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1 Polysaccharide II surface anchoring, the Achilles' heel of

2 *Clostridioides difficile*.

3
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21 **Abstract**

22 Cell wall glycopolymers (CWPGs) in Gram-positive bacteria have been reported to be
23 involved in several bacterial processes. These polymers, pillars for proteins and S-layer,
24 are essential for the bacterial surface set-up, could be essential for growth, and, in
25 pathogens, participate most often in virulence. CWGPs are covalently anchored to the
26 peptidoglycan by Lcp proteins that belong to the LytR-CpsA-PSr family. This anchoring,
27 important for growth, was reported as essential for some bacteria such as *Bacillus*
28 *subtilis*, but the reason why CWGPs anchoring is essential remained unknown. We
29 studied LcpA and LcpB of *Clostridioides difficile* (*C. difficile*) and showed that they have
30 a redundant activity. To delete both *lcp* genes, we set up the first conditional-lethal
31 mutant method in *C. difficile* and showed that polysaccharide II (PSII) anchoring at the
32 bacterial surface is essential for *C. difficile* survival. In the conditional-lethal mutant, *C.*
33 *difficile* morphology was impaired, suggesting that peptidoglycan synthesis was affected.
34 Because Lcp proteins are transferring CWPGs from the C55-undecaprenyl phosphate,
35 also needed in the peptidoglycan synthesis process, we assumed that there was a
36 competition between the PSII and the peptidoglycan synthesis pathways. We confirmed
37 that UDP-MurNAc-pentapeptide precursor was accumulated, showing that
38 peptidoglycan synthesis was blocked. Our results provided an explanation for the
39 essentiality of PSII anchoring in *C. difficile* and suggest that the essentiality of the
40 anchoring of CWPGs in other bacteria can also be explained by the blocking of
41 peptidoglycan synthesis. To conclude, our results suggest that Lcps are potential new
42 targets to combat *C. difficile* infection.

43

44 **Importance**

45 Cell wall glycopolymers (CWGPs) in gram-positive bacteria have been reported to be
46 involved in several bacterial processes. The CWGPs anchoring to the peptidoglycan is
47 important for growth and virulence. We set up the first conditional-lethal mutant method
48 in *C. difficile* to study LcpA and LcpB involved in the anchoring of the CWGPs to the
49 peptidoglycan. This study offers new tools to reveal the role of essential genes in *C.*
50 *difficile*. LcpA and LcpB activity was shown to be essential, suggesting that they are
51 potential new targets to combat *C. difficile* infection. In this study, we also showed that
52 there is a competition between the polysaccharide II synthesis pathway and the
53 peptidoglycan synthesis that probably exists in other Gram-positive bacteria. A better
54 understanding of these mechanisms allows us to define the Lcp proteins as a
55 therapeutic target for a potential design of a novel antibiotic against pathogenic Gram-
56 positive bacteria.

57

58 **Introduction**

59 In recent years, there has been an increasing interest in cell wall glycopolymers
60 (CWGPs) in Gram-positive bacteria for their role in bacterial physiology and
61 pathogenicity. These polymers represent up to 50% of the dry weight of the cell wall (1).
62 CWGPs are covalently linked to peptidoglycan (PG). They support surface proteins (like
63 Cwp in *Clostridioides difficile* or SLH in *Bacillus subtilis*) that are non-covalently
64 anchored at the very end of CWGPs (2, 3). Most of them are essential and involved in
65 cell division and cell shape maintenance (for review (4)). In pathogens, they are
66 essential for virulence (5–11). They are therefore thought to be targets for the
67 conception of new antimicrobial molecules (12, 13).

68 CWGPs anchoring is of major importance for the physiology of Gram-positive
69 bacteria. This process was shown to be done by proteins belonging to the LytR-CpsA-
70 PSr (LCP) family. Members of this protein family are widespread in the bacterial world
71 as they were identified in eight different bacterial phyla (14). The Lcp enzymes transfer
72 CWGPs from a lipid carrier, the C₅₅-undecaprenyl phosphate (C₅₅P) to the nascent or
73 mature PG (15–19). Lcp proteins are therefore key players in bacterial surface
74 assembly. In Gram-positive bacteria, several copies of *lcp* genes are often observed but
75 the gene products can have distinct catalytic activities. For example, in *B. subtilis*, three
76 Lcp proteins have been identified and one of them (TagU) has a stronger activity than
77 the two others (20). In *M. tuberculosis*, the only Lcp is essential (21). Finally, in
78 *Staphylococcus aureus* (*S. aureus*), LcpA is the main transferase of teichoic acids
79 whereas LcpC is dedicated to the capsular polysaccharides transfer (19). The Lcp
80 proteins are at least partially redundant in *B. subtilis* (22), *S. aureus* (23, 24), and
81 *Streptococcus pneumoniae* (25, 26). Besides, the Lcp proteins are good targets for

82 specific inhibitors development because their soluble catalytic domain is extracellular
83 (accessible to immune system cells) and they have no homologs in mammals (14). In *C.*
84 *difficile*, Lcps were studied individually (27), but their redundancy and essentiality for
85 survival have never been assessed experimentally.

86 *Clostridioides difficile* (previously known as *Clostridium difficile*) is a Gram-
87 positive, motile, strictly anaerobic, and spore-forming enteric pathogen. *C. difficile*
88 infections (CDIs) are a primary cause of nosocomial diarrhea and antibiotic-associated
89 colitis (28). Besides, the incidence and the number of severe clinical forms have been
90 increasing in recent years, due to emerging hypervirulent and antibiotic-resistant strains
91 (including *C. difficile* ribotype 027) (29). Consequently, *C. difficile* is considered an
92 urgent threat to public health by the Centers for Disease Control and prevention (30).
93 Moreover, multiple resistance mechanisms to currently used antibiotics, often mediated
94 by plasmid acquisition (31, 32), are observed and cause concerns about future
95 treatment options for CDI management. Therefore, developing new strategies and
96 discovering new bacterial targets is necessary.

97 In *C. difficile*, three CWPGs have been identified: two teichoic acids (TA)
98 anchored in the peptidoglycan (polysaccharides I and II, (33)) and one lipoteichoic acid
99 (LTA) anchored directly in the membrane (34). Only the polysaccharide II (PSII) and the
100 LTA are conserved among *C. difficile* strains. All the biosynthesis genes of these
101 glycopolymers are encoded in a single locus of the chromosome. All the genes predicted
102 to encode enzymes involved in PSII synthesis are reported to be essential for bacterial
103 survival (3, 35), but surprisingly not *lcpA* and *lcpB* genes encoding PSII anchoring
104 proteins (27). Note that Cwp proteins, including the S-layer protein SlpA, are non-
105 covalently linked to the PSII (3).

106 In this study, we focused on PSII. Its biosynthesis is predicted to be initiated by
107 the transferase CD2783, transferring the first sugar unit (UDP-Glucose) on the C₅₅P lipid
108 carrier. Then, several cytoplasmic glycosyltransferases catalyze the transfer of sugar
109 units on the chain. When finished, the chain is flipped outside the cell by the flippase
110 MviN (27) and transferred to the pre-existing chains to form a C₅₅P-polymerized PSII
111 molecule. PSII is then transferred from the lipid carrier to the PG by LcpA and LcpB (27).
112 In this work, we studied the two Lcps of *C. difficile* to evaluate the importance of a
113 correct polysaccharide anchoring in the physiology of the bacterium. We wanted to
114 determine if the *lcp* genes were essential for survival.

115

116

117

118 **Results**

119 Construction of *lcp* single mutants

120 To facilitate the screen of the allelic exchange technique in *C. difficile* (36), we decided
121 to replace the open reading frame of *lcpA* and *lcpB* with the open reading frame of the
122 *catP* gene expressing the thiamphenicol resistance. To that aim, we constructed the
123 pJV10 vector that harbors an *ermB* gene (Figure S1) conferring erythromycin resistance.
124 In the genome of the 630 strain, two copies of the *ermB* gene are found. In contrast, the
125 630 Δ *erm* harbors only one *ermB* gene (37), which is usually not expressed. However,
126 we were unable to conjugate the pJV10 plasmid in the 630 Δ *erm* that became, in these
127 conditions, resistant to erythromycin, probably because the remaining *ermB* gene was
128 sufficiently expressed during the conjugation process. Therefore, we chose to construct
129 a “true” 630 Δ *erm* by deleting both *ermB* genes directly from the clinical 630 strain and
130 obtained the JMV1 strain.

131 We first deleted *lcpA* and *lcpB* separately in the JMV1 strain using the allelic exchange
132 method (36). Thanks to the presence of the *catP* gene, after the selection of the first
133 crossing over (36), a simple restreak on a petri dish in the presence of thiamphenicol
134 allows the identification of potential mutant clones. The JMV3 (Δ *lcpA*) strain was easily
135 obtained (21 mutant clones were thiamphenicol resistant out of 25) whereas the JMV4
136 (Δ *lcpB*) strain was quite hard to get (3 mutant clones were thiamphenicol resistant out of
137 187), suggesting that *lcpB* plays an important role for *C. difficile* growth.

138

139 *lcpA* and *lcpB* are redundant

140 We first confirmed that the *lcpB* mutant (JMV4) showed a growth defect (Figure S2).
141 Then, we observed the morphology of the mutant cells in classical optic microscopy
142 (Figure 1A) and measured the cell length and width (Figure 1C and 1D), allowing us to
143 determine a percentage of “normal morphology” (Figure 1B). Contrary to the Δ *lcpA*
144 mutant bacteria (JMV3) whose morphology is normal, almost 35% of the Δ *lcpB* (JMV4)
145 cells were curved or inflated (Figures 1 and S3). Cells were also significantly longer and
146 thicker than the JMV1 cells (Figures 1C and 1D). These observed morphological and
147 growth defects in the absence of *lcpB* confirmed the previous results obtained by
148 Vedantam *et al.* (27) and suggest that LcpB plays a major role in anchoring the PSII to
149 the peptidoglycan.

150 Besides, we observed that bacterial morphology and growth were restored in the strains
151 JMV4 + pMEZ12 (complementation plasmid bearing *lcpA*, named thereafter *p**lcpA* for
152 simplification) and JMV4 + pJV21 (complementation plasmid bearing *lcpB*, named
153 thereafter *p**lcpB* for simplification), as shown in Figures 1A and S2. Indeed, the
154 abnormal cell ratio was reduced to 4% and 6% when complementation with *lcpA* or *lcpB*
155 was introduced (Figure 1B). These results suggest that LcpA can compensate for the
156 absence of LcpB in anchoring the PSII to the peptidoglycan and that both Lcp proteins
157 have redundant functions in *C. difficile*.

158 Considering the absence of phenotype in the JMV3 strain, we wondered if *lcpA* was
159 expressed and we assessed the expression of *lcpA* and *lcpB* by a measurement of the
160 promoter activity (by beta-glucuronidase assay). As shown in Figures 2A and 2B, *lcpA*
161 and *lcpB* had constitutive expression, respectively with a mean of 230 and 35 Miller
162 units, but *lcpA* is transcribed at a higher level than *lcpB*. This result suggested, that even
163 if transcribed at a low level, *lcpB* is important for cell growth and morphology.

164
165 The $\Delta lcpA$ (JMV3) and $\Delta lcpB$ (JMV4) mutant strains present a normal
166 surface protein profile but an altered PSII layer

167 Because Cwp proteins are non-covalently anchored to the PSII, we analyzed the S-layer
168 content (Figure S4). We found no differences between the CWP proteins of the parental
169 strain and the single mutants. To assess the presence of PSII at the bacterial surface,
170 we purified the PSII, checked that it was non-contaminated with LTA by NMR (Figure
171 S5), and coupled it with BSA. After immunization, we obtained specific antibodies able to
172 recognize the PSII (Figure S6). Using a super-resolution microscope, the JMV1 parental
173 strain showed a homogenous and continuous layer of PSII along the bacterium. In
174 contrast, both JMV3 and JMV4 mutant strains showed an altered PSII layer (Figure 3).
175 The JMV3 cells presented a holed layer of PSII. The JMV4 mutant strain presented a
176 smooth PSII layer. The alteration of the PSII deposition at the surface was present in
177 both mutants but the PSII layer was differently altered in the JMV3 and JMV4 strains,
178 suggesting that even though redundant in activity, LcpA and LcpB have slightly different
179 roles in PSII anchoring at the bacterial surface.

180
181 **PSII anchoring is essential for *C. difficile* survival**

182 Once the single mutants were obtained and their phenotypes confirmed, we tried to get
183 a double mutant strain to assess the essentiality of the PSII anchoring for *C. difficile*
184 survival. The first strategy was to use our improved allelic exchange method using the
185 pJV13 plasmid and the *C. difficile* JMV1 strain. Despite the facilitated screening of
186 mutants, we failed to isolate a double *lcp* mutant over the 450 clones tested. This result

187 suggested that deleting both *lcpA* and *lcpB* genes was not possible, maybe because
188 of the essentiality of both LcpA and LcpB.

