on the catalytic subunit (6-9). CipA further contains a cellulose-binding module (CBM), which anchors the array of catalytic components to the cellulose surface (4, 10, 11).

Searching the genome sequence of *C. thermocellum* revealed more than 70 genes encoding dockerin-containing proteins, which are presumed to be the cellulosome components (12, 13). Thus, including the genes encoding the cellulosome components, the scaffold proteins, and the free enzymes but without counting the regulatory and sugar-transport genes, there are likely more than 100 genes involved in biomass degradation by this bacterium. How the organism regulates the expression of such a large number of genes and proteins for biomass degradation is an intriguing question, yet so little is known. The issue is further complicated by the fact that biomass is typically a solid substrate incapable of diffusing into the cell to regulate gene expression.

It has been demonstrated that production of the overall cellulase activity by *C. thermocellum* is influenced by the carbon source (14-18). But it is not clear how many individual genes are subject to carbon source regulation. Recent studies focus on a few specific cellulase components. The most abundant catalytic component of the cellulosome is an exoglucanase called CelS (10, 11, 19-24). At the protein level, CelS (25, 26) and CipA (26) are upregulated by

growth on cellulose as compared to cellobiose. In addition, growth rate has been shown to affect the expression of several cellulase genes. The expression of *celS* is growth rate-dependent as revealed by chemostat experiments (25, 27). Similarly, the transcript levels of *cipA*, *olpB*, *orf2p*, *celB*, *celG*, and *celD* are dependent on growth rate (28, 29). In contrast, the expression of *sdbA* and *xynC* are independent from growth rate.

Despite these studies, molecular mechanisms governing the carbon-source regulation of the cellulase biosynthesis in this bacterium remain unidentified. Here we report the first cellulase gene transcriptional regulatory protein, GlyR3, of *C. thermocellum*. GlyR3 specifically binds to an 18-bp near perfect palindrome in the promoter region of the non-cellulosomal cellulase gene *celC*. GlyR3 is shown to repress *celC* in an *in vitro* transcription assay. The repression is reversed by laminaribiose, a β-1-3 linked glucose dimer, which inhibits GlyR3's DNA-binding activity. The negative regulation is the first cellulase regulation mechanism found in *C. thermocellum*. Since *celC*, *glyR3*, and *licA* are co-transcribed into a polycistronic mRNA (M. Newcomb and J.H. D. Wu, submitted for publication), these three genes form a cellulase operon, the first demonstrated in *C. thermocellum*.

Results

GlyR3 Structure. GlyR3 (353 amino acids) is homologous to LacI (360 amino acids) of *Escherichia coli* (27% identical and 49% similar; Fig. 1). BLAST search (30) revealed two other *C. thermocellum* proteins homologous to LacI, GlyR1 (342 amino acids, 22% identical and 43% similar) and GlyR2 (345 amino acids, 29% identical and 49% similar). GlyR3 was particularly interesting because its gene is a member of the *celC* gene cluster and is co-transcribed with *celC* and *licA*, two cellulase or hemicellulase genes (Fig. 2A; M. Newcomb and J.H. D. Wu, submitted

for publication). GlyR3, as GlyR1 and GlyR2, contains two distinct domains (31, 32): a helix-turn-helix DNA-binding motif at the N-terminal end and a sugar-binding domain at the C-terminal end (Fig 2B), suggesting that it is a regulatory protein controlled by a sugar. The location of *glyR3* suggests that GlyR3 controls the expression of the *celC* gene cluster by binding to its promoter region.

rGlyR3 Binds to the *celC* Promoter Region. To study the function of GlyR3, we cloned its gene into *E. coli* with a chitin-binding domain (CBD) fused to the C-terminus of the recombinant protein. Fusion with the CBD facilitated purification by affinity chromatography using chitin beads as the affinity ligand. rGlyR3 was cleaved off from the CBD, which bound to the chitin bead, by dithiothreitol (DTT) treatment and appeared as the predominant protein species with the expected size (39,330 daltons) on an SDS-gel (data not shown). The ability of rGlyR3 to bind to the promoter region of the *celC* gene cluster was examined by EMSA (electrophoretic mobility shift assay). The EMSA probe, prepared by PCR using biotin-labeled primers 3 and 5 (Table 1), represented the DNA sequence 100 to 200 bp upstream from the start codon of the *celC* gene, considered as the promoter region. In EMSA, adding rGlyR3 to the reaction resulted in gel-shift of the probe (lane 2, Fig. 3), indicating that rGlyR3 binds to the *celC* promoter region. On the other hand, under the same condition, rGlyR3 did not bind to the probe representing the CipA promoter region (data not shown), indicating that the binding of rGlyR3 is specific. The apparent dissociation constant (K_D), estimated as the concentration of rGlyR3 needed to shift 50% of the probe, was 4×10^{-14} M.

To determine that GlyR3 is indeed expressed *in vivo* and the protein thus expressed binds to the same sequence, the EMSA was carried out using the cell lysate of *C. thermocellum* as the

source of the DNA-binding protein. Although the lysate of the cellobiose-grown cells failed to bind to the *celC* promoter probe in two different concentrations (lanes 3-4, Fig. 3), the lysate of the lichenan-grown cells retarded the probe's gel mobility to the same level as rGlyR3 (lane 5, Fig. 3). To verify that the lysate protein responsible for this shift is indeed GlyR3, we eluted the shifted band from the EMSA gel and subjected it to SDS-PAGE analysis. The silver-stained protein, which was the only protein detected, had an apparent molecular weight of 39 kD as expected for GlyR3 (data not shown). The 39 kD protein was further eluted from the SDS-gel. MALDI-TOF (matrix assisted laser desorption/ionization time of flight) analysis demonstrated that the eluted protein was GlyR3 (33% sequence coverage; data not shown). These results indicate that GlyR3 is induced by lichenan and binds specifically to the *celC* promoter region.

