

## **Supplementary information**

**Mechanisms involved in xyloglucan catabolism by the cellulosome-producing bacterium**

***Ruminiclostridium cellulolyticum***

Julie Ravachol<sup>1</sup>, Pascale de Philip<sup>1</sup>, Romain Borne<sup>1</sup>, Pascal Mansuelle<sup>2</sup>, María J. Maté<sup>3</sup>,

Stéphanie Perret<sup>1</sup> and Henri-Pierre Fierobe<sup>1\*</sup>

<sup>1</sup>Aix-Marseille Université-CNRS, Laboratoire de Chimie Bactérienne, UMR7283, IMM, 31  
chemin Joseph Aiguier, F-13402 Marseille, France.

<sup>2</sup>Plate-forme de Protéomique, IMM, 31 chemin Joseph Aiguier, F-13402 Marseille, France.

<sup>3</sup>Aix-Marseille Université-CNRS, Laboratoire d'Architecture et Fonction des Macromolécules  
Biologiques, UMR7257, Parc Technologique de Luminy, F-13288 Marseille, France.

\*To whom correspondence should be sent: hpfierob@imm.cnrs.fr

Supplementary Table S1: Kinetic parameters of the hydrolytic activities of Cel9U, Cel9X, Cel44O and Xgh74A on tamarind xyloglucan

Enzyme	$k_{cat}^a$	$K_m^b$	$k_{cat}/K_m^c$
Cel9U <sup>d</sup>	$2,302 \pm 157$	$7.5 \pm 0.15$	307
Cel9X <sup>d</sup>	$6,560 \pm 231$	$8.4 \pm 0.4$	781
Cel44O	$970 \pm 38$	$0.21 \pm 0.06$	4,619
Xgh74A	$2,304 \pm 78$	$0.37 \pm 0.01$	6,227

<sup>a</sup>values are given in  $\mu\text{mol}$  of products released per  $\mu\text{mol}$  of enzyme  $\times \text{min}^{-1}$ .

<sup>b</sup>values are given in  $\text{g} \times \text{L}^{-1}$  of xyloglucan.

<sup>c</sup>values are given in  $\mu\text{mol}$  of products released per  $\mu\text{mol}$  of enzyme  $\times \text{min}^{-1} \text{L} \times \text{g}^{-1}$ .

<sup>d</sup>data are from reference<sup>19</sup>.

Supplementary Table S2: Specific activity of the  $\beta$ -glucosidase GH3A on 1 mM celooligosaccharides.

Substrate	Specific activity <sup>a</sup>
Cellobiose	9.0 ± 0.20 <sup>b</sup>
Cellotriose	12.4 ± 1.3
Cellotetraose	11.6 ± 1.3
Cellopentaose	14.0 ± 2.3
Cellohexaose	10.7 ± 0.6

<sup>a</sup>values are given in  $\mu\text{mol}$  of products released per  $\mu\text{mol}$  of enzyme  $\times \text{min}^{-1}$ .

<sup>b</sup>the data show the mean and standard deviation of two replicates.

Supplementary Table S3: MALDI-TOF analyses of the products released during the sequential degradation of XXXG by successive rounds of incubation with either the  $\alpha$ -xylosidase or the  $\beta$ -glucosidase.

Corresponding steps in Figures 9c or 9d	Composition	Expected m/z [M+Na] <sup>+</sup>	Observed m/z [M+Na] <sup>+</sup>
Substrate	XXXG <sup>a</sup>	1,085.338	1,085.306
9c step 1 (+ $\alpha$ -xylosidase)	GXXG	953.296	953.322
9c step 2 (+ $\beta$ -glucosidase)	XXG	791.243	791.237
9c step 3 (+ $\alpha$ -xylosidase)	GXG	659.201	659.137
9c step 4 (+ $\beta$ -glucosidase)	XG	497.148	497.131
Substrate	XXXG	1,085.338	1,085.306
9d step 1 (+ $\beta$ -glucosidase)	XXXG	1,085.338	1,085.290
9d step 2 (+ $\alpha$ -xylosidase)	GXXG	953.296	953.209
9d step 3 (+ $\beta$ -glucosidase)	XXG	791.243	791.198
9d step 4 (+ $\alpha$ -xylosidase)	GXG	659.201	659.139
9d step 5 (+ $\beta$ -glucosidase)	XG	497.148	497.081

<sup>a</sup>see Fig. 1 for xyloglucan motif abbreviations.