189 To assess the essentiality of *lcp* genes in *C. difficile*, we elaborated a new strategy
190 based on the construction of a conditional-lethal mutant (Figure S7). The first step was
191 to insert an extra copy of *lcpB* under the control of a P_{tet} promoter in the *ermB* locus of
192 the 630, to mimic the JMV1 strain by removing both *ermB* genes, giving rise to the JMV2
193 strain. The second step was to perform the deletion of both *lcpA* and *lcpB* in the JMV2
194 strain using pJV13 plasmid in the presence of 100 ng.mL⁻¹ of anhydrotetracycline (ATc).
195 We obtained the conditional-lethal mutant strain JMV6 that was not able to grow without
196 induction of the additional copy of *lcpB* (Figures 4A and S8). To confirm this phenotype,
197 conditional-lethal mutant strain (JMV6) was grown in the presence of 10 or 50 ng.mL⁻¹ of
198 ATc and then plated on a Petri dish with no or up to 250 ng.mL⁻¹ (Figure 4A). No growth
199 was observed on plates at 10 ng.mL⁻¹ ATc or less, showing that the presence of at least
200 one *lcp* is essential for *C. difficile* growth. In liquid culture, conditional-lethal mutant strain
201 (JMV6) in the presence of 10 ng.mL⁻¹ had an impaired growth that was restored by
202 adding 50 ng.mL⁻¹ of ATc (Figure 4B). Without ATc, growth was restored when *lcpA* was
203 present (on *plcpA* plasmid) confirming the redundancy of Lcp activity. We also assessed
204 the morphology using microscopy and confirmed that the conditional-lethal mutant strain
205 (JMV6) grown with 10 ng.mL⁻¹ of ATc had a marked phenotype with ellipsoid cells
206 shorter and thicker than the JMV1 cells (Figure 5). In the presence of 50 ng.mL⁻¹ of ATc,
207 some bacilli were curved and long but the rod shape was restored with comparable cell
208 width and increased cell length compared to JMV1 cells (Figure 5). Finally, the addition
209 of *plcpA* or *plcpB* fully restored the bacterial shape, similarly to the controls (JMV1 and
210 JMV2 strains). Our results showed that the absence of *lcpA* and *lcpB* is lethal for *C.*

211 *difficile* and suggested that PSII anchoring is essential for *C. difficile* growth. In addition,
212 this result suggested that only *lcpA* and *lcpB* are involved in PSII anchoring.

213

214 PSII remains at the bacterial surface in the JMV6 strain

215 To analyze the localization of PSII at the bacterial surface when its anchoring is impaired
216 due to the limitation of *LcpA* and *LcpB*, the conditional-lethal mutant strain (JMV6) was
217 cultured with 10 ng.mL⁻¹ or 50 ng.mL⁻¹ of ATc (Figure 6). We used the JMV2 strain as a
218 control, which has a second copy of *lcpB* (*P_{tet}-lcpB* copy at the *ermB* locus). This strain
219 has a similar phenotype to the JMV1 strain confirming that overexpression of *lcpB*, due
220 to the induction of the second copy, does not affect PSII anchoring and bacterial
221 morphology. In the conditional-lethal mutant strain (JMV6), we confirmed that a low
222 induction of *lcpB* (10 ng.mL⁻¹ of ATc) leads to ellipsoid cells. The rod shape was restored
223 in the presence of 50 ng.mL⁻¹ of ATc with or without *lcpA*. Moreover, PSII was still
224 localized at the bacterial surface of the JMV6 strain in the presence of 10 ng.mL⁻¹ of ATc
225 (Figure 6, JMV6 (ATc 10)). This result was surprising because, according to the previous
226 study of Chu *et al.* (27), PSII was expected to be found in the supernatant fraction. Our
227 results suggested that the PSII, after its synthesis was still anchored to its lipid carrier at
228 the plasmic membrane, in accordance with the models (20, 27).

229

230 Part of the surface PSII and Cwp proteins is released in the JMV6 strain

231 To assess the impact of a defect of PSII anchoring to PG, we analyzed the presence of
232 PSII at the bacterial surface and in the supernatant by dot blot analysis (Figure 7). In the
233 JMV1 parental strain and the JMV2 control strain (*P_{tet}-lcpB*), the PSII was found in the

234 bacterial fraction (pellet), suggesting that it was only associated with the bacterial
235 surface. The same result was observed for the single *lcp* mutant strains JMV3 and
236 JMV4. Conversely, in the conditional-lethal *lcp* mutant (JMV6) with 10 ng.mL⁻¹ of ATc,
237 PSII was found at the bacterial surface and released in the culture supernatant. This
238 release of PSII is decreased in the presence of 50 ng.mL⁻¹ of ATc. The phenotype is
239 completely restored in the conditional-lethal mutant strain (JMV6) in the presence of
240 *lcpA* and 50 ng.mL⁻¹ of ATc.

241 Because the PSII was released in the supernatant, we assessed whether the Cwp
242 proteins, which are non-covalently linked to the PSII, were also found in the supernatant.
243 We showed that the Cwp amount was decreased at the bacterial surface of the
244 conditional-lethal mutant strain (JMV6) in the presence of 10 ng.mL⁻¹ ATc induction, in
245 comparison with the JMV1, JMV2, and JMV6+*lcpA* strains (Figure 8A). Cwp proteins of
246 the conditional-lethal mutant strain (JMV6) strain in the presence of 10 ng.mL⁻¹ were
247 found in the supernatant. In comparison, in the presence of 50 ng.mL⁻¹, Cwp proteins
248 from the JMV6 strain were more abundant at the bacterial surface. To further
249 characterize which proteins were concerned, we performed a western blot analysis.
250 These analyses allowed us to identify two proteins of the Cwp family, Cwp66 and SlpA,
251 in the supernatant of the conditional-lethal mutant strain (JMV6) strain (Figures 8D and
252 8F). Accordingly, Cwp66 was absent from the surface protein extracts (Figure 8C) and
253 SlpA was found in a lower quantity than in other strains (Figure 8E). It is to note that
254 SlpA precursor (uncleaved) was found in the conditional-lethal mutant strain (JMV6),
255 suggesting a maturation defect. We analyzed the autolysis profile of all strains to
256 investigate why the PSII and the Cwp proteins were found in the supernatant (Figure 9).
257 We found that the single *lcp* mutants JMV3 and JMV4 autolyzed more rapidly than the

258 parental strain (Figure 9A) and that this phenotype was absent when they were
259 complemented with either *p/lcpA* or *p/lcpB*. The conditional-lethal mutant JMV6 autolyzed
260 also more rapidly than the JMV1 strain (Figure 9B). Again, the impaired phenotype was
261 fully restored in the presence of 50 ng.mL⁻¹ of ATc and *lcpA*. These results suggested
262 that the conditional-lethal mutant strain (JMV6) is lysing more rapidly than the parental
263 strain, explaining the partial release of the PSII into the culture supernatant.

264
265 **Cytoplasmic PG precursors accumulate in response to impaired PSII**
266 **anchoring to PG**

267 Because the PSII is attached to the C₅₅P carrier during its biosynthesis and until an Lcp
268 protein anchors it to the peptidoglycan, we hypothesized that the PSII transfer
269 impairment from the C₅₅P carrier to the peptidoglycan may limit the availability of this
270 lipid carrier for peptidoglycan synthesis. The extraction of cytoplasmic peptidoglycan
271 precursors was performed for JMV1, conditional-lethal mutant strain JMV6 (10 ng.mL⁻¹
272 ATc), and conditional-lethal mutant strain JMV6 + *p/lcpA* (50 ng.mL⁻¹ ATc) (Figure 10). In
273 the JMV1 strain, only peak 1 was found (Figure 10A). In the two other tested strains
274 (Figures 10B and 10C), peak 1 and peak 2 were found. Mass spectrometry analyses
275 (Figure 10D) indicated that the precursor in peak 1 was UDP-MurNAc-pentapeptide.
276 Analysis of the precursor in peak 2 by tandem mass spectrometry indicated that it
277 differed from UDP-MurNAc-pentapeptide by the amidation of the side-chain carboxyl of
278 the diaminopimelyl (DAP) residue located at the 3rd position of the pentapeptide stem.
279 This amidation, attributed to AsnB, was only reported once, when *C. difficile* was grown
280 in the presence of vancomycin at a sublethal concentration (38). A third peak (Figure

281 10B and C) was not identified. UDP-MurNAc-pentapeptide was 21-fold more abundant
282 in JMV6 grown in the presence of 10 ng.mL⁻¹ of ATc than in the parental JMV1 strain.
283 The accumulation of UDP-MurNAc-pentapeptide was less abundant (6 fold instead of 21
284 fold) in the JMV6 + *p/lcpA* strain, in the presence of 50 ng.mL⁻¹ of ATc. These results
285 establish that impaired PSII anchoring to peptidoglycan results in the accumulation of
286 the UDP-MurNAc-pentapeptide peptidoglycan precursor. This accumulation is likely to
287 result from a limited availability of the C₅₅P lipid carrier for peptidoglycan synthesis due
288 to its sequestration in lipid-linked PSII precursors.

289

290 **Discussion**

291 In this study, we characterized LcpA and LcpB as responsible for PSII anchoring
292 to *C. difficile* PG. In addition, we showed that the activity of these proteins is essential for
293 the viability of *C. difficile* probably because of an interference with the PG synthesis.

294 In well-studied Gram-positive models like *B. subtilis*, *S. pneumoniae*, and *S.*
295 *aureus*, *lcp* genes are found in multiple copies in the genome and are at least partially
296 redundant (22–26). Our study confirmed that growth of a *lcpB* mutant strain is
297 associated with morphological defects, contrary to a *lcpA* mutant strain (27). *lcpB*
298 appears then to be more important than *lcpA*, yet *lcpB* is expressed at a lower level than
299 *lcpA*. The morphological and growth defects of the *lcpB* mutant were restored by
300 overexpression of *lcpA*. The overexpression may localize LcpA differently than in the
301 parental strain, allowing the complementation by compensating the absence of LcpB at
302 the bacterial surface and suggests that LcpA and LcpB have partially redundant
303 functions. Similarly, in other bacteria, yet redundant in activity, one Lcp has a

304 predominant role, and its absence impacts bacterial physiology more than the others
305 (22, 39, 40).. Our immunofluorescence study (Figure 3) showed that the PSII layer is
306 altered in both single mutants but differently, suggesting that these distinct phenotypes
307 can be due to a different localization of the two Lcps at the surface. It is to note that
308 LcpB is predicted to have a transmembrane domain and LcpA only has a signal peptide
309 domain (<https://www.ebi.ac.uk/interpro/>), suggesting that LcpB is localized at the
310 membrane and LcpA is secreted. Since the PSII is linked to the C₅₅P at the membrane,
311 a membranous Lcp (LcpB in *C. difficile*) may be more efficient in transferring it from the
312 C₅₅P to PG. In contrast, LcpA should be less efficient because of its lack of an N-
313 terminal transmembrane domain which is untypical among Lcp proteins, since they
314 usually have at least a transmembrane domain (14).

315 Lcp proteins are phosphotransferases according to Kawai *et al.* (22) or
316 peptidoglycan-glycopolymer ligase according to Schaefer *et al.* (40). However, in *lcp*
317 mutants of *S. aureus* and *B. subtilis*, CWGPs were found to be released (22, 23, 27).
318 There is a discrepancy between these data and the theoretical CWGP synthesis and
319 transfer of the CWGPs from the C₅₅P to the PG. This was explained in *S. aureus* by the
320 activity of CapA1 that catalyzes the cleavage of the pyrophosphate linkage between the
321 CWGP and the C₅₅P, releasing the CWGP into the supernatant in the absence of Lcp
322 proteins. In contrast, in *S. pneumoniae* (26) and our study, we reported that the CWGPs
323 were found both in the supernatant and at the bacterial surface. In our work, it is difficult
324 to know whether this PSII localization is due to the presence of a low level of LcpB
325 (JMV6 in the presence of 10 ng.mL⁻¹ of ATc) or if PSII is still anchored to C₅₅P carrier at
326 the surface. In *C. difficile*, one gene encodes a putative protein similar to that of CapA1

327 from *S. aureus* (CD630_11190, 19% of identity and 45% of similarity) and none was
328 found in the *S. pneumoniae* R6 genome. The CD630-11190 putative lipoprotein may
329 have another function than CapA1, but we can't exclude that the observed release of
330 PSII into the supernatant may be due to this protein, together with the observed bacterial
331 lysis (Figure 9).

332 Additionally, we showed that PSII release in the conditional-lethal strain was
333 associated with the release of the Cwp66 and SlpA surface proteins in the supernatant.
334 Indeed, we were able to detect SlpA at the bacterial surface which is the most abundant
335 surface protein in *C. difficile*, but not Cwp66, suggesting that most of the Cwp proteins
336 are not localized at the bacterial surface anymore. In parallel, we observed that SlpA
337 was only partially matured in the JMV6 strain, suggesting that Cwp84 was not efficient in
338 its cleavage. This defect in SlpA cleavage may be due to the Cwp84 localization that
339 was suggested to be first active when positioned at the surface, then released after an
340 auto maturation, and finally fully active and reassociated to the bacterial surface (41).
341 This last step may be missing due to a probable association with the released PSII
342 instead of the bacterial surface, explaining the partial defect in SlpA cleavage.

343 Blocking indirectly the recycling of C₅₅P, for example with cell wall synthesis
344 inhibitors (such as bacitracin and vancomycin), leads to an accumulation of UDP-
345 MurNAc-pentapeptide in the cytoplasm and then bacterial death (42). Because the PSII
346 is predicted to be anchored on the C₅₅P lipid carrier during its biosynthesis (3, 27) and
347 until it is transferred by Lcp proteins to the PG (19), we hypothesized that an impairment
348 in PSII anchoring could lead to a blocking of peptidoglycan biosynthesis through a
349 competition between the C₅₅P linked PSII and the synthesis of lipid II that requires free

350 C₅₅P. Our results suggest that the sequestration of C₅₅P-linked PSII blocks the transfer
351 of the UDP-MurNAc-pentapeptide to free C₅₅P, leading to its accumulation in the
352 cytoplasm. During this accumulation, the UDP-MurNAc-pentapeptide is amidated
353 (Figure 10). This amidation of a peptidoglycan precursor was already observed and
354 mediated by AsnB in *C. difficile*, but only in the presence of vancomycin (38). As
355 vancomycin also targets lipid II, we can hypothesize that the accumulation of UDP-
356 MurNAc-pentapeptide may induce the expression of *asnB* leading to the amidation of
357 peptidoglycan precursors.