Determination of the GlyR3 Binding Site by DNase I Footprinting. To determine the GlyR3 binding site, we developed a non-isotope DNase I footprinting technique. In this method, a fluorescein-labeled DNA fragment corresponding to the 200 bp region immediately upstream of the start codon of *celC* was partially digested by DNase I in the presence and absence of rGlyR3. The digested products were resolved by capillary electrophoresis and detected by using a fluorescence detector. As shown in Fig. 4, the fluorescence signals of a stretch of 18 bp were suppressed by rGlyR3 (comparing panels A and B). The protected region corresponds to an 18 bp palindromic sequence, typical for a DNA-binding site, with only one mismatch: AATGAACGC GCGTACATT (Fig. 4C). The ability of rGlyR3 to bind to this 18 bp sequence was verified by competitive EMSA, in which an excessive amount of unlabeled, double-stranded 18 bp sequence was used to compete for binding to rGlyR3 with the biotin-labeled 100 bp *celC* promoter probe previously mentioned (Fig. 3). As shown in Fig. 5, the unlabeled 18 bp sequence

at 100-fold concentration completely inhibited the binding of rGlyR3 to the 100 bp *celC* promoter probe (lane 3). In contrast, an unrelated 18 bp sequence from another site of the *celC* promoter region (probes 8 and 9, Table 1) failed to compete in the EMSA at the same concentration (lane 4; Fig. 5). These results indicate that rGlyR3 binds specifically to the 18 bp palindromic sequence.

Laminaribiose Inhibits GlyR3 Binding to the *celC* Promoter Region. The existence of a sugar-binding domain suggests that the DNA-binding activity of GlyR3 is regulated by a sugar. Various sugars were examined for their effects on the GlyR3's DNA-binding activity using EMSA. Among all the sugars tested, only laminaribiose, a β-1,3 linked glucose disaccharide, was found to inhibit rGlyR3's ability to bind the 100 bp *celC* promoter probe at the concentration of 15 mM (lane 3, Fig. 6A). In contrast, cellobiose at the same concentration had no effect (lane 4, Fig. 6A). Other sugars, including cellotriose, cellotetraose, cellopentose, glucose, sucrose, lactose, maltose and gentibiose, as cellobiose, showed little effect on the binding reaction (data not shown). Laminaribiose similarly inhibited the formation of the DNA-protein complex when the 18 bp binding site was used as the probe (Fig. 6B). The inhibition was dose dependent with an observable inhibitory effect at 0.5 mM laminaribiose (lane 2).

rGlyR3 Is a Negative Regulator Subject to Inactivation by Laminaribiose as Revealed by *in vitro* Transcription Assay. To determine if GlyR3 serves as a transcription regulator for the expression of *celC*, we examined its ability to modulate the transcription of *celC* in an *in vitro* transcription assay. The assay utilized a DNA template consisting of the *celC* promoter region and the 5' end of the *celC* gene. The resulting *celC* transcript was quantified by using

quantitative reverse transcriptase- (RT-) mediated, Real-Time PCR. As shown in Fig. 7A, transcription of *celC* was repressed by rGlyR3 in a dose-dependent manner. Furthermore, laminaribiose reversed the repressive effect of rGlyR3, also in a dose-dependent manner (columns 1-4, Fig. 7B). The rGlyR3-repressed transcription was completely restored at 10 mM laminaribiose (column 4). In contrast, cellobiose did not reverse the adverse effect of rGlyR3 (column 6). Laminaribiose alone at 10 mM had little effect on transcription (column 5). These results indicate that rGlyR3 serves as a negative regulator for the *celC* gene in these experiments, presumably by binding to the promoter region. The gene is induced by laminaribiose, which inactivates the binding.

Discussion

C. thermocellum produces a highly complicated biomass-degrading enzyme system, including the cellulosome that contains more than 70 subunits and many free enzymes. Despite intensive studies, how the organism coordinates the expression of such a large number of enzymes to degrade a particular biomass substrate or a mixture of substrates remains elusive.

GlyR3 is the first transcriptional regulator of glycosyl hydrolase genes identified in *C. thermocellum*. It binds specifically to a near perfect 18-bp palindrome in the *celC* promoter region. Its binding site notably bears similarity to many previously reported binding sites for transcriptional regulators that are homologous to LacI and control carbon metabolism in a variety of microorganisms (Table 2). The dissociation constant (K_D) for GlyR3 is estimated to be 4×10^{-14} M. This is near the same order of magnitude as the value for LacI ($K_D = 10^{-13}$ M) (33). At this

time, we cannot rule out the possibility of the existence of a second binding site with a lower affinity as has been reported for LacI.