Supplementary Table S4: list of primers used

**Primers used for overexpression in *E. coli* of selected genes**

Protein (gene locus)	Primer name	5'-3' primer sequence
Cel44O (Ccel_0429)	44Of 44Or	AAAAAAACCATGGCTGCCAGTGACGCAATAAACG AAAAAAACTCGAGCCAATCAATTGAATCAACATACATT
Xgh74A (Ccel_1207)	Ccel_1207f Ccel_1207r	TTTTTCCATGGCAAATGGCCCCGTAAGCGCCCCGTATAATTGGAA GGGGGGCTCGAGAAATGAGGTAATTATTCCCAATAAATAAC
Gal42A (Ccel_2451)	2451ncof 2451mnf 2451mnr 2451xhor	TTTTTCCATGGATAAATATATGCTTATTGGTATG CTAAAGGATITTCACGGCGGACGTC GACGTCCGCCG TGAAATCCTTAG TTTTCTCGAGTATTAGCTTTAGCACTTTACGTCA
Glu3A (Ccel_2454)	2454Ncof 2454Xhor	AAAAACCATGGAATACCGATCAGATAGATAAAAAAAATTGATGAAC AAAAACTCGAGCAGAGCAAGAGCTATAGCTATCG
Xyl31A (Ccel_2455)	2455Ncof 2455Xhor	TATATACCATGGCTAAATTCTAAATGGATACTGGATGAGT TTTTCTCGAGTAGAATTCTACTGTATAACTGCCAGTAGA
SBP <sub>2458</sub> (Ccel_2458)	SBPf SBPrev	AATTCCATATGCACCACCACCAACGCTTGACCAAACCGGGAACCGACAGC AATTCTCGAGTTATTACTGTTCTGCAGCCTGTTGGCGGG
Cel9Xt	XdokeTf XdokeTR X830f	GCATTCGCCAACAGTAATTGTCAAGGTACTCCTTACTAAATTACGGC GCCGTATAATTAGTAGAAGGAGTACCTGACAAATTACTGTTGGCGAATGC CCCCCAGGTCAAGATAGGA
9X-44O	9X44Of 9X44Or pETrev	CAGTAATTGTCAGGTAAAACCTCCATAGCTGCCAGTGACGCAATAAACG CGTTTATTGCGTCACTGGCAGCTATGGAGTTTCACCTGACAAATTACTG ATGTTGACAGCTTATCATCGA