358 UDP-MurNAc-pentapeptide accumulation suggested that the PG synthesis is
359 blocked and explained the essentiality of Lcp activity in *C. difficile*. In *B. subtilis*, CWGPs
360 are dispensable for cell viability (43), but the absence of the three Lcps is lethal (22).
361 Similarly, in *Mycobacterium tuberculosis*, Lcp1, the unique Lcp, was shown to be
362 essential (44). In other bacterial species, this essentiality was not reported, but the
363 absence of Lcp led to defects in growth, morphology, and virulence (23, 40, 45). Our
364 results confirmed the importance of the Lcp proteins in bacterial cell wall organization
365 and their essentiality for bacterial physiology and fitness. Since Lcp proteins are mainly
366 found in Gram-positive and especially in pathogens, they are very good targets for the
367 research of a new class of antibacterial drugs to counteract the emergence of multidrug-
368 resistant bacteria.

369

370 **Materials and methods**

371 **Bacterial strains and growth conditions**

372 The strains used and constructed in this study are listed in Table 1. All *C. difficile* strains
373 of this study are isogenic derivatives of the clinical 630 strain (46). *C. difficile* was grown
374 in a Brain-Heart Infusion medium (BHI, BD Difco) at 37°C in anaerobic conditions
375 (Jacomex, 5% H₂ - 5% CO₂ - 90% N₂). When needed, BHI was supplemented with 1%
376 defibrinated horse blood, thiamphenicol (Th, 7.5 µg.mL⁻¹), aztreonam (Az, 16 µg.mL⁻¹,
377 used to kill parental *E. coli* during the conjugation process), or erythromycin (Er, 5
378 µg.mL⁻¹). Anhydrotetracycline (ATc) was used to induce the P_{tet} promoter (concentration
379 from 5 to 250 ng.mL⁻¹). Growth curves were obtained using a SpectraMax plate reader
380 (Molecular devices). *Escherichia coli* was grown aerobically in LB medium at 37°C,
381 supplemented when needed with ampicillin (Amp, 100 µg.mL⁻¹), chloramphenicol (Cm,
382 25 µg.mL⁻¹), kanamycin (Kn, 40 µg.mL⁻¹), spectinomycin (Spec, 100 µg.mL⁻¹) or
383 erythromycin (Er, 150 µg.mL⁻¹).

384

385 **Molecular biology**

386 According to the manufacturer's instructions, the plasmid extractions, gel extraction, and
387 PCR purifications were achieved using the Omega E.Z.N.A Plasmid DNA Mini Kit, Gel
388 extraction Kit, and Cycle Pure Kit. PCRs were carried out using high-fidelity Phusion
389 DNA polymerase for gene amplification on genomic DNA and mutant screening of *C.*
390 *difficile*. In contrast, the Taq DNA polymerase was used for screening steps in *E. coli*.

391

392 **Construction of plasmids**

393 A list of plasmids and primers used in this study can be found in Tables 1 (plasmids),
394 S1, and S2 (primers). The construction of all plasmids is detailed in Text S1. The
395 plasmids used in this study were constructed using either the Gibson assembly protocol
396 from NEB (47) or the Golden Gate assembly from NEB (48, 49) cloning techniques. For
397 Golden Gate assembly, the primers were designed using the NEB Builder® assembly
398 tool.

399

400 Mutant strains construction

401 Plasmids were transferred from *E. coli* HB101 (pRK24) to *C. difficile* via heterogramic
402 conjugation (between *E. coli* and *C. difficile*), following the previously described protocol
403 (50). The single and double cross-over events were screened based on the pseudo-
404 suicide plasmid pMSR following the appropriate protocol described by Peltier (36), with
405 some modifications. As we replace the ORFs with a *catP* gene, a first quick screen for
406 the second crossing-over event is done by restreaking clones on BHI supplemented with
407 a thiamphenicol agar plate. Then, only Th^R clones are checked by PCR using
408 appropriate primers (Table S2).

409

410 Construction of JMV1, JMV3, and JMV4 strains

411 The JMV1 strain is an $\Delta ermB$ region derivative of the clinical 630 strain. The deletion
412 was made by replacing the complete *ermB* region [genes CD630_20100 (*ermB*),
413 CD630_20091, CD630_20090, CD630_20080, CD630_20071, CD630_20070 (*ermB*)]
414 with a spectinomycin resistance gene. This replacement was made by allelic exchange
415 technique (36) using the pJV8 plasmid.

416 The single *lcp* mutants JMV3 and JMV4 are derivatives of the JMV1 strain, where the
417 ORF was replaced with a thiamphenicol resistance gene. The deletion of CD630_27650
418 (*lcpA*) and CD630_27660 (*lcpB*) was made by allelic exchange using respectively
419 deletion plasmids pJV11 and pJV12. The mutants were PCR-verified using the primers
420 couples JV85/JV90, JV86/JV91 for JMV3 mutant, and JV88/JV90, JV87/JV91 for JMV4
421 strain (Table S2).

422

423 Conditional-lethal mutant construction

424 The insertion of the P_{tet} -*lcpB* in the *erm* locus was made using the pJV27 plasmid and
425 the resulting strain JMV2 was PCR-verified using the JV99/JV100 primers. Then, the
426 deletion of both *lcp* genes was made using the pJV13 plasmid and the use of 100
427 ng.mL⁻¹ of ATc, giving rise to the conditional-lethal mutant strain JMV6, which can be
428 PCR-checked using primers JV85/JV90 and JV91/JV87 (Table 2).

429

430 Beta-glucuronidase assay

431 The beta-glucuronidase assay was performed as described in Ammam *et al.*, 2020 (38).

432

433 Growth and autolysis curves

434 Growth and autolysis curves were performed using the SpectraMax® plate reader. To
435 ensure anaerobic conditions, the 96-wells plates were filmed with an adhesive film in the
436 anaerobic chamber. The cultures were launched in BHI at an approximate optical
437 density of 0.1 from overnight pre-culture of different strains. Growth and autolysis curves
438 were performed at 37°C.

439

440 Cwp proteins and supernatant proteins extractions

441 Cwp proteins were isolated from intact *C. difficile* bacteria using low-pH glycine as
442 described previously by Fagan *et al.* (51). The optical density was systematically
443 adjusted to 1 for all strains before protein extraction. Supernatant proteins fraction was
444 obtained by harvesting bacteria (20,000 x g, 15 min, 4 °C) from overnight cultures
445 previously adjusted to an optical density (600 nm) of 1, and then precipitated with
446 trichloroacetic acid 10% (on ice, 4 hours). The pellet is finally resuspended in Tris 50
447 mM pH 7.4.

448

449 Preparation of antigens and antibodies against PSII and SlpA

450 Surface polysaccharide II was isolated using the protocol of Cox (52). The detection of
451 glycopolymers in fPLC fractions was accomplished by the phenol-sulfuric assay (53).
452 The fractions of interest were freeze-dried and analyzed by ¹H and ³¹P NMR (ENS Lyon)
453 to confirm the PSII purification. Purified NMR-confirmed PSII was then conjugated to
454 bovine serum albumin (BSA). The coupling reaction proceeded according to the protocol
455 described by Romano (54), with cyanoborohydride (NaBH₃CN) as a coupling agent. The
456 resulting glycoconjugate antigen (PSII-BSA) was submitted to Covalab (France) for
457 rabbit immunization (four injections with 50 µg of the glycoconjugate per animal).
458 Specificity of the purified PSII was confirmed by dot blot and NMR-confirmed,
459 peptidoglycan (PG), and PG-PSII extracts.

460 SlpA was purified as described by Bruxelle *et al.* (55) and was submitted to Covalab
461 (France) for guinea pig immunization (four injections with 22.5 µg of the protein per
462 animal). Specificity of the polyclonal antibodies was performed by western blot.

463

464 Immunodetection

465 For the Western blot analyses, the following antibodies were used: anti-SlpA antibodies
466 (guinea pig) diluted at 1:5,000 and anti-Cwp66 antibodies (rabbit) diluted at 1:10,000.
467 For the dot blot analysis, anti-PSII antibodies (rabbit) diluted 1:10,000 were used.
468 Antibody binding was revealed with anti-rabbit Immobilon Western Chemiluminescent
469 HRP Substrate (Merck) and revelation was performed on Fusion Fx Imaging System
470 (Vilber Lourmat).

471

472 PSII visualization by Super-Resolution Confocal microscope

473 A 16 h culture was diluted to obtain 10^8 cells.mL⁻¹ thanks to a Kovalslide system, and 20
474 µL of this diluted culture was deposited on a thin round coverslip. After drying, the slides
475 were stained in TBS-tween BSA 5%, washed, and incubated with the primary antibody
476 (anti-PSII, 1:200) for 1h, with the secondary antibody (StarRED® from Abberior, 1:500)
477 for 1h, and finally with Hoechst (1:2000) to visualize DNA. Washings were performed
478 between each step. Finally, the coverslip was mounted on a slide with mounting medium
479 Abberior Mount Solid® and stored overnight at 4°C before imaging on a STEDYCON
480 super-resolution microscope (Abberior).

481

482 PG cytoplasmic precursors extraction and analysis

483 The protocol described previously by Cremniter *et al.* (56) was used with some
484 modifications. Bacteria were grown in 500 mL brain heart infusion broth overnight and
485 submitted to ice-cold formic acid (47mL, 1.1M) extraction for 30 min at 4 °C, without
486 prior bacitracin treatment.

487 To allow comparison of the different strains whose culture optical density was not equal,
488 we calculated the ratio peak area/optical density, presented in the results. The extract
489 was centrifuged (7,000 x *g* for 15 min at 4 °C) and the supernatant was loaded to a gel
490 filtration column (Sephadex G-25) for desalting. The fraction of elution was lyophilized
491 and resuspended in 10 mL water. 100 µL of this cytoplasmic precursor solution was
492 loaded onto an *rp*HPLC in a C18 column (Hypersil GOLD aQ; 250 x 4.6 mm; 3 µm,
493 Thermo Scientific) at a flow rate of 1 ml/min. A linear gradient (0 to 20 %) was applied
494 between 13 and 33 min at 25 °C (buffer A, 50 mM ammonium formate pH 4.4; buffer B,
495 100 % Methanol). Absorbance was monitored at 262 nm and the peak corresponding to
496 the major cytoplasmic precursor was collected, lyophilized, resuspended in 20 µL of
497 water. Ten µL were analyzed by mass spectrometry on a Bruker Daltonics maXis high-
498 resolution mass spectrometer (Bremen, Germany) operating in the positive mode
499 (Analytical platform of the Muséum National d'Histoire Naturelle, Paris, France). Mass
500 spectral data were explored using Bruker Compass DataAnalysis 4.3.

501

502 Statistics

503 Statistical analyses were conducted using GraphPad Prism (version 9.0.0, GraphPad
504 Software, San Diego, California USA, www.graphpad.com). The *p-value* is indicated for
505 all comparisons when differences are statistically significant.

506

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514

515 **Footnotes**

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517

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523

524

525 **References**

- 526 1. Neuhaus FC, Baddiley J. 2003. A continuum of anionic charge: structures and functions of D-alanyl-
527 teichoic acids in gram-positive bacteria. *Microbiol Mol Biol Rev* 67:686–723.
- 528 2. Mesnage S, Fontaine T, Mignot T, Delepierre M, Mock M, Fouet A. 2000. Bacterial SLH domain
529 proteins are non-covalently anchored to the cell surface via a conserved mechanism involving wall
530 polysaccharide pyruvylation. *EMBO J* 19:4473–4484.
- 531 3. Willing SE, Candela T, Shaw HA, Seager Z, Mesnage S, Fagan RP, Fairweather NF. 2015. *Clostridium*
532 *difficile* surface proteins are anchored to the cell wall using CWB2 motifs that recognise the anionic
533 polymer PSII. *Mol Microbiol* 96:596–608.
- 534 4. Swoboda JG, Campbell J, Meredith TC, Walker S. 2010. Wall Teichoic Acid Function, Biosynthesis,
535 and Inhibition. *ChemBioChem* 11:35–45.
- 536 5. Weidenmaier C, Peschel A, Xiong Y-Q, Kristian SA, Dietz K, Yeaman MR, Bayer AS. 2005. Lack of wall
537 teichoic acids in *Staphylococcus aureus* leads to reduced interactions with endothelial cells and to
538 attenuated virulence in a rabbit model of endocarditis. *J Infect Dis* 191:1771–1777.
- 539 6. Weidenmaier C, Peschel A, Kempf VAJ, Lucindo N, Yeaman MR, Bayer AS. 2005. DltABCD- and
540 MprF-mediated cell envelope modifications of *Staphylococcus aureus* confer resistance to platelet
541 microbicidal proteins and contribute to virulence in a rabbit endocarditis model. *Infect Immun*
542 73:8033–8038.
- 543 7. Collins LV, Kristian SA, Weidenmaier C, Faigle M, Van Kessel KPM, Van Strijp JAG, Götz F,
544 Neumeister B, Peschel A. 2002. *Staphylococcus aureus* strains lacking D-alanine modifications of
545 teichoic acids are highly susceptible to human neutrophil killing and are virulence attenuated in
546 mice. *J Infect Dis* 186:214–219.