The role of GlyR3 as a negative regulator is evidenced by the results of the *in vitro* transcription assay, in which the transcription of *celC* was repressed by GlyR3 in a dose-dependent manner. The repression is presumed to be due to the binding of GlyR3 to the 18 bp binding site (the operator) in the promoter region. Laminaribiose serves as an inducer, presumably by binding to the sugar-binding domain of GlyR3 and inhibiting its DNA-binding activity. Since we demonstrated that *celC-glyR3-licA* are co-transcribed (M. Newcomb and J.H. D. Wu, submitted for publication), the three genes therefore form an operon repressible by GlyR3 and inducible by laminaribiose. The *celC* operon thus is similar to the *lac* operon, both operating in a negative mode. On the other hand, since *glyR3* is part of the *celC* operon, induction of the operon would increase the level of the repressor and create a feedback loop. A continuous supply of the inducer, laminaribiose, would be needed to keep the operon in the induced state. In this regard, the *celC* operon functions like the *E. coli hut* operon, in which the repressor is part of the operon. In the absence of a continuous supply of the inducer, we expect the induction of the operon to be transient. In the soil bacterium *Thermobifida fusca,* a similar regulator, CelR, has been reported (34). CelR binds to a 14 bp inverted repeat in the promoter region of each of the six cellulase genes. The binding is inactivated by cellobiose, the presumed inducer. Recently data suggest that laminaribiose might also be involved in the induction (35).

Both CelC (36, 37) and LicA (38) are active on polysaccharides containing β-1,3 glucan such as lichenan and laminarin. In addition, callose, a plant cell wall polysaccharide, consists of β-1,3 linked glucose. Constitutive low-level expression of the *celC* operon likely generates low levels of CelC and LicA. When a substrate containing β-1,3 glucan becomes available, these two

enzymes would generate the inducer, laminaribiose, as the hydrolysis product. Laminaribiose diffused or transported into the cell would turn on the operon for the biosynthesis of more enzymes. This regulation scheme is corroborated by our observation that GlyR3 was detected in the cell lysate only when the bacterium was grown on lichenan. This regulation scheme further implies that CelC and LicA are the major β-1,3 glucan-degrading enzymes in this bacterium. LicA has indeed been reported to be the major enzyme that degrades β-1,3 glucan (38). LicA was characterized as an endo-1,3(4)-β-glucanase active on barley-β-glucan and laminarin. It was shown to be upregulated when growing on laminarin or barley-β-glucan as opposed to cellobiose or cellulose. We independently found that *C. thermocellum* grows on laminaribiose as the sole carbon source (data not shown). These results are consistent with the proposed regulation mechanism of the *celC* operon presented above. It is noteworthy that both CelC and LicA are non-cellulosomal enzymes, suggesting that degradation of β-1,3 glucan does not benefit from the enzymes serving as the cellulosomal components in *C. thermocellum*.

Our results indicate that, despite the water insolubility of the biomass substrates, coordination of the expression of biomass-degrading enzymes can be accomplished through soluble sugars. The *celC* operon as a unit of gene regulation provides the first clue to the puzzle of how the bacterium coordinates the biosynthesis of such a large number of glycosyl hydrolases. GlyR3 is the first transcription regulator found in *C. thermocellum*. It is also the first time laminaribiose is found to serve as an inducer. Foreseeably, more transcription factors and inducers will be found, which will further illuminate how the bacterium commands a myriad of enzymes to attack the complicated biomass substrate containing many different forms of glycans. The results will be particular illuminating in understanding if a particular set of the cellulosome

components are selected by the bacterium to optimize its activity on a particular biomass substrate.

Materials and Methods

Bacterial Strains and Plasmids. *C. thermocellum* ATCC 27405 was used as the source for genomic DNA, RNA, and cell lysates. *E. coli* Top10 (Invitrogen) was used as the cloning host for plasmid PTXB1 (New England Biolabs). *E. coli* strain BL21(DE3) (Stratagene) was used for expressing recombinant GlyR3.

Culture Conditions. *C. thermocellum* was grown in Hungate tubes or anaerobic flasks in chemically-defined MJ medium (39) containing 0.5% carbon source (cellobiose, lichenan, or laminaribiose). Seed cultures were grown on cellobiose. The cultures were incubated at 60º C. *E. coli* strains containing recombinant plasmids were grown at 37º C in a shaker or on agar plates containing Luria-Bertani medium (40) supplemented with 0.1 mg/ml ampicillin. Isopropylthiogalactoside (IPTG; 50 mM) was used to induce the expression of cloned *glyR3*.

Cloning of *glyR3*. PCR was employed to clone *glyR3* using *C. thermocellum* genomic DNA as the template, primers 1 and 2, (Table 1), which incorporated the *EcoR*V and *Xho*I restriction sites, respectively, and a hi-fidelity DNA polymerase (Extensor; ABgene). The PCR product was digested with *EcoR*V and *Xho*I, cloned into the *Nru*I and *Xho*I sites of pTXB1, and transformed by electroporation into *E. coli* TOP10 cells. Restriction digests and DNA sequencing using the dye termination cycle sequencing method and a Model 3100 Genetic Analyzer (Applied Biosystems) were used to verify the cloned gene.

Expression and Purification of rGlyR3. *E. coli* BL21(DE3) harboring pTXB1 containing the clone *glyR3* was induced with 50 mM IPTG in the exponential growth phase for four hours. The cells were harvested by centrifugation and lyzed by sonication. rGlyR3 in the lysate was purified by affinity chromatography using chitin beads as the affinity ligand following the IMPACT system protocol (New England Biolabs). The purified protein was concentrated by ultrafiltration using a Microsep 3K column (Pall) and examined for size and purity using an SDS-PAGE on a 12% gel (41).

Protein Assay. Protein concentrations were determined using the Bradford (42) reagent (Bio-Rad) and bovine serum albumin (Sigma) as a standard.