**Primers used for qPCR experiments designed with the Primer-BLAST tool**

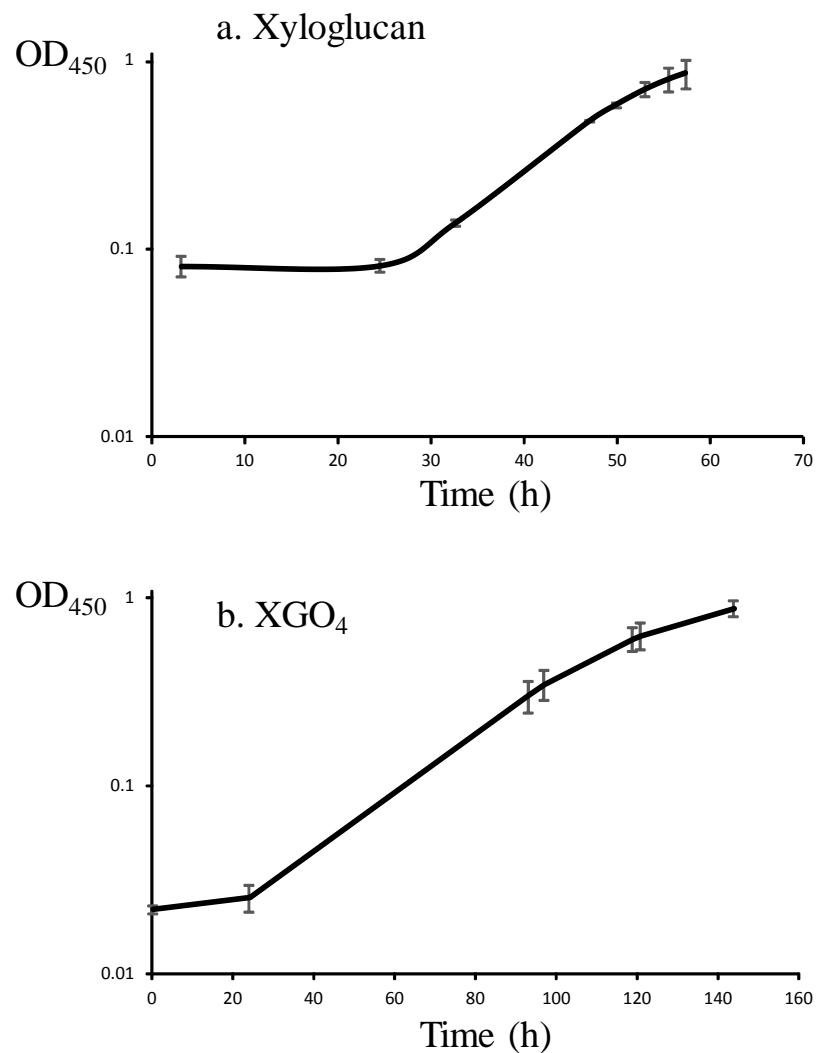
Protein (gene locus)	Primer name	5'-3' primer sequence
Gal42A (Ccel_2451)	2451f 2451r	CTCGTGGATGTCGCCAAAAGT CACCACTCATGGITAAGCCG
Regulator (Ccel_2452)	2452f 2452r	CGGCAAGCTCGGAAATCTT CGTCCCACAGAACGAAACAA
Sensor (Ccel_2453)	2453f 2453r	CAGCACCATGTGGGATAACG CGTATAACGGCGTACCAAAGC
Glu3A (Ccel_2454)	2454f 2454r	TGCTGCCAATAACCAAGGAGA TCCGTAATCAACTGACGGCT
Xyl31A (Ccel_2455)	2455f 2455r	TACGGTTGGGAGAGCGATT TCCAACGATTCGCCCTCAAC
TMD <sub>2456</sub> (Ccel_2456)	2456f 2456r	GAAGTCAAGCGTGGTTGGTT CCACAAACTCCAAGCGTCA
TMD <sub>2457</sub> (Ccel_2457)	2457f 2457r	TGCTTAATCTGGGGCTTCGT CAAGAATGGGAACCGAGAGG
SBP <sub>2458</sub> (Ccel_2458)	2458f 2458r	TGGCAAAGCACGGAGATAAC CCTCGGAAGGAGTAATGGGA
Cel44O (Ccel_0429)	0429f 0429r	AGCACCGTCAGAAAGATGGA AGAGAGCCGGTCACTGICA
Cel9U (Ccel_0755)	0755f 0755r	CGGTAAAGACGGAGGGAAAGT ATTGTAATCCCCGGCATCGT
Xgh74A (Ccel_1207)	1207f 1207r	GAAGCGGTAAACGGACTTTGG GGGITCCAATGTTCTCCTGC
Cel9X (Ccel_2621)	2621f 2621r	TACTGAGTGGCAGCACGTA AGCCGGATATGCTTTCCCT
RpoD (Ccel_0541)	RpoDdir RpoDrev	AAACATAGTCAGAAAGTAGAAAAG CTATACTAACAAACCAAGCCTTAAG
16S rRNA (Ccel_R0018)	16s235F 16s235R	CTATGTTCTGAGTGCCGG ATACTTATTGTGTTAACTCCGG