- 547 8. Fisher N, Shetron-Rama L, Herring-Palmer A, Heffernan B, Bergman N, Hanna P. 2006. The *dlt*ABCD
548 operon of *Bacillus anthracis* Sterne is required for virulence and resistance to peptide, enzymatic,
549 and cellular mediators of innate immunity. *J Bacteriol* 188:1301–1309.
- 550 9. Spears PA, Havell EA, Hamrick TS, Goforth JB, Levine AL, Abraham ST, Heiss C, Azadi P, Orndorff PE.
551 2016. *Listeria monocytogenes* wall teichoic acid decoration in virulence and cell-to-cell spread. *Mol*
552 *Microbiol* 101:714–730.
- 553 10. Meireles D, Pombinho R, Carvalho F, Sousa S, Cabanes D. 2020. *Listeria monocytogenes* Wall
554 Teichoic Acid Glycosylation Promotes Surface Anchoring of Virulence Factors, Resistance to
555 Antimicrobial Peptides, and Decreased Susceptibility to Antibiotics. *Pathogens* 9:E290.
- 556 11. Kharat AS, Denapaite D, Gehre F, Brückner R, Vollmer W, Hakenbeck R, Tomasz A. 2008. Different
557 pathways of choline metabolism in two choline-independent strains of *Streptococcus pneumoniae*
558 and their impact on virulence. *J Bacteriol* 190:5907–5914.
- 559 12. Lee SH, Wang H, Labroli M, Koseoglu S, Zuck P, Mayhood T, Gill C, Mann P, Sher X, Ha S, Yang S-W,
560 Mandal M, Yang C, Liang L, Tan Z, Tawa P, Hou Y, Kuvelkar R, DeVito K, Wen X, Xiao J, Batchlett M,
561 Balibar CJ, Liu J, Xiao J, Murgolo N, Garlisi CG, Sheth PR, Flattery A, Su J, Tan C, Roemer T. 2016.
562 TarO-specific inhibitors of wall teichoic acid biosynthesis restore β -lactam efficacy against
563 methicillin-resistant staphylococci. *Science Translational Medicine* 8:329ra32-329ra32.
- 564 13. Sewell EW, Brown ED. 2014. Taking aim at wall teichoic acid synthesis: new biology and new leads
565 for antibiotics. 1. *J Antibiot* 67:43–51.
- 566 14. Hübscher J, Lüthy L, Berger-Bächli B, Stutzmann Meier P. 2008. Phylogenetic distribution and
567 membrane topology of the LytR-CpsA-Psr protein family. *BMC Genomics* 9:617.

- 568 15. Atilano ML, Pereira PM, Yates J, Reed P, Veiga H, Pinho MG, Filipe SR. 2010. Teichoic acids are
569 temporal and spatial regulators of peptidoglycan cross-linking in *Staphylococcus aureus*. Proc Natl
570 Acad Sci U S A 107:18991–18996.
- 571 16. Schlag M, Biswas R, Krismer B, Kohler T, Zoll S, Yu W, Schwarz H, Peschel A, Götz F. 2010. Role of
572 staphylococcal wall teichoic acid in targeting the major autolysin Atl. Mol Microbiol 75:864–873.
- 573 17. Bhavsar AP, Truant R, Brown ED. 2005. The TagB protein in *Bacillus subtilis* 168 is an intracellular
574 peripheral membrane protein that can incorporate glycerol phosphate onto a membrane-bound
575 acceptor in vitro. J Biol Chem 280:36691–36700.
- 576 18. Andre G, Deghorain M, Bron PA, van Swam II, Kleerebezem M, Hols P, Dufrene YF. 2011.
577 Fluorescence and atomic force microscopy imaging of wall teichoic acids in *Lactobacillus*
578 *plantarum*. ACS Chem Biol 6:366–376.
- 579 19. Rausch M, Deisinger JP, Ulm H, Müller A, Li W, Hardt P, Wang X, Li X, Sylvester M, Engeser M,
580 Vollmer W, Müller CE, Sahl HG, Lee JC, Schneider T. 2019. Coordination of capsule assembly and
581 cell wall biosynthesis in *Staphylococcus aureus*. Nat Commun 10:1404.
- 582 20. Gale RT, Li FKK, Sun T, Strynadka NCJ, Brown ED. 2017. *B. subtilis* LytR-CpsA-Psr Enzymes Transfer
583 Wall Teichoic Acids from Authentic Lipid-Linked Substrates to Mature Peptidoglycan In Vitro. Cell
584 Chem Biol 24:1537-1546.e4.
- 585 21. Malm S, Maaß S, Schaible UE, Ehlers S, Niemann S. 2018. In vivo virulence of *Mycobacterium*
586 *tuberculosis* depends on a single homologue of the LytR-CpsA-Psr proteins. Sci Rep 8:3936.

- 587 22. Kawai Y, Marles-Wright J, Cleverley RM, Emmins R, Ishikawa S, Kuwano M, Heinz N, Bui NK,
588 Hoyland CN, Ogasawara N, Lewis RJ, Vollmer W, Daniel RA, Errington J. 2011. A widespread family
589 of bacterial cell wall assembly proteins. *EMBO J* 30:4931–4941.
- 590 23. Chan YGY, Frankel MB, Dengler V, Schneewind O, Missiakas D. 2013. *Staphylococcus aureus*
591 mutants lacking the LytR-CpsA-Psr family of enzymes release cell wall teichoic acids into the
592 extracellular medium. *J Bacteriol* 195:4650–4659.
- 593 24. Chan YG-Y, Kim HK, Schneewind O, Missiakas D. 2014. The capsular polysaccharide of
594 *Staphylococcus aureus* is attached to peptidoglycan by the LytR-CpsA-Psr (LCP) family of enzymes. *J*
595 *Biol Chem* 289:15680–15690.
- 596 25. Yother J. 2011. Capsules of *Streptococcus pneumoniae* and other bacteria: paradigms for
597 polysaccharide biosynthesis and regulation. *Annu Rev Microbiol* 65:563–581.
- 598 26. Eberhardt A, Hoyland CN, Vollmer D, Bisle S, Cleverley RM, Johnsborg O, Håvarstein LS, Lewis RJ,
599 Vollmer W. 2012. Attachment of capsular polysaccharide to the cell wall in *Streptococcus*
600 *pneumoniae*. *Microb Drug Resist* 18:240–255.
- 601 27. Chu M, Mallozzi MJG, Roxas BP, Bertolo L, Monteiro MA, Agellon A, Viswanathan VK, Vedantam G.
602 2016. A *Clostridium difficile* Cell Wall Glycopolymer Locus Influences Bacterial Shape,
603 Polysaccharide Production and Virulence. *PLoS Pathog* 12:e1005946.
- 604 28. Bartlett JG, Taylor NS, Chang T, Dzink J. 1980. Clinical and laboratory observations in *Clostridium*
605 *difficile* colitis. *Am J Clin Nutr* 33:2521–2526.
- 606 29. Zilberberg MD, Shorr AF, Kollef MH. 2008. Increase in adult *Clostridium difficile*-related
607 hospitalizations and case-fatality rate, United States, 2000-2005. *Emerg Infect Dis* 14:929–931.

- 608 30. Centers for Disease Control and Prevention (U.S.). 2019. Antibiotic resistance threats in the United
609 States, 2019. Centers for Disease Control and Prevention (U.S.).
- 610 31. Pu M, Cho JM, Cunningham SA, Behera GK, Becker S, Amjad T, Greenwood-Quaintance KE,
611 Mendes-Soares H, Jones-Hall Y, Jeraldo PR, Chen J, Dunny G, Patel R, Kashyap PC. 2021. Plasmid
612 Acquisition Alters Vancomycin Susceptibility in *Clostridioides difficile*. *Gastroenterology* 160:941-
613 945.e8.
- 614 32. Boekhoud IM, Hornung BVH, Sevilla E, Harmanus C, Bos-Sanders IMJG, Terveer EM, Bolea R, Corver
615 J, Kuijper EJ, Smits WK. 2020. Plasmid-mediated metronidazole resistance in *Clostridioides difficile*.
616 *Nat Commun* 11:598.
- 617 33. Ganeshapillai J, Vinogradov E, Rousseau J, Weese JS, Monteiro MA. 2008. *Clostridium difficile* cell-
618 surface polysaccharides composed of pentaglycosyl and hexaglycosyl phosphate repeating units.
619 *Carbohydr Res* 343:703–710.
- 620 34. Reid CW, Vinogradov E, Li J, Jarrell HC, Logan SM, Brisson J-R. 2012. Structural characterization of
621 surface glycans from *Clostridium difficile*. *Carbohydr Res* 354:65–73.
- 622 35. Dembek M, Barquist L, Boinett CJ, Cain AK, Mayho M, Lawley TD, Fairweather NF, Fagan RP. 2015.
623 High-throughput analysis of gene essentiality and sporulation in *Clostridium difficile*. *MBio*
624 6:e02383.
- 625 36. Peltier J, Hamiot A, Garneau JR, Boudry P, Maikova A, Hajnsdorf E, Fortier L-C, Dupuy B, Soutourina
626 O. 2020. Type I toxin-antitoxin systems contribute to the maintenance of mobile genetic elements
627 in *Clostridioides difficile*. *Commun Biol* 3:718.

- 628 37. Hussain HA, Roberts AP, Mullany P. 2005. Generation of an erythromycin-sensitive derivative of
629 *Clostridium difficile* strain 630 (630Deltaerm) and demonstration that the conjugative transposon
630 Tn916DeltaE enters the genome of this strain at multiple sites. *J Med Microbiol* 54:137–141.
- 631 38. Ammam F, Patin D, Coullon H, Blanot D, Lambert T, Mengin-Lecreulx D, Candela T. 2020. AsnB is
632 responsible for peptidoglycan precursor amidation in *Clostridium difficile* in the presence of
633 vancomycin. *Microbiology (Reading)* 166:567–578.
- 634 39. Liszewski Zilla M, Chan YGY, Lunderberg JM, Schneewind O, Missiakas D. 2015. LytR-CpsA-Psr
635 enzymes as determinants of *Bacillus anthracis* secondary cell wall polysaccharide assembly. *J*
636 *Bacteriol* 197:343–353.
- 637 40. Schaefer K, Matano LM, Qiao Y, Kahne D, Walker S. 2017. In vitro reconstitution demonstrates the
638 cell wall ligase activity of LCP proteins. *Nat Chem Biol* 13:396–401.
- 639 41. ChapetónMontes D, Candela T, Collignon A, Janoir C. 2011. Localization of the *Clostridium difficile*
640 cysteine protease Cwp84 and insights into its maturation process. *J Bacteriol* 193:5314–5321.
- 641 42. Hashizume H, Sawa R, Harada S, Igarashi M, Adachi H, Nishimura Y, Nomoto A. 2011. Tripropeptin C
642 Blocks the Lipid Cycle of Cell Wall Biosynthesis by Complex Formation with Undecaprenyl
643 Pyrophosphate. *Antimicrobial Agents and Chemotherapy* 55:3821–3828.
- 644 43. D’Elia MA, Millar KE, Beveridge TJ, Brown ED. 2006. Wall teichoic acid polymers are dispensable for
645 cell viability in *Bacillus subtilis*. *J Bacteriol* 188:8313–8316.
- 646 44. Harrison J, Lloyd G, Joe M, Lowary TL, Reynolds E, Walters-Morgan H, Bhatt A, Lovering A, Besra GS,
647 Alderwick LJ. 2016. Lcp1 Is a Phosphotransferase Responsible for Ligating Arabinogalactan to
648 Peptidoglycan in *Mycobacterium tuberculosis*. *mBio* 7:e00972-16.

- 649 45. Ballister ER, Samanovic MI, Darwin KH. 2019. *Mycobacterium tuberculosis* Rv2700 Contributes to
650 Cell Envelope Integrity and Virulence. *J Bacteriol* 201:e00228-19.
- 651 46. Sebahia M, Wren BW, Mullany P, Fairweather NF, Minton N, Stabler R, Thomson NR, Roberts AP,
652 Cerdeño-Tárraga AM, Wang H, Holden MTG, Wright A, Churcher C, Quail MA, Baker S, Bason N,
653 Brooks K, Chillingworth T, Cronin A, Davis P, Dowd L, Fraser A, Feltwell T, Hance Z, Holroyd S, Jagels
654 K, Moule S, Mungall K, Price C, Rabinowitsch E, Sharp S, Simmonds M, Stevens K, Unwin L,
655 Whithead S, Dupuy B, Dougan G, Barrell B, Parkhill J. 2006. The multidrug-resistant human
656 pathogen *Clostridium difficile* has a highly mobile, mosaic genome. *Nat Genet* 38:779–786.
- 657 47. Gibson DG, Glass JI, Lartigue C, Noskov VN, Chuang R-Y, Algire MA, Benders GA, Montague MG, Ma
658 L, Moodie MM, Merryman C, Vashee S, Krishnakumar R, Assad-Garcia N, Andrews-Pfannkoch C,
659 Denisova EA, Young L, Qi Z-Q, Segall-Shapiro TH, Calvey CH, Parmar PP, Hutchison CA, Smith HO,
660 Venter JC. 2010. Creation of a bacterial cell controlled by a chemically synthesized genome. *Science*
661 329:52–56.
- 662 48. Pryor JM, Potapov V, Kucera RB, Bilotti K, Cantor EJ, Lohman GJS. 2020. Enabling one-pot Golden
663 Gate assemblies of unprecedented complexity using data-optimized assembly design. *PLoS One*
664 15:e0238592.
- 665 49. Pryor JM, Potapov V, Bilotti K, Pokhrel N, Lohman GJS. 2022. Rapid 40 kb Genome Construction
666 from 52 Parts through Data-optimized Assembly Design. *ACS Synth Biol* 11:2036–2042.
- 667 50. Cartman ST, Kelly ML, Heeg D, Heap JT, Minton NP. 2012. Precise manipulation of the *Clostridium*
668 *difficile* chromosome reveals a lack of association between the *tcdC* genotype and toxin
669 production. *Appl Environ Microbiol* 78:4683–4690.
- 670 51. Fagan R, Fairweather N. 2010. Dissecting the cell surface. *Methods Mol Biol* 646:117–134.