Electrophoresis Mobility Shift Assay (EMSA). The 100 bp EMSA probe was made by PCR using Taq DNA polymerase (Thermostart; ABgene), primer 3 labeled with biotin, and primer 5 (Table 1). The 18 bp probe consisted of complementary DNA fragments annealed by heating to 94º C and slowly cooling to room temperature (probes 6 and 7, Table 1). All EMSA experiments were performed on 4% polyacrylamide gels in Tris-Borate-EDTA buffer (45 mM Tris-borate, 1 mM EDTA). Each EMSA reaction mixture contained 500 ng poly (dI-dC), 1X Lightshift EMSA kit binding buffer (Pierce), 1X Lightshift loading dye (Pierce), and appropriate amounts of the DNA probe and protein preparations. Sugars were added in some experiments to test their inhibitory effect as indicated. EMSA gels were electroblotted onto Biodyne B membrane (Pall Corporation). Signal development followed the Lightshift Chemiluminescent EMSA kit protocol (Pierce) using Biomax films (Kodak) for luminescence detection.

DNase I Footprinting. PCR was used to amplify the 200 bp *celC* promoter region using primer 3 labeled with fluorescein and primer 4 (Table 1). The reaction mixture contained 400 ng of the amplified DNA fragment, binding buffer (10 mM Tris, 50 mM KCl, 1 mM DTT), 300 ng dI-dC,

1 U DNase I (Invitrogen), and with or without 60 ng rGlyR3. After incubation at 37º C for 7 min, 1 mM EDTA was added and the mixture was heated to 70º C for 15 min. The DNase I-digested DNA products were resolved and detected using a Model 3100 Genetic Analyzer (Applied Biosystems).

***in vitro* Transcription Assay.** In this assay (43, 44), the DNA template was generated using primers 10 and 11 (Table 1) to amplify the 200 bp *celC* promoter region along with the first 650 bp of *celC* of the *C. thermocellum* genomic DNA. Each assay mixture contained 10 µl *C. thermocellum* cell lysate (cellobiose-grown), 2 µl RNase inhibitor (RNase Out; Invitrogen), 1X RNA polymerase buffer, 1 µg DNA template, 25 nM rNTP's, different amounts of rGlyR3 and laminaribiose, and DEPC-water to a total volume of 50 µl. The reactions were incubated at 60º C for 50 min. The resulting RNA was isolated using the Trizol method (Invitrogen), subjected to DNase I digestion, reverse transcribed using random primers, and quantified using Real-Time PCR with the primers specific to *celC* as described below.

Quatitative Real-Time PCR. Each reaction mixture contained 1 µl cDNA template, 7.5 µl SYBR Green Supermix (Bio-Rad), 5.75 µl water, and 250 nM of each primer (primers 12 and 13, Table 1). Real-Time PCR was carried out using a iCycler IQ (Bio-Rad).

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Figure Legends

Fig. 1. Alignment of GlyR1, GlyR2, GlyR3, and LacI. The putative DNA-binding domain of GlyR3 is underlined and the putative sugar-binding domain is bolded. "*****", identical residues; ":", conserved residues; "." semi-conserved residues according to the convention of the European Bioinformatics Institute (http://www.ebi.ac.uk/clustalw/). GenBank accession numbers: GlyR1: ZP_00509723, GlyR2: ZP_00503684, GlyR3: ZP_00504673.

Fig. 2. Schematic drawing of the *celC* operon (*A*) and the domain structure of GlyR3 (*B*) of *C. thermocellum*.

Fig. 3. Binding of rGlyR3 to the *celC* promoter region as revealed by EMSA. All reactions contained 5 ng of a biotin-labeled 100 bp DNA fragment corresponding to the *celC* promoter region. Lanes: 1, no protein; 2, rGlyR3 (1 ng); 3-4, cell lysate from the cellobiose-grown *C. thermocellum* culture (200 ng and 500 ng protein, respectively); 5, cell lysate from the lichenan-grown *C. thermocellum* culture (120 ng protein). The shifted band from lane 5 was excised and subjected to MALDI-TOF analysis, confirming the binding protein to be GlyR3.

Fig. 4. GlyR3 DNA-binding site as determined by DNase I footprinting analysis. The flourescein-labeled, 200 bp DNA fragment corresponding to the *celC* promoter region was subjected to DNase I digestion without (*A*) and with (*B*) rGlyR3. The digested products were resolved by capillary electrophoresis and detected by a fluorescence detector. The DNA

sequence corresponding to the suppressed peaks (Protected Region) is palindromic with one mismatch (*C*). The peaks shown in red are the internal size standards.

Fig. 5. Competitive EMSA confirming the rGlyR3 DNA-binding site. All reactions contained 5 ng of a biotin-labeled 100 bp DNA fragment corresponding to the *celC* promoter region. Lanes: 1, no protein; 2, 0.5 ng rGlyR3; 3, 0.5 ng rGlyR3 and 100-fold unlabeled 18 bp binding site; 4, 0.5 ng rGlyR3 and 100-fold unlabeled18 bp control fragment.

Fig. 6. Inhibition of GlyR3 DNA-binding activity by laminaribiose as analyzed by EMSA. (*A*) 100 bp DNA fragment corresponding to the *celC* promoter region as the probe. All reactions contained 5 ng biotin-labeled probe. Lanes: 1, probe only; 2, probe and 0.5 ng rGlyR3; 3-4, probe and 0.5 ng rGlyR3 plus 15 mM of laminaribiose and cellobiose, respectively. (*B*) 18 bp GlyR3 DNA-binding site as the probe. All reactions contained 5 ng biotin-labeled probe and 0.5 ng rGlyR3. Lanes: 1, no laminaribiose, 2-5, 0.5, 1, 5, and 10 mM laminaribiose, respectively.