**Primers used for construction of *R. cellulolyticum* mutant strain MTL2458**

Protein (gene locus)	Primer name	5'-3' primer sequence
<b>SBP<sub>2458</sub> (Ccel_2458)</b>	IBS-SBP	AAAAAAAGCTTATAATTATCCTTACATGCCGCCGTCGTGCGCCAGATAGGGTG
	EBS1d-SBP	CAGATTGTACAATGTGGTGATAACAGATAAGTCGCCGTCCCTAACTTACCTTCTTGT
	EBS2-SBP	TGAACGCAAGTTCTAATTTCGGITGCATGTCGATAGAGGAAAGTGTCT
	EBS	CGAAATTAGAAACTTGCCTTCAGTAAC
<b>Em<sup>R</sup></b>	SBPf	GGGTGGATTATTCACTGTTGA
	SBPr	GGTTGGCAAGAGCGACGGTATGGTG
<b>Em<sup>R</sup></b>	ramF	ACCGCGTTATTTGATAAAAATAATAATAGTGGG
	ramR	ACCGCGTGCAGCTCATAGAATTATTCCTCCCG

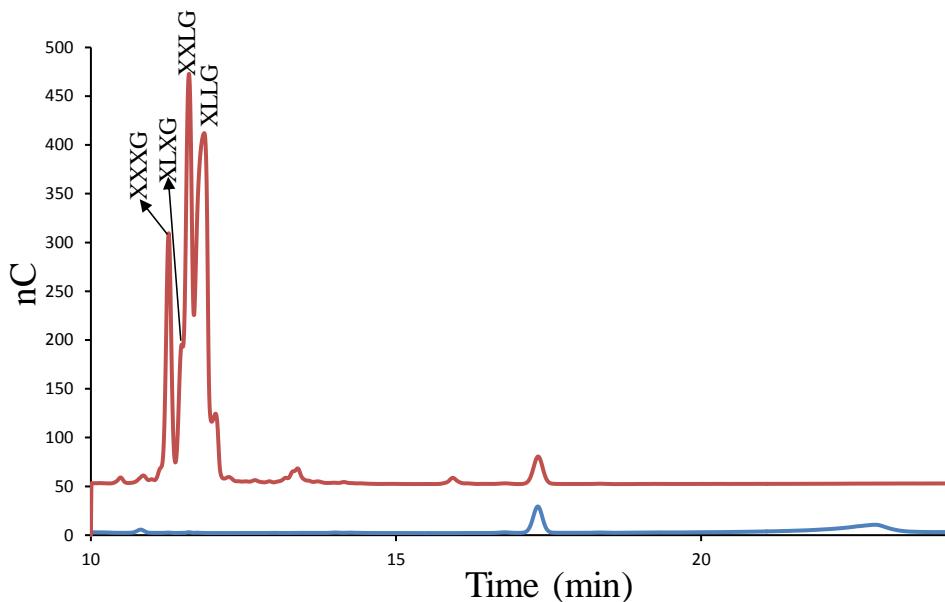
**Supplementary Figure S1: Growth on minimal medium supplemented with a) tamarind xyloglucan or b) XGO<sub>4</sub> at 3.5 g/L.**

The data show the mean of three independent experiments and the bars represent the standard deviation. Cultures on minimal medium supplemented with tamarind xyloglucan (**a**) or XGO<sub>4</sub> (**b**) were used as inoculum (1/20).