- 671 52. Cox AD, St Michael F, Aubry A, Cairns CM, Strong PCR, Hayes AC, Logan SM. 2013. Investigating the
672 candidacy of a lipoteichoic acid-based glycoconjugate as a vaccine to combat *Clostridium difficile*
673 infection. *Glycoconj J* 30:843–855.
- 674 53. DuBois Michel, Gilles KA, Hamilton JK, Rebers PA, Smith Fred. 1956. Colorimetric Method for
675 Determination of Sugars and Related Substances. *Anal Chem* 28:350–356.
- 676 54. Romano MR, Leuzzi R, Cappelletti E, Tontini M, Nilo A, Proietti D, Berti F, Costantino P, Adamo R,
677 Scarselli M. 2014. Recombinant *Clostridium difficile* toxin fragments as carrier protein for PSII
678 surface polysaccharide preserve their neutralizing activity. *Toxins (Basel)* 6:1385–1396.
- 679 55. Bruxelle J-F, Mizrahi A, Hoys S, Collignon A, Janoir C, Péchiné S. 2016. Immunogenic properties of
680 the surface layer precursor of *Clostridium difficile* and vaccination assays in animal models.
681 *Anaerobe* 37:78–84.
- 682 56. Cremniter J, Mainardi J-L, Josseaume N, Quincampoix J-C, Dubost L, Hugonnet J-E, Marie A,
683 Gutmann L, Rice LB, Arthur M. 2006. Novel mechanism of resistance to glycopeptide antibiotics in
684 *Enterococcus faecium*. *J Biol Chem* 281:32254–32262.
- 685 57. Trieu-Cuot P, Carlier C, Poyart-Salmeron C, Courvalin P. 1990. A pair of mobilizable shuttle vectors
686 conferring resistance to spectinomycin for molecular cloning in *Escherichia coli* and in Gram-
687 positive bacteria. *Nucleic Acids Research* 18:4296.
- 688 58. Fagan RP, Fairweather NF. 2011. *Clostridium difficile* Has Two Parallel and Essential Sec Secretion
689 Systems. *J Biol Chem* 286:27483–27493.
- 690 59. Heap JT, Pennington OJ, Cartman ST, Minton NP. 2009. A modular system for *Clostridium* shuttle
691 plasmids. *J Microbiol Methods* 78:79–85.

692

693 **Figures legends**

694 Figure 1

695 **The $\Delta lcpB$ mutant (JMV4) presents curved, inflated, longer and larger cells than**
696 **the parental strain JMV1.**

697 **A.** JMV3 ($\Delta lcpA$) and JMV4 ($\Delta lcpB$) single mutants were analyzed in optic microscopy
698 and complemented with pMTL84222 (vector), *pTcpA* (plasmid carrying *lcpA* expressed
699 with its own promoter) or *pTcpB* (plasmid carrying *lcpB* expressed with its own promoter).

700 Scale bar represents 20 μ m. **B.** The percentage of abnormal (curved, thick, or inflated)
701 cells among total cells was calculated by measuring more than 100 cells for each strain.

702 **C.** Cell length of the parental strain JMV1, JMV3 and JMV4 complemented with the
703 vector (pMTL84222), *pTcpA* or *pTcpB*. **D.** Cell width of the parental strain JMV1, JMV3
704 and JMV4 complemented with the vector (pMTL84222), *pTcpA* or *pTcpB*. For B, C and D,
705 the number above each group data represents the number of cells counted. **** means
706 student t-test *p-value* is < 0.0001.

707

708 Figure 2

709 **Both *lcpA* and *lcpB* have a constitutive expression**

710 GusA activity measured for *lcpA* (**A**) and *lcpB* (**B**) promoters GusA activity (blue curve)
711 was measured in Miller Units and growth (red curve) was followed by measuring the
712 optical density at 600 nm (OD_{600nm}) for 8 hours.

713

714 Figure 3

715 **Both $\Delta lcpA$ and $\Delta lcpB$ exhibit an altered PSII layer at the surface.**

716 Immunofluorescence assay of JMV1, JMV3 and JMV4 strains, was observed using
717 super-resolution microscope. Bacteria were stained for DNA (DAPI, blue) and PSII (anti-
718 PSII, green). The merged picture shows both localizations simultaneously (scale bar
719 represents 20 μm). The panel shows a magnify part of the picture (scale bar represents
720 2 μm).

721

722 Figure 4

723 **The *lcp* conditional-lethal mutant (JMV6) is not able to grow without ATc induction**
724 **of the P_{tet} -*lcpB* copy.**

725 **A.** JMV1 and JMV2 grown in liquid culture were diluted and plated on BHI agar petri
726 dishes. JMV6 grown in liquid culture in the presence of 10 (JMV6 (ATC 10)) or 50
727 ng.mL^{-1} (JMV6 (ATc 50)) of ATc was diluted and plated on BHI agar petri dishes. The
728 control strain, JMV6 harboring the plasmid *p/cpA* grown in liquid culture in the presence
729 of 50 ng.mL^{-1} of ATc (JMV6 + *p/cpA* (ATc 50)) was diluted and plated on BHI agar petri
730 dishes. Petri dishes contained ATc from 0 to 250 ng.mL^{-1} in the BHI agar medium. **B.**
731 JMV1, JMV2, JMV6 and JMV6 + *p/cpA* were grown in the presence of 50 ng.mL^{-1} of ATc
732 and then, the growth was measured for 20h (1200 minutes) without ATc (JMV1, JMV6 +
733 *p/cpA*), in the presence of 10 ng.mL^{-1} of ATc (JMV6 (ATc 10)) or in the presence of 50
734 ng.mL^{-1} of ATc (JMV2 (ATc 50), JMV6 (ATc 50), JMV6 + *p/cpA* (ATc 50)). The graph
735 represents the mean of 3 independent experiments.

736

737 Figure 5

738 **In the presence of 10 ng.mL⁻¹ of ATc, the *lcp* conditional-lethal mutant (JMV6)**
739 **loses its rod shape.**

740 **A.** JMV1, JMV6 + *p_{lcpA}*, JMV6 + *p_{lcpB}*, JMV2 in the presence of 50 ng.mL⁻¹ (JMV2
741 (ATc 50)) of ATc and JMV6 in the presence of 10 (JMV6 (ATc 10)) or 50 ng.mL⁻¹ (JMV6
742 (ATc 50)) of ATc were observed in optic microscopy. The scale bar represents 20 μm.

743 **B and C.** Cell length (**B**) and cell width (**C**) of bacteria from each strain observed in **A**.
744 were measured. The number above each group data represents the number of cells
745 counted. **** means student t-test *p-value* is < 0.0001.

746

747 Figure 6

748 **In the presence of 10 ng.mL⁻¹ of ATc , the *lcp* conditional-lethal mutant (JMV6)**
749 **loses its rod shape but PSII is still detected at the surface.**

750 Immunofluorescence assay of JMV1, JMV2 in the presence of 50 ng.mL⁻¹ (JMV2
751 (ATc50)), JMV6 in the presence of 10 ng.mL⁻¹ (JMV6 (ATc10)), JMV6 in the presence of
752 50 ng.mL⁻¹ (JMV6 (ATc50)) and JMV6 + *p_{lcpA}* in the presence of 50 ng.mL⁻¹ (JMV6 +
753 *p_{lcpA}* (ATc50)) strains was observed using super-resolution microscope. Bacteria were
754 stained for DNA (DAPI, blue) and PSII (anti-PSII, green). The merged picture shows
755 both localizations simultaneously (scale bar represents 20μm). The panel shows a
756 magnify part of the picture (scale bar represents 2μm).

757

758 Figure 7

759 **PSII is released into the supernatant of the JMV6 strain in the presence of**
760 **10 ng.mL⁻¹ of ATc**

761 Dot blot analysis using specific antibodies targeting PSII was performed on the bacterial
762 surface content (pellet) and supernatant content (culture supernatant) from JMV1, JMV2
763 JMV3, JMV4, JMV6 grown in the presence of 10 ng.mL⁻¹ of Atc (JMV6 (Atc 10)), JMV6
764 grown in the presence of 50 ng.mL⁻¹ of Atc (JMV6 (Atc 50)) and JMV6 *p/cpA* grown in
765 the presence of 50 ng.mL⁻¹ of Atc (JMV6 + *p/cpA* (Atc 50)). Each content was diluted up
766 to 1:64. PG-PSII is used as positive control and PG as a negative control.

767

768 Figure 8

769 **PSII anchoring impairment is associated with Cwp proteins released in the culture**
770 **supernatant.**

771 Characterization of surface (**A, C, E**) and supernatant (**B, D, F**) protein profiles from
772 JMV1, JMV2, JMV6 and JMV6 + *p/cpA* grown in the absence of Atc (-) or in the
773 presence of 10 ng.mL⁻¹ of Atc (10) or in the presence of 50 ng.mL⁻¹ of Atc (50).
774 Coomassie blue staining (**A, B**), anti-Cwp66 Western blots (**C, D**) and anti-SlpA Western
775 blots (**E, F**) were performed. The protein ladder is graduated in kg Dalton (kDa). MW:
776 molecular weight.

777

778 Figure 9

779 **PSII anchoring mutants present an autolysis phenotype**

780 Autolysis of JMV1, JMV3 and JMV4, harboring the empty plasmid pMTL84222 (+
781 vector), the *p/cpA* plasmid (+ *p/cpA*) or the *p/cpB* plasmid (+ *p/cpB*) were measured and
782 presented in **A**. Autolysis of JMV1, JMV2 grown in the presence of 50 ng.mL⁻¹ of ATc
783 (50), JMV6 + *p/cpA*, JMV6 grown in the presence of 10 ng.mL⁻¹ of ATc (JMV6 (ATc10)),
784 JMV6 grown in the presence of 50 ng.mL⁻¹ of ATc (JMV6 (ATc50)) and JMV6 + *p/cpA*

785 grown in the presence of 50 ng.mL⁻¹ of ATc (JMV6 + *p/**cpA* (ATc50)), were measured
786 and presented in **B**. The optical density was measured for 3 hours (180 minutes) and the
787 result is presented as a cell survival percentage. The graph represents the mean of 3
788 independent experiments.

789

790 Figure 10

791 **PG cytoplasmic precursors accumulate when PSII anchoring is impaired**

792 **A, B** and **C**. Purification and quantification of UDP-MurNAc-pentapeptide from JMV1 (**A**),
793 JMV6 grown in the presence of 10 ng.mL⁻¹ of ATc (JMV6 (ATc10)) (**B**), JMV6 + *p/**cpA*
794 grown in the presence of 50 ng.mL⁻¹ of ATc (JMV6 + *p/**cpA* (ATc50)) (**C**) was performed.
795 **D**. A table represents each peak area and area/optical density ratio. In addition, the
796 observed and calculated monoisotopic masses obtained after mass spectrometry
797 analysis are presented in the two last columns. mAU = milli Arbitrary Unit, Da = Dalton

798

799 **Supplemental figures legends**

800 Figure S1

801 **Graphic map of the pJV10 plasmid used to construct deletion plasmids of the *lcp***

802 On this graphic map of the pJV10 plasmid, created by Serial Cloner, the spectinomycin
803 resistance gene flanked by Bsal sites to allow Golden Gate assembly, an erythromycin
804 resistance gene, and the P_{tet}-CD2517 (Toxin) from the pMSR to facilitate
805 counterselection during the allelic exchange are shown.

806

807 Figure S2

808 **The Δ *lcpB* strain presents an altered growth**

809 Growth curve of single mutant strains of *lcpA* (JMV3) and *lcpB* (JMV4), harboring either
810 the pMTL84222, or the *plcpA* or *plcpB* plasmid. The growth was observed in BHI
811 medium for 17 hours (1020 minutes). The graph represents the mean of 3 independent
812 experiments.

813

814 Figure S3

815 **The Δ *lcpB* mutant (JMV4) is thicker, curved, or inflated in liquid culture.**

816 These panels present additional pictures of the JMV4 strain observed in optic
817 microscopy. The scale bar represents 20 μ m.

818

819 Figure S4

820 **The single *lcp* mutants JMV3 and JMV4 exhibit a normal S-layer content**

821 This Coomassie staining of Cwp protein extractions shows that the Cwp content of the
822 S-layer of JMV1, JMV3 and JMV4 harboring either pMTL84222 (vector), *plcpA* or *plcpB*
823 plasmid. The protein ladder is graduated in kg Dalton (kDa). MW: molecular weight.

824

825 Figure S5

826 **The PSII was obtained and the absence of contamination with LTA was confirmed
827 by NMR.**

828 ^1H (A) and ^{31}P (B) NMR spectra of the PSII extracted from culture pellets of the 630
829 strain. Two samples were sent for analysis, named PSII 3.2 and PSII 2.6. Both were
830 confirmed to contain PSII. The chemical shift is measured in part-per-million (ppm).

831

832 Figure S6

833 **The immunization led to antibodies production and these antibodies showed good**
834 **specificity for the PSII**

835 This dot blot assay shows that the antibodies produced by the rabbits recognize well the
836 RMN-verified PSII (**A**) of *C. difficile* and the PG linked PSII (PG-PSII) (**A** and **C**) and do
837 not cross-react with peptidoglycan (**A** and **C**) or lipoteichoic acid (LTA) (**C**) of *C. difficile*.
838 Moreover, different samples at different stages of the purification process were tested
839 (**B**). Briefly, PSII purification protocol was performed as followed (white boxes, steps of
840 PSII purification, yellow boxes, potential contaminant molecules) : 1 litter of *C. difficile*
841 culture was pelleted. Pellet was washed in PBS and boiled in water for 30 minutes. After
842 centrifugation, pellet (a) was tested to know whether some PSII were not recovered. The
843 supernatant was further used for purification and a TCA precipitation was performed.
844 After centrifugation, pellet (b) was tested to know whether some PSII was not recovered;
845 it was resuspended in water and centrifuged again, giving pellet (c). The supernatant (d)
846 was dialyzed and applied on fPLC. PSII was recovered, dosage was performed by
847 phenol sulfuric method and PSII was analyzed by NMR.

848

849 Figure S7

850 **A new strategy designed to construct a conditional-lethal mutant in *C. difficile***

851 Schematic representation of the strategy used to create a conditional-lethal mutant of *C.*
852 *difficile* *lcpA* and *lcpB* genes. The strategy consists in three major steps: first the
853 insertion of an inducible copy of *lcpB* in the *erm* locus of the chromosome (under control
854 of P_{tet}), then the deletion of both *lcpA* and *lcpB* by replacing the ORFs with a *catP* gene,
855 and finally the control of the *l* expression of *lcpB* thanks to ATc induction.