Fig. 7. Laminaribiose induction of *celC* by inactivating GlyR3 as revealed by *in vitro* transcription assay. (*A*) Relative transcript level determined by quantitative RT-PCR in the presence of various amounts of rGlyR3. (*B*) Relative transcript level in the presence of rGlyR3 and cellobiose or various amounts of laminaribiose. The data represent the averages of the results from triplicate experiments. Vertical bars represent standard deviations.

Table 1

Primer and probe sequences

No.	Sequence[1,2]
1	**F:** *glyR3*-F-*EcoR*V-GCGCGATATCACCAGTGAAGAAATAGCAAAATTA
2	**R:** *glyR3*-R-*Xho*I-GCGCCTCGAGGAATTCCAAAGCCCTCTTGGTT
3	**F:** Entire_*celC*Prom-F-biotin (or fluorescien)-CCGAATAAAAACTGGACAGAG
4	**R:** Entire_*celC*Prom-R-Unlab-TCCTCCTGAAATATTGTGTTTTA
5	**R:** *celC*Prom_1st_100bp-R-Unlab-TGAAACCATTTAACACTGGATTAT
6	**F:** BS-F-Biotin(or Unlab)-AATGAACGCGCGTACATT
7	**R:** BS-R-Unlab-AATGTACGCGCGTTCATT
8	**F:** Control 18-mer-F-Unlab-AACTGGACAGAGAAGAAG
9	**R:** Control 18-mer-R-Unlab-CTTCTTCTCTGTCCAGTT
10	**F:** Invt-F-CCGAATAAAAACTGGACAGAAG
11	**R:** Invt-R-CCAGTGGGCTTTCTGATGC
12	**F:** *celC*-F-CGGGAACATATTGCCTTTGAAC
13	**R:** *celC*-R-GGTGGAATCAATTTCCCTGATTG

[1]F: Forward, R: Reverse

[2]Restriction sites are underlined.

Table 2

The DNA-binding half-sites of GlyR3 and other regulatory proteins in the GalR/LacI family[1]

Regulator	Sequence[2]	Species
GlyR3	**AATGAACGC**	*C. thermocellum*
CelR	**TG**GGA**GC**	*T. fusca*
LacI	**TTG**TGA**GC**	*E. coli*
CcpA	**TG**TAA**GC**	*B. subtilis*
GalR	**GTG**KAA**NC**	*E. coli*
GalS	**GTG**KAA**NC**	*E. coli*

[1] CelR-GalS binding half-sites were taken from (34).

[2] K = G/T, N = any base; conserved nucleotides are bolded.

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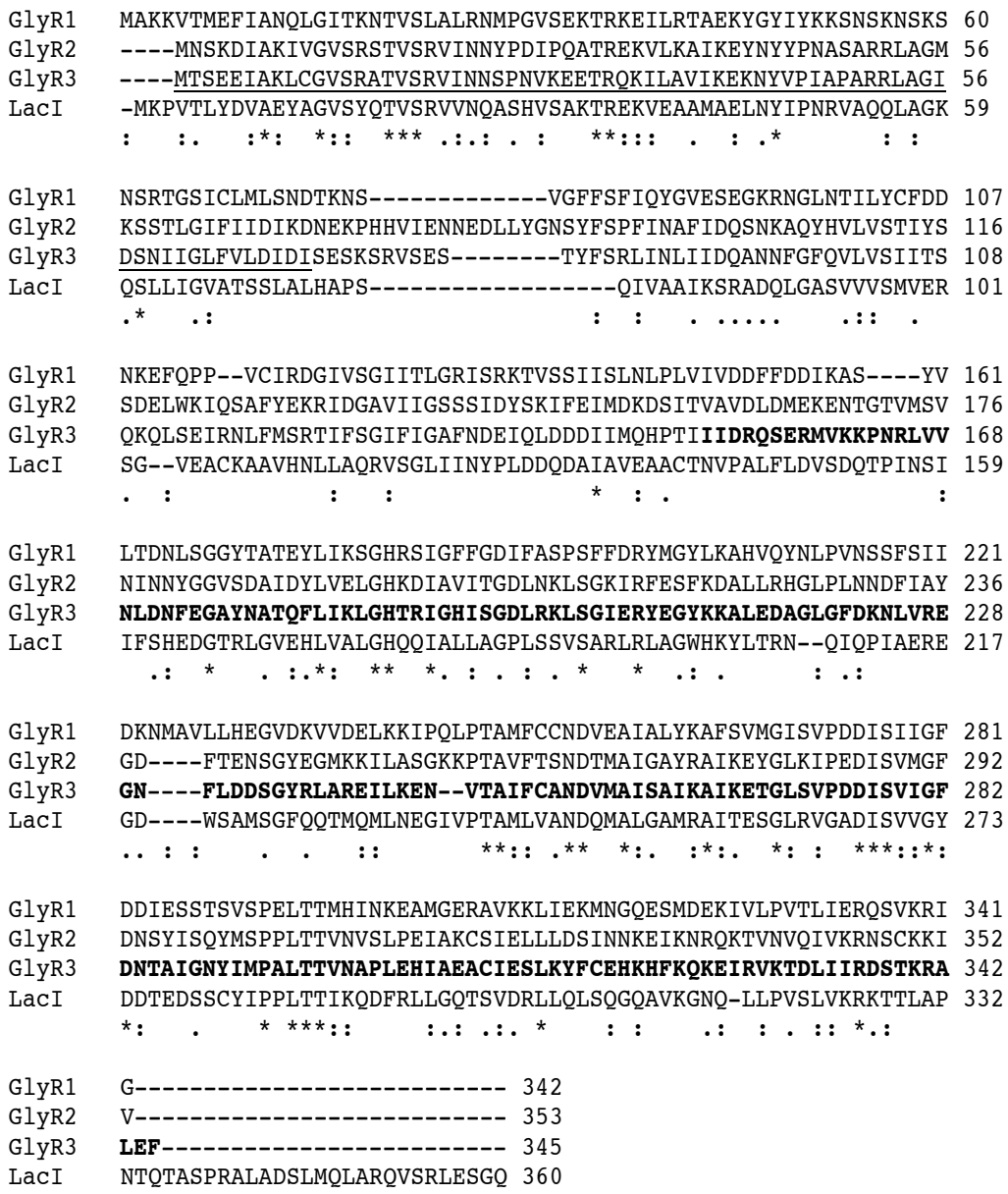