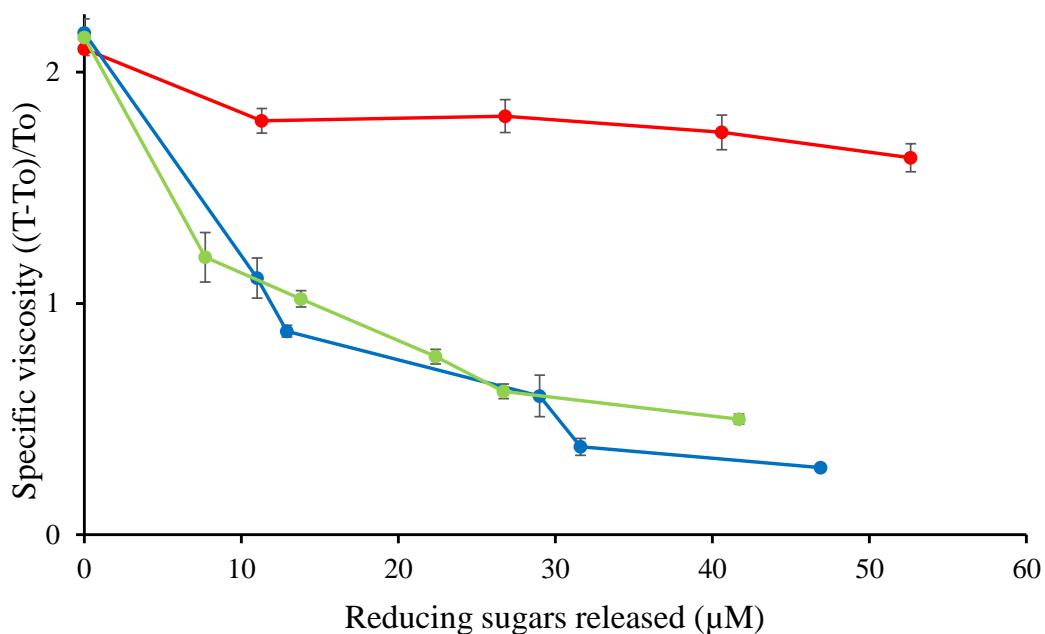
**Supplementary Figure S2: Complete degradation of 3.5 g/L xyloglucan by Cel9X.**

Xyloglucan was incubated for 24 h at 37°C with no (blue) or 0.5 µM of Cel9X (red). The obtained sugars are indicated on top of each peak. The mixture of XGO<sub>4</sub> oligosaccharides served to prepare the XGO<sub>4</sub>-based minimal medium used for growth of *R. cellulolyticum* (Figure S1) and mRNA extraction subsequently used for reverse transcription and quantitative PCR experiments (Figure 7).



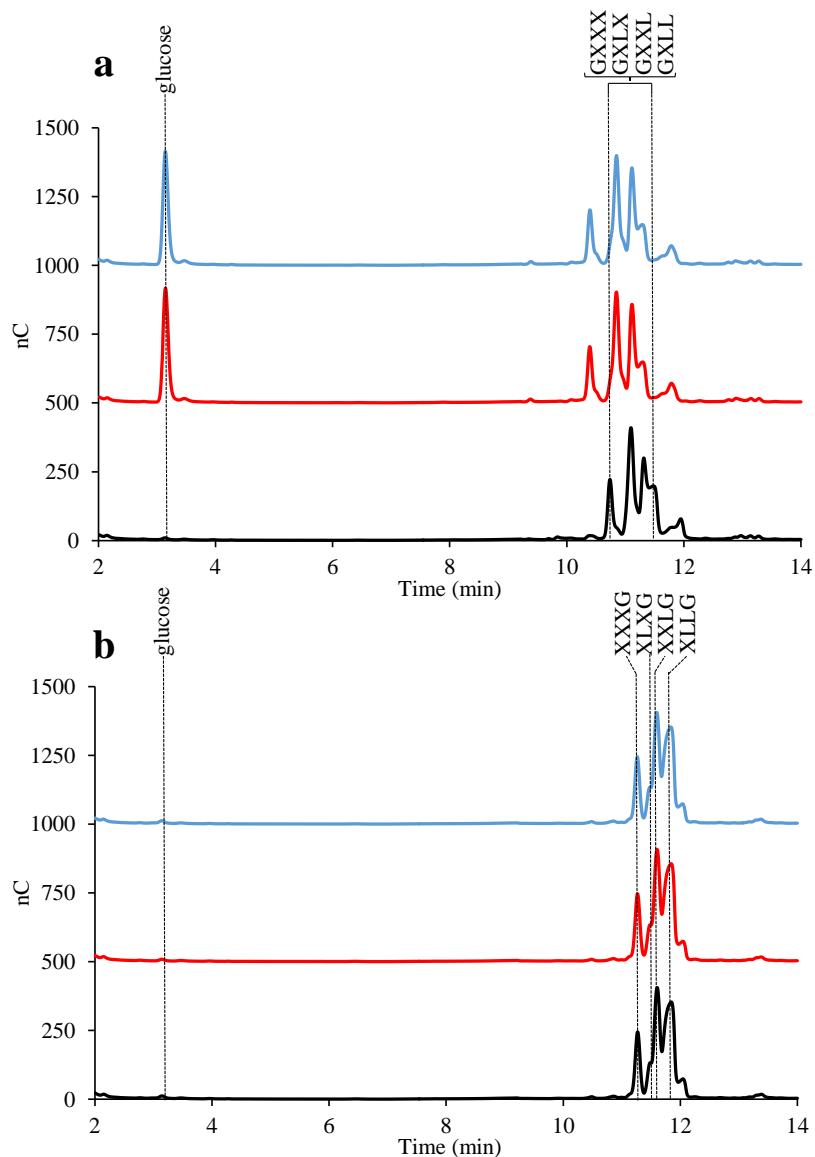
**Supplementary Figure S3: Changes in relative xyloglucan viscosity versus reducing sugars released by Cel9X, Cel44O and Xgh74A.**