856

857 Figure S8

858 **The anchoring of PSII is essential for *C. difficile* growth**

859 The conditional-lethal mutant pre-cultured overnight in liquid BHI in the presence of 50
860 ng.mL⁻¹ATc is not able to grow on a BHI plate without ATc but grows correctly in the
861 presence of ATc at 50 ng.mL⁻¹.

862

863

864

865 Tables :

866

867 Table 1. Bacterial strains and plasmids used in this study.

Name	Genotype or primer sequence	Source or reference
Bacterial strains		
<i>Escherichia coli</i>		
TG1	<i>E. coli</i> k12 (F', <i>tra</i> D36, <i>lacIq</i> , Δ <i>lacZ</i> , MIS, <i>pro</i> A+B+/SupE, Δ (<i>hdsM-mcrB</i>))	Laboratory stock
HB101 pRK24	<i>E. coli</i> (pRK24) (F - Δ (<i>gpt-proA</i>) 62 Leu B6 <i>gln</i> V44 <i>ara</i> -14 <i>galK2 lacY1</i> Δ (<i>mcrC-mrr</i>) <i>rps</i> L20 (<i>srf</i> ^t) <i>xyl</i> -5 <i>mlt</i> -1 <i>rec</i> A13, pRK24	Laboratory stock
<i>Clostridioides difficile</i>		
630	Clinical strain, Erm ^R	Sebahia <i>et al.</i> 2006 (46)
630 Δ <i>erm</i>	Derivative of 630 strain, Erm ^S	Hussain <i>et al.</i> 2005 (37)
JMV1	Derivative of 630 strain, Erm ^S , Δ (<i>CD630_20100</i> , <i>CD630_20091</i> , <i>CD630_20090</i> , <i>CD630_20080</i> , <i>CD630_20071</i> , <i>CD630_20070</i>)	This work
JMV2 (630 P _{tet} ⁻ <i>lcpB</i>)	Derivative of 630 strain, Erm ^S , Δ (<i>CD630_20100</i> , <i>CD630_20091</i> , <i>CD630_20090</i> , <i>CD630_20080</i> , <i>CD630_20071</i> , <i>CD630_20070</i>)::P _{tet} ⁻ <i>lcpB</i>	This work
JMV3 (Δ <i>lcpA</i>)	JMV1 Δ <i>lcpA</i>	This work
JMV4	JMV1 Δ <i>lcpB</i>	This work
JMV5 (Δ <i>lcpB</i> P _{tet} ⁻ <i>lcpB</i>)	JMV2 Δ <i>lcpB</i>	This work
JMV6 (Δ <i>lcpA</i> Δ <i>lcpB</i> P _{tet} ⁻ <i>lcpB</i>)	JMV2 Δ <i>lcpA</i> Δ <i>lcpB</i>	This work
Plasmids and vectors		
pMSR	Circular cloning vector, 5624 nucleotides, <i>catP</i> , <i>alacZ</i> , P _{tet} - <i>CD2517</i> (toxin), pseudo-suicide plasmid, Cm ^R	Gift from J. Peltier (36)
pBLUNT	Linear cloning vector from Invitrogen, Kn ^R	Invitrogen

pAT28	Mobilizable shuttle plasmid, Spc ^R	Trieu-Cuot <i>et al.</i> 1990 (57)
pRPF185	P _{ter} -gusA Tm ^R expression and cloning vector	Fagan <i>et al.</i> 2011 (58)
pMTL-83151	Cm ^R cloning vector, pCB102 replicative origin	Heap <i>et al.</i> 2009 (59)
pMTL-84151	Cm ^R cloning vector, pCD6 replicative origin	
pMTL-84222	Erm ^R cloning vector, pCD6 replicative origin	
pJV4	pBLUNTΩaadA, spectinomycin resistance gene flanked by Bsal sites, Kn ^R	This work
pJV5	pMSR derivative, used to construct pJV8, Cm ^R and Sp ^R	This work
pJV6	pMTL-83151ΔcatPΩermB, Erm ^R	This work
pJV7	pMSRΩaadA, spectinomycin resistance gene flanked by Bsal sites, Cm ^R and Sp ^R	This work
pJV8	pMSR derivative, plasmid used for Erm locus deletion, Cm ^R and Sp ^R	This work
pJV10	pJV7ΔcatPΩermB, Erm ^R and Sp ^R	This work
pJV11	pJV10 derivative, plasmid used for lcpA deletion plasmid, Erm ^R	This work
pJV12	pJV10 derivative, plasmid used for lcpB deletion plasmid, Erm ^R	This work
pJV13	pJV10 derivative, plasmid used for lcp region deletion, Erm ^R	This work
pTC131	pMTL-84151ΩaadA, spectinomycin resistance gene flanked by Bsal sites, Cm ^R and Sp ^R	This work
pMEZ5	pTC131ΔcatPΩermB, Erm ^R and Sp ^R	This work
p/lcpA (pMEZ12)	pMEZ-5ΩP _{lcpA} -lcpA, Erm ^R	This work
pJV20	pTC131ΩP _{lcpB} -lcpB, Cm ^R	This work
p/lcpB (pJV21)	pMTL-84222ΩP _{lcpB} -lcpB, Erm ^R	This work
pJV27	pJV8ΩP _{ter} -lcpB, Cm ^R	This work
pMDR1	pTC131ΩaphAΩgusA, Cm ^R and Kn ^R	This work
pMDR2	pMDR1ΔaphAΩaadA, Cm ^R and Sp ^R	This work
pMDR5	pMDR2ΔaadAΩP _{lcpB} , Cm ^R	This work
pMDR8	pMDR2ΔaadAΩP _{lcpA} , Cm ^R	This work

870 Authors contributions

871 Conceptualization: TC, JMV

872 Funding acquisition: TC, JMV,CJ

873 Experimental work: JMV, TC

874 PSII purification and RMN: JMV, LE, SDQ

875 PG precursors experiment: YL, JH, MA, JMV

876 Supervision: TC

877 Writing original draft: TC, JMV

878 Validation: JMV, TC, LE, SDQ, YL, JH, MA, CJ

879

880 Conflicts of interest

881 The authors declare that they have no conflicts of interest with the contents of this
882 article.

883

884 Abbreviations used

885 ATc: anhydrotetracycline

886 CWGPs: cell wall glycopolymers

887 MW: molecular weight

888 PSII: polysaccharide II

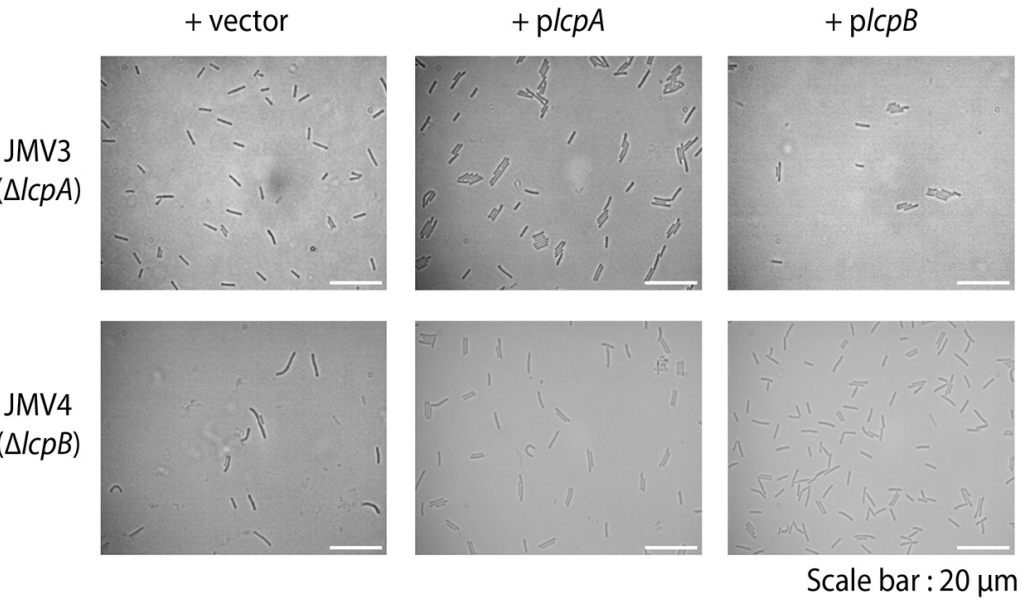
889 PG: peptidoglycan

890 C₅₅P: C₅₅-undecaprenyl phosphate

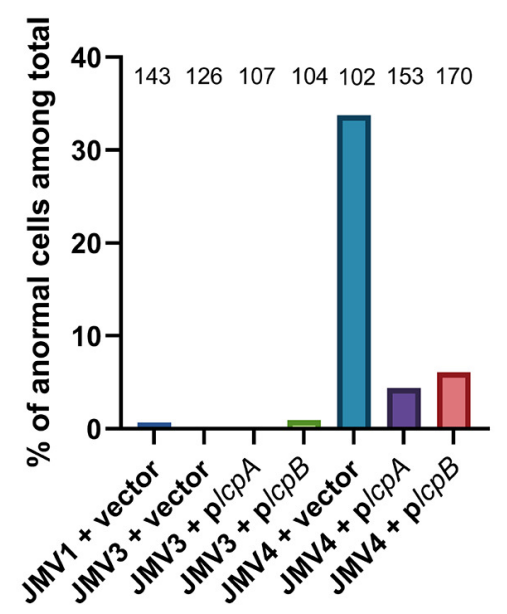
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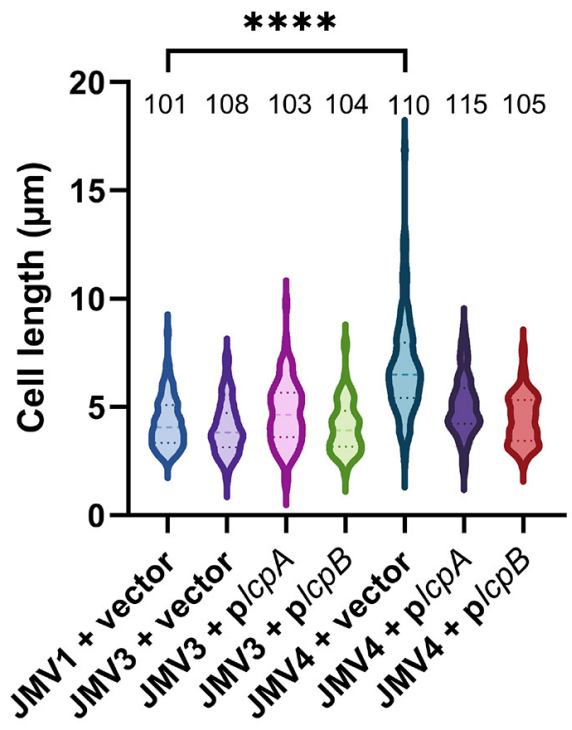
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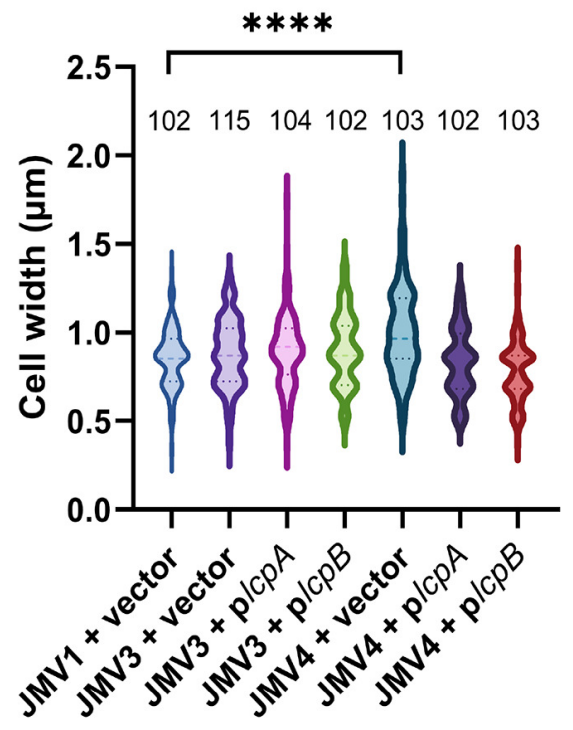
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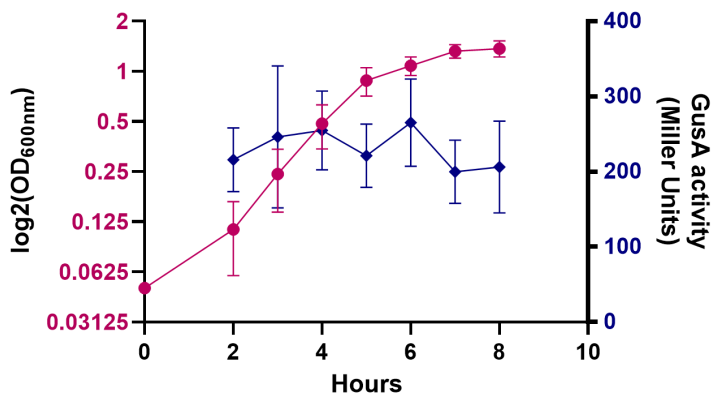
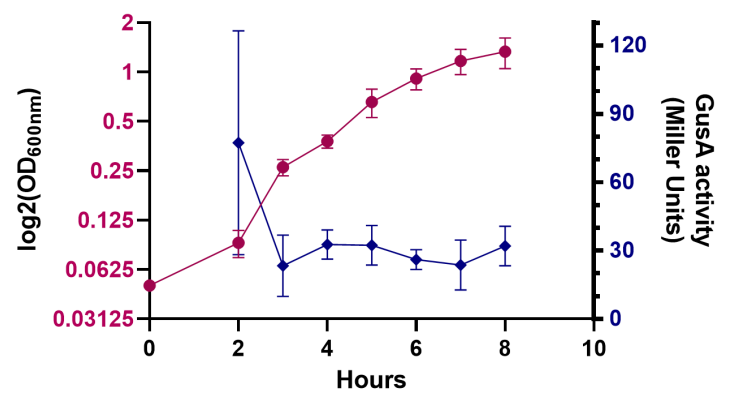