Newcomb, Chen and Wu,
Fig. 1

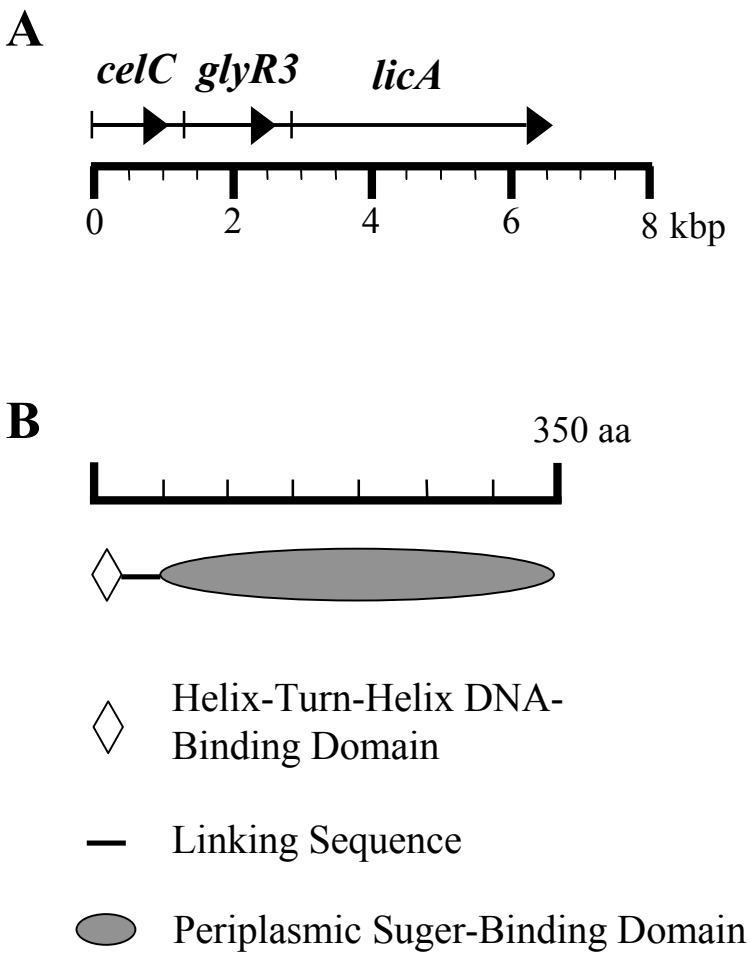

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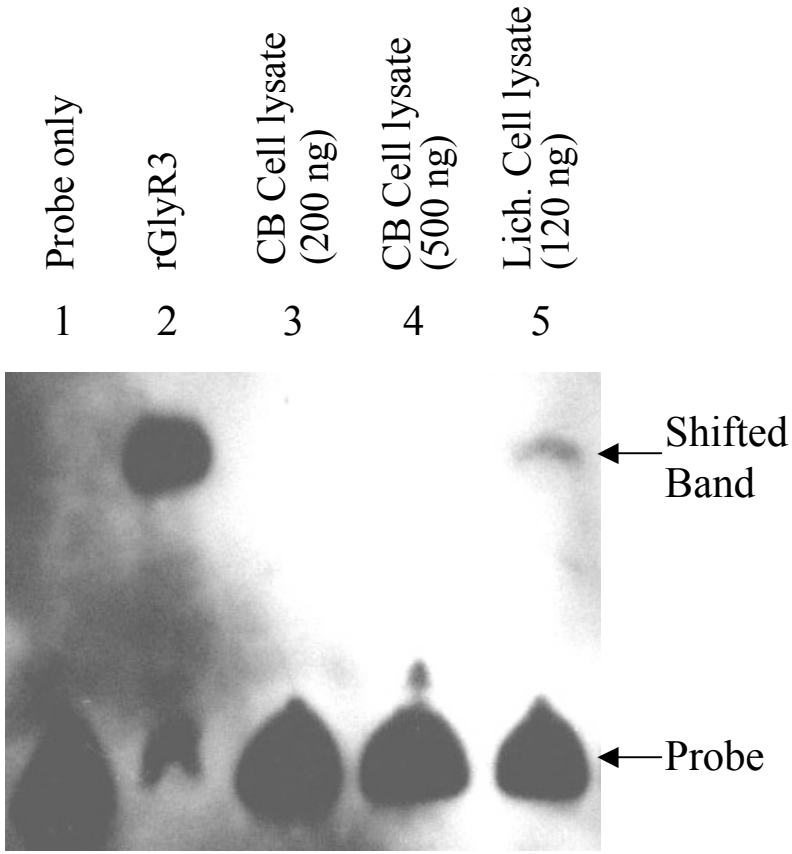
Fig. 2