Green line, Cel9X; blue line, Cel44O; red line, Xgh74A. The data show the mean and standard deviation of three independent experiments. The specific viscosity was determined as  $((T - T_0)/T_0)$  where  $T$  and  $T_0$  correspond to the flow time of xyloglucan with enzyme and the flow time of buffer, respectively.



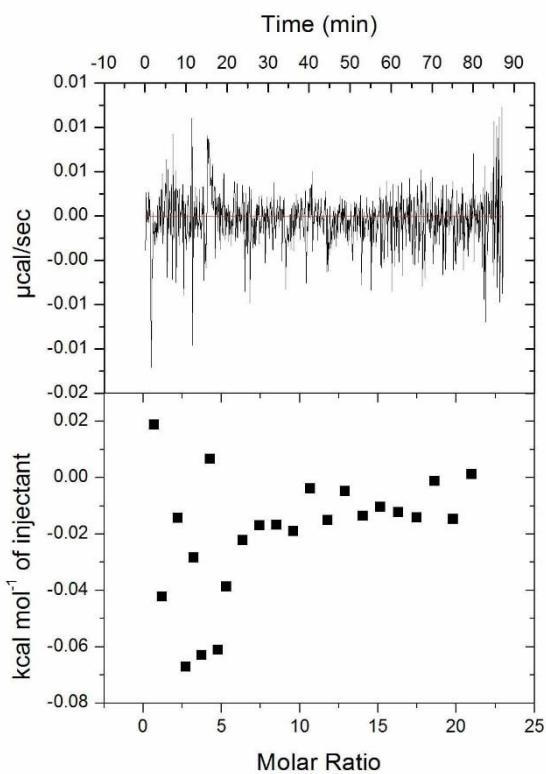
**Supplementary Figure S4: HPAEC-PAD analysis of the action of the  $\beta$ -glucosidase Glu3A on the end products generated by a) Cel44O and b) Cel9X on xyloglucan.**

Xyloglucan (3.5 g/L) was incubated for 24 h at 37°C with 0.5  $\mu$ M of Cel44O (**a**) or 0.5  $\mu$ M of Cel9X (**b**), prior heating at 100 °C for 5 min. The xyloglucan oligosaccharides obtained in each case (black lines, **a** and **b**) were then incubated with 1  $\mu$ M of Glu3A for 30 min (red lines, **a** and **b**) or 2 h (blue lines, **a** and **b**). The obtained sugars are indicated on top of each peak.



**Figure S5: Lack of interaction between the SBP<sub>2458</sub> and isoprimeverose observed by ITC.**

The upper part of each panel shows the raw binding heats and the lower part shows the integrated binding heats minus the dilution control heats. The SBP was at 40  $\mu$ M and the ligand at 4 mM. Similar ITC data were obtained for cellobiose, cellotetraose, glucose, xylose and galactose.



**Figure S6: Growth of wild-type and mutant MTL2458 strains of *R. cellulolyticum* on minimal medium supplemented with a) cellobiose (2 g/L) or b) tamarind xyloglucan (3.5 g/L).**

The cultures were inoculated (1/33) with cellobiose (2 g/L) grown precultures. The data show the mean of three independent experiments for wild type (black squares) and MTL2458 (open squares) strains, respectively. Bars represent the standard deviations.