C



D



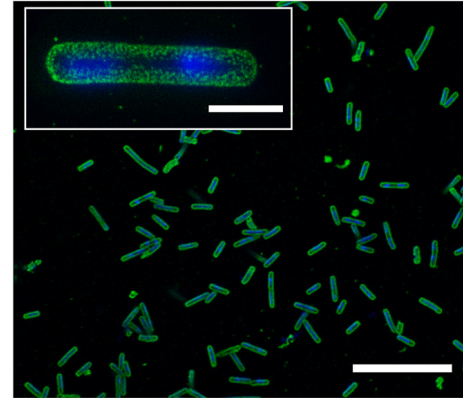
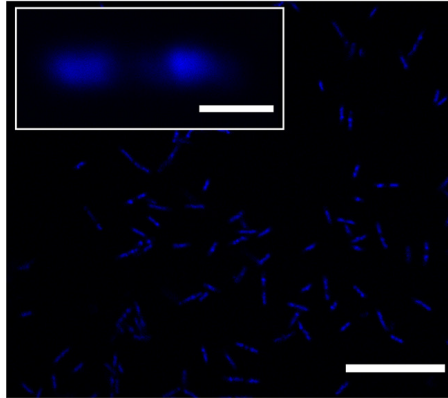
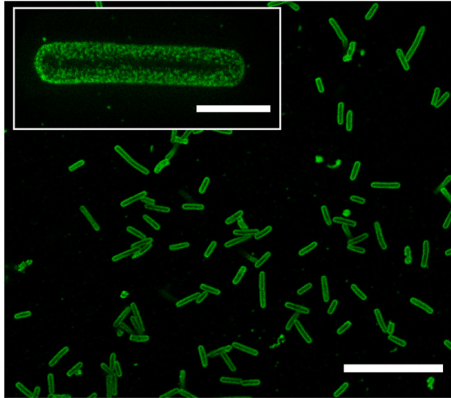
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Anti-PSII

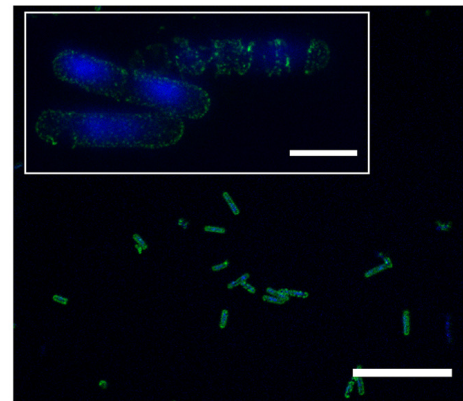
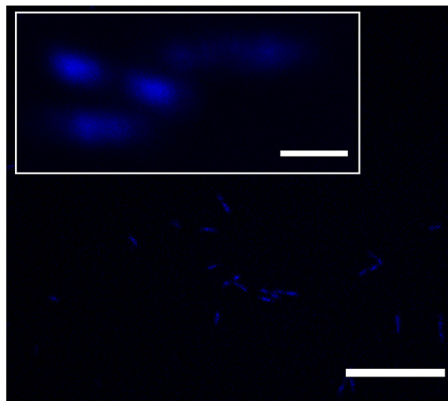
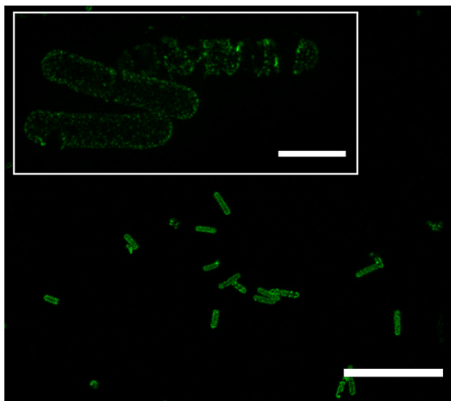
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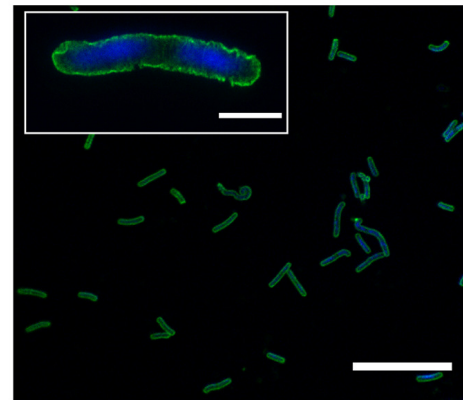
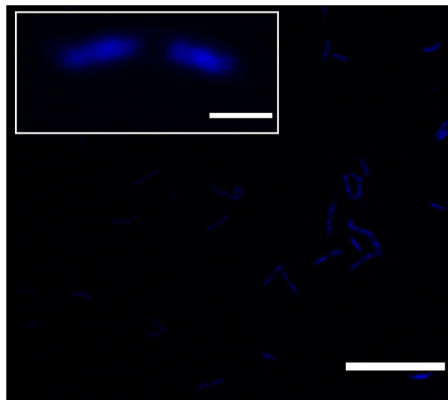
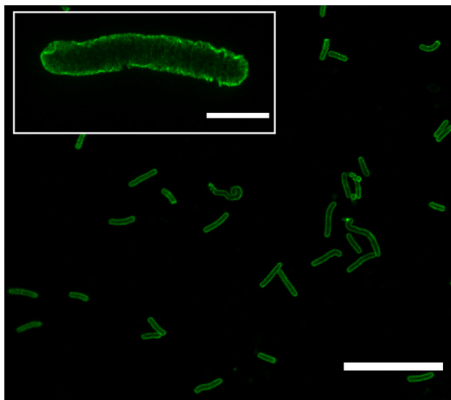
JMV1



JMV3

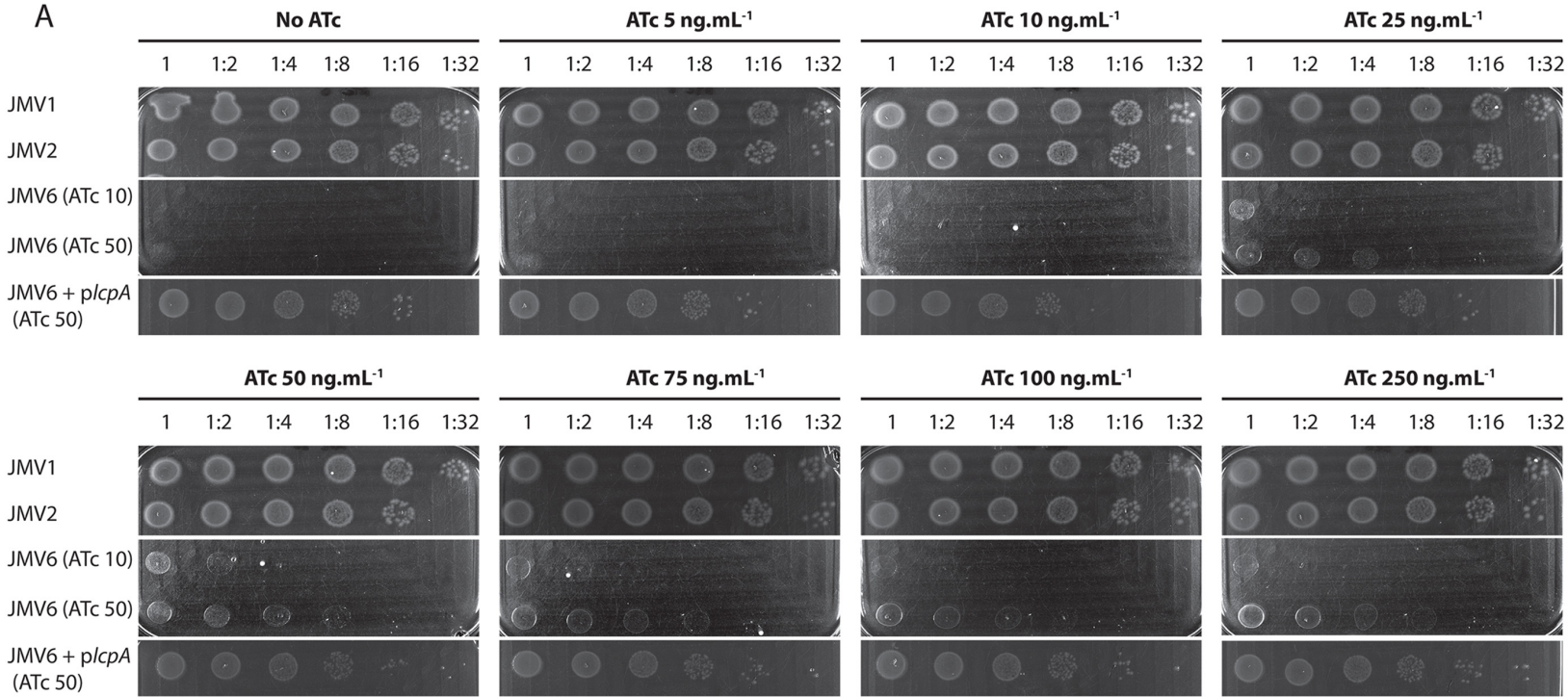


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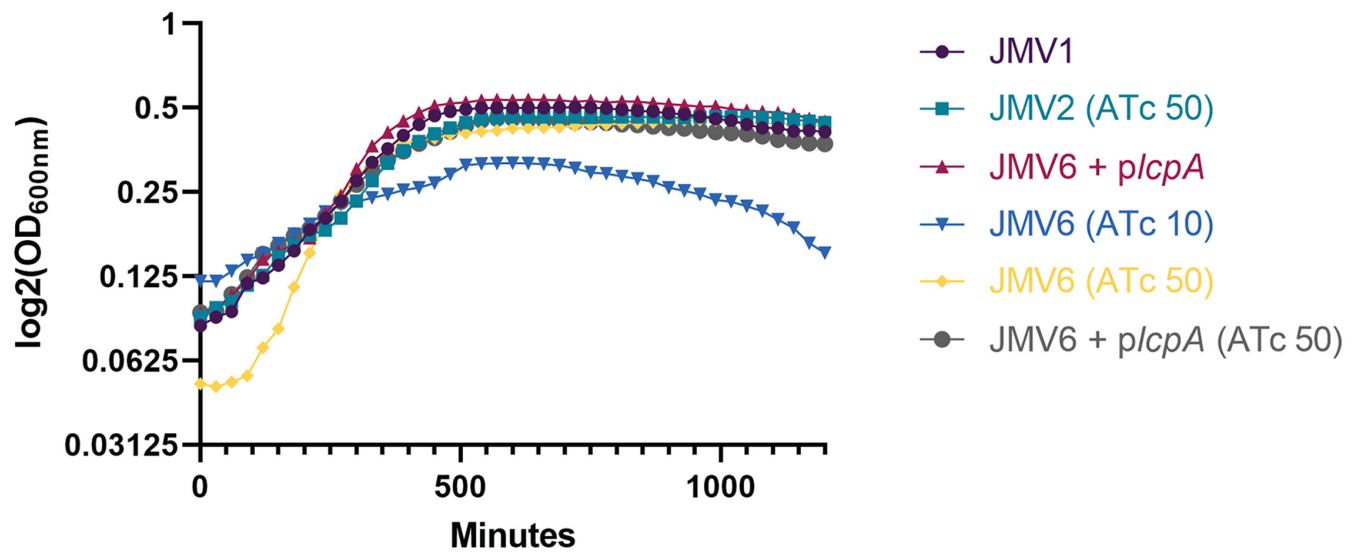