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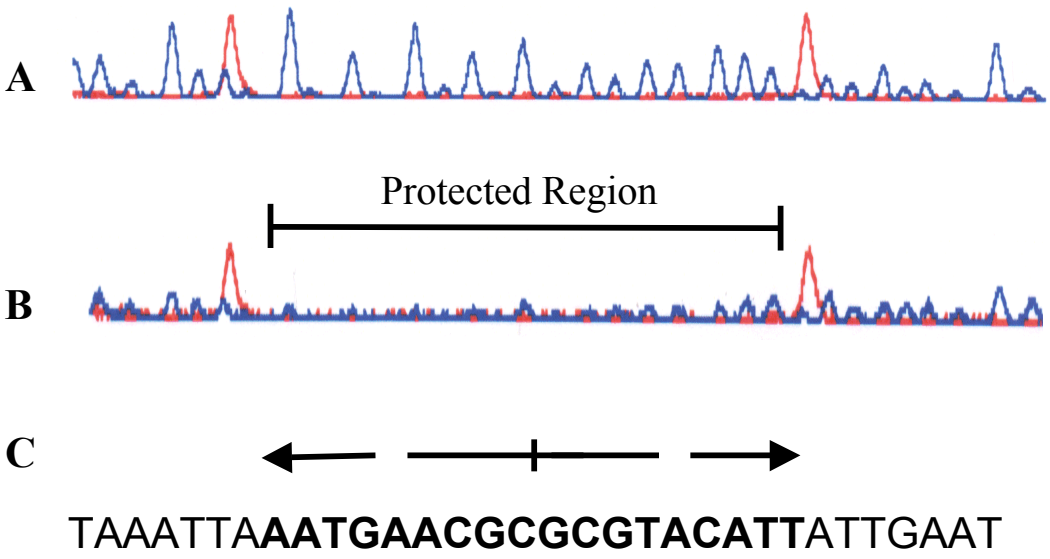

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Fig. 4

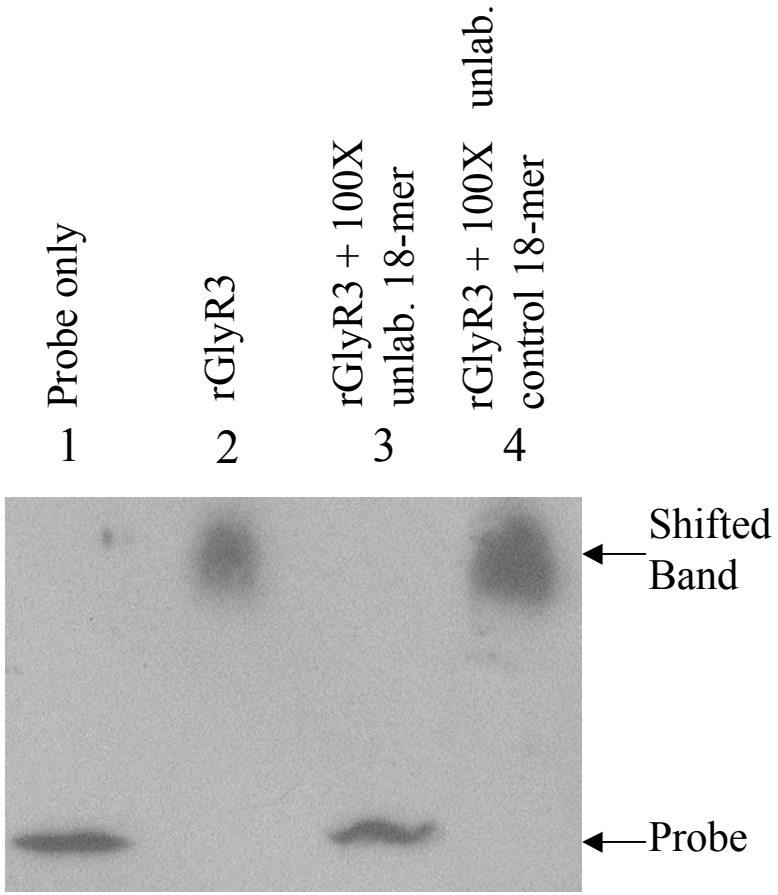

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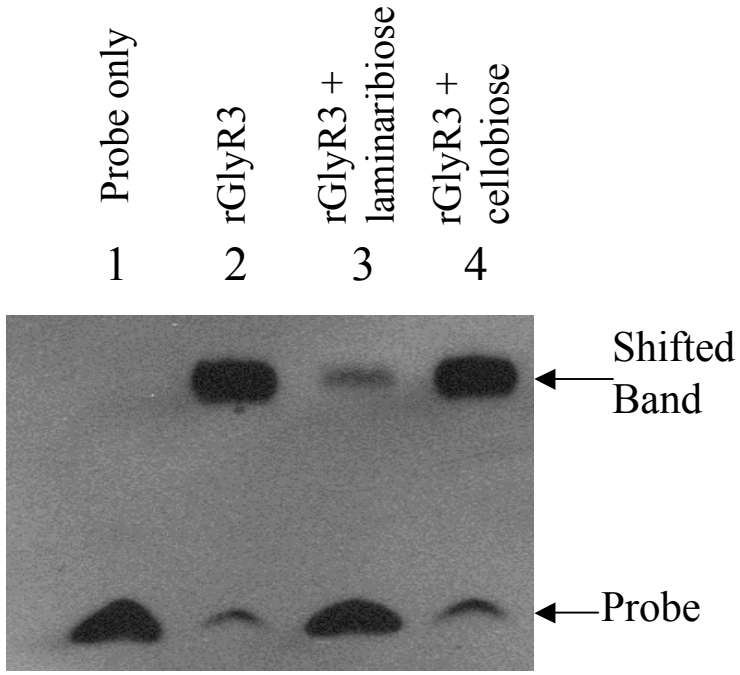
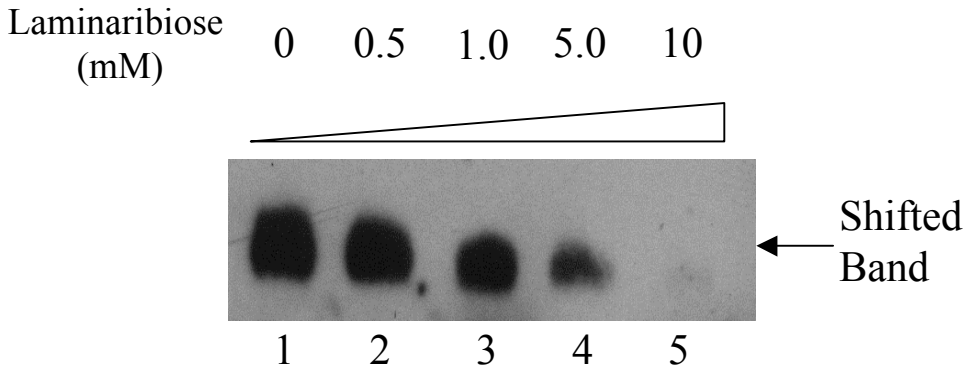
Fig. 5

A 100 bp Probe

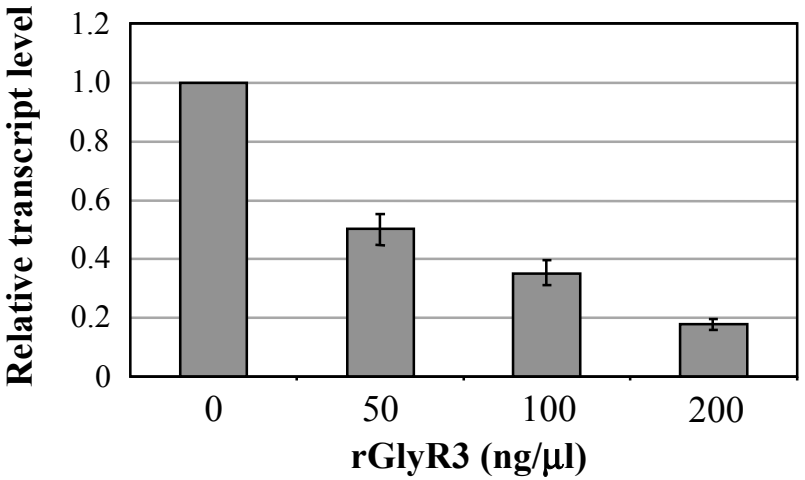


B 18 bp Probe



Newcomb, Chen and Wu, Fig. 6

A



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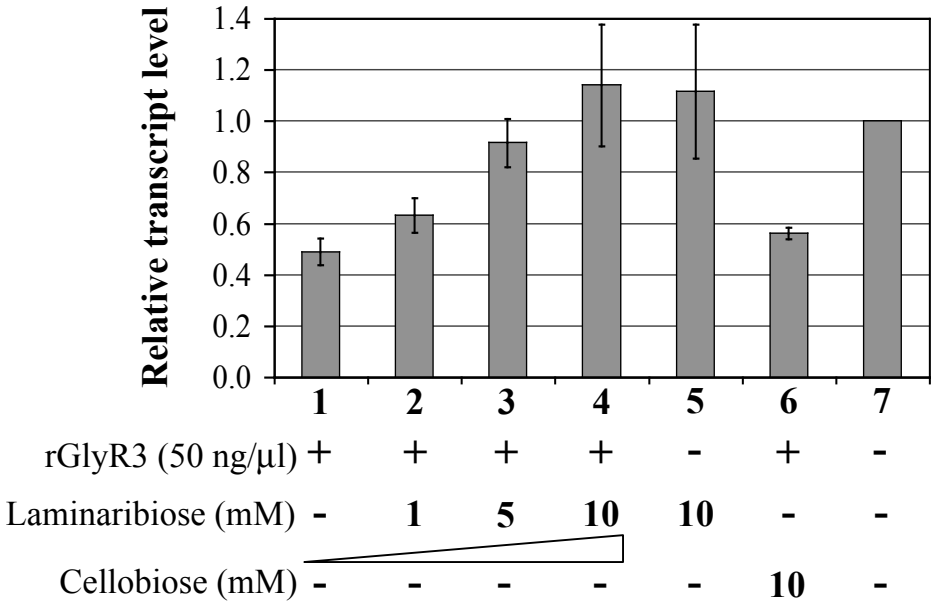

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Fig. 7