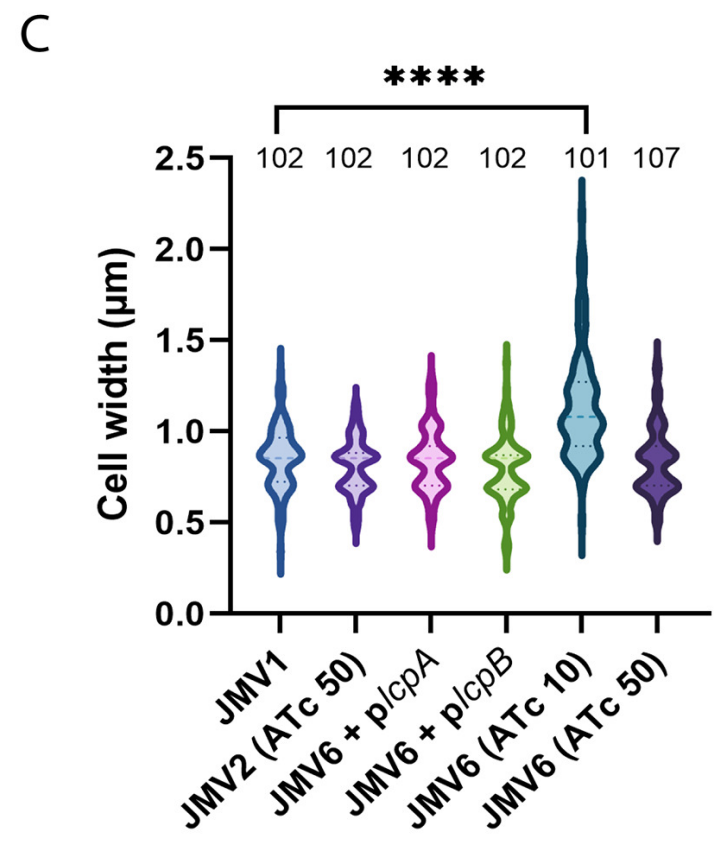
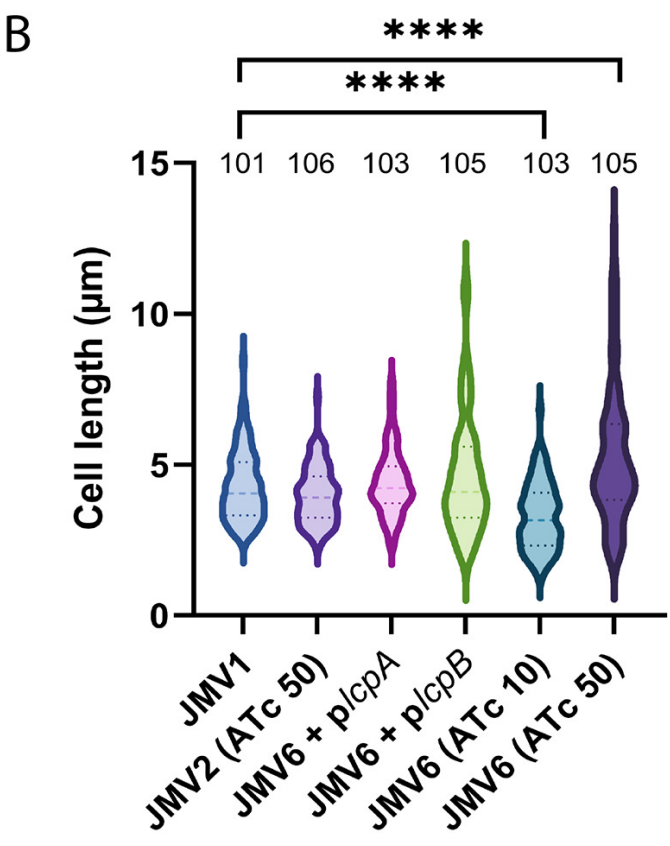
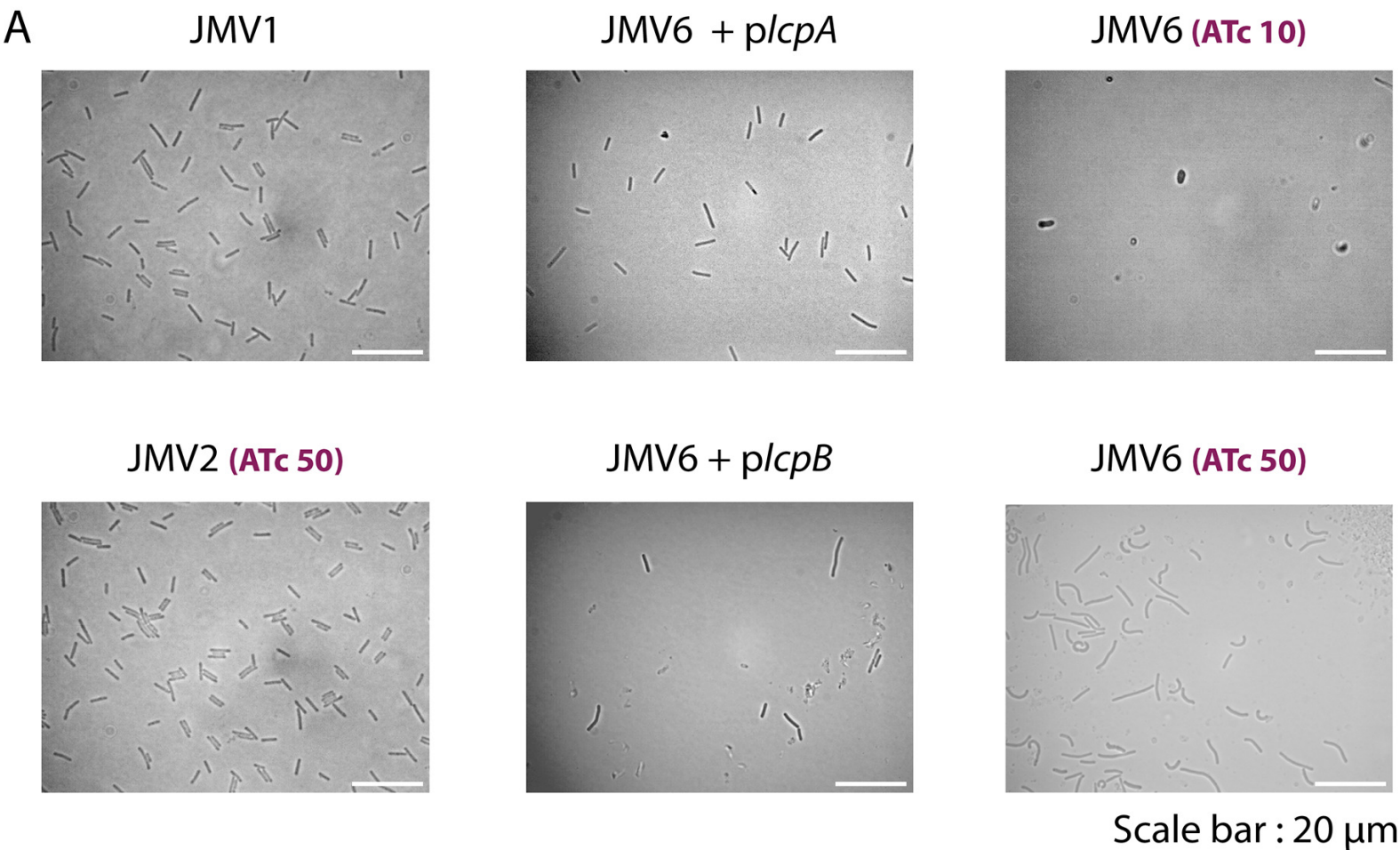
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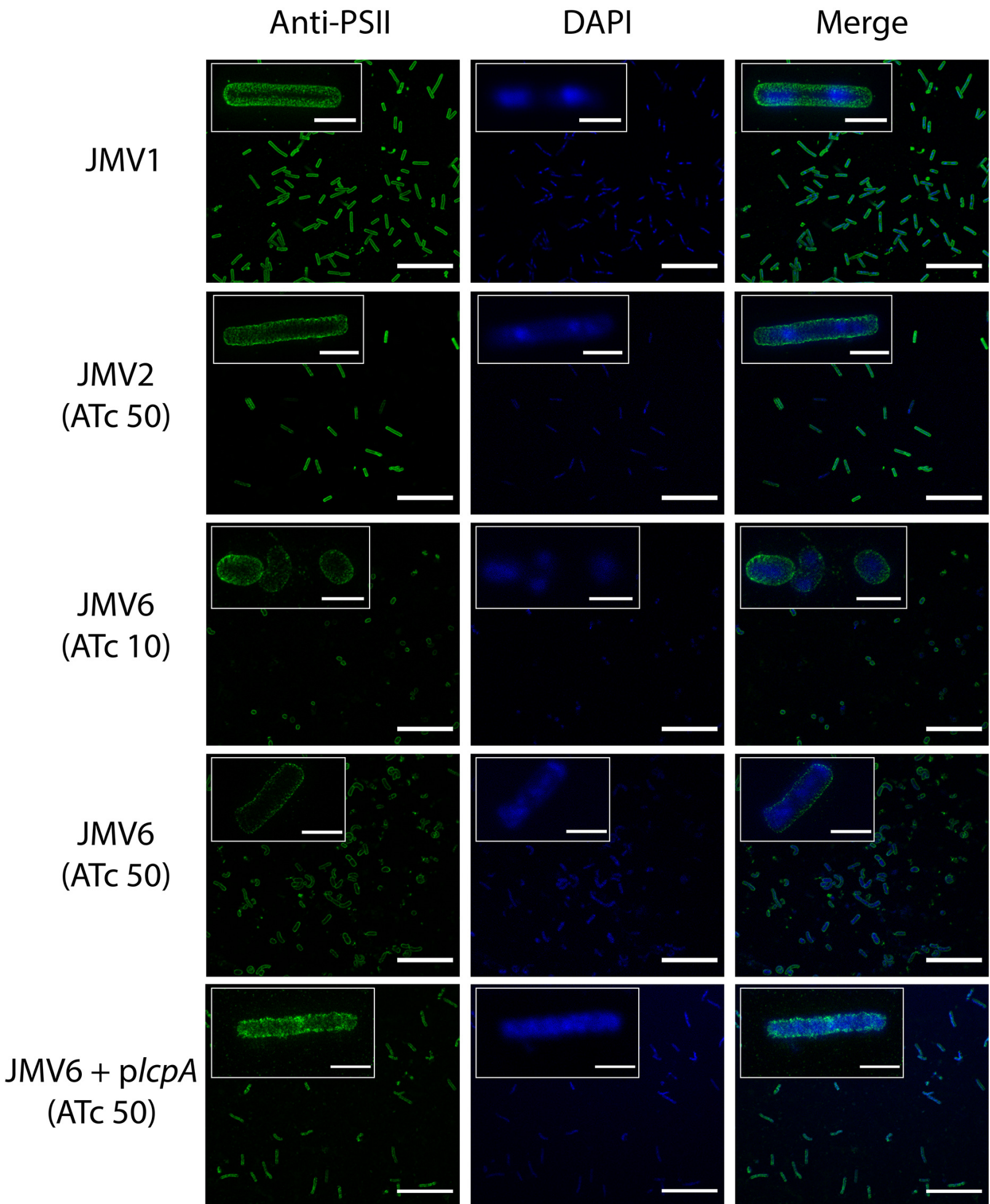
A



B







Scale bars : inserts = 2 μm large views = 20 μm

Pellet

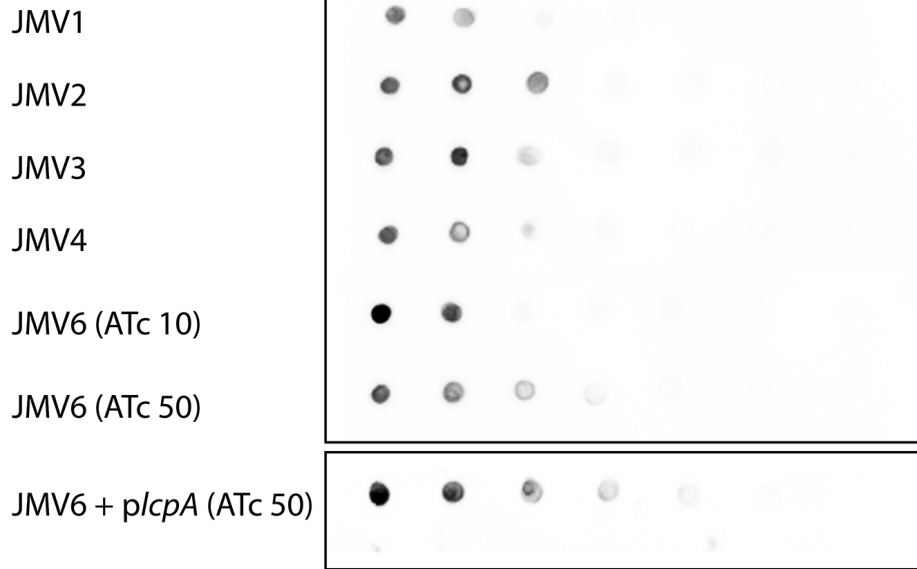
Culture supernatant

PG-PSII PG
| |

PG-PSII PG
| |

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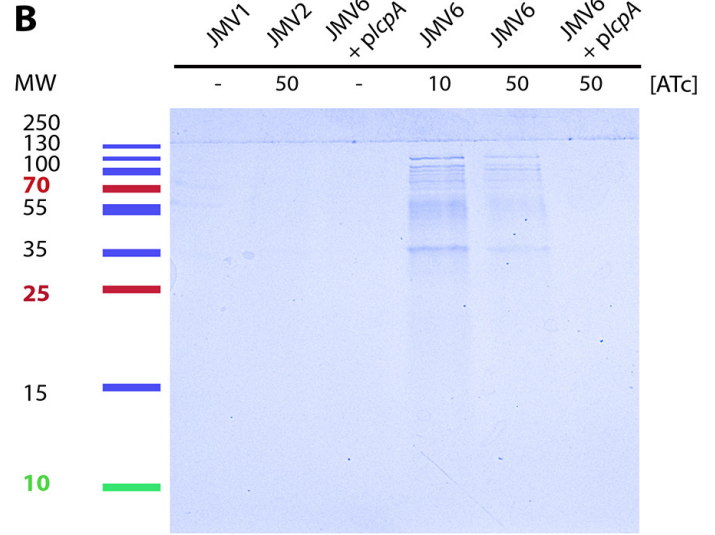
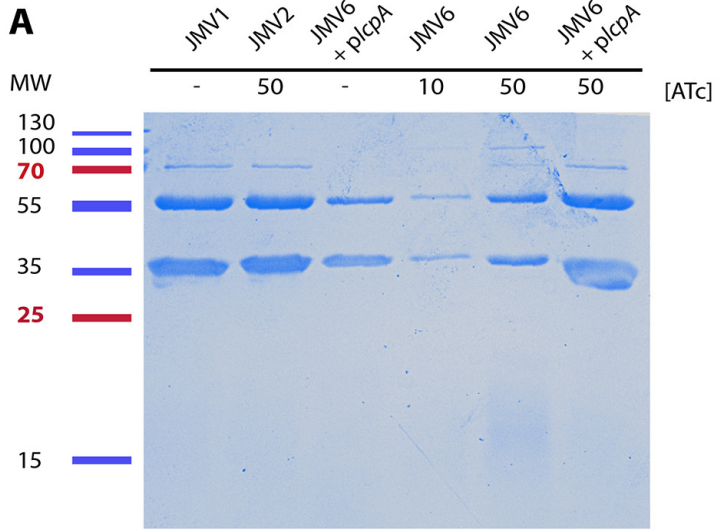
1 1:2 1:4 1:8 1:16 1:32 1:64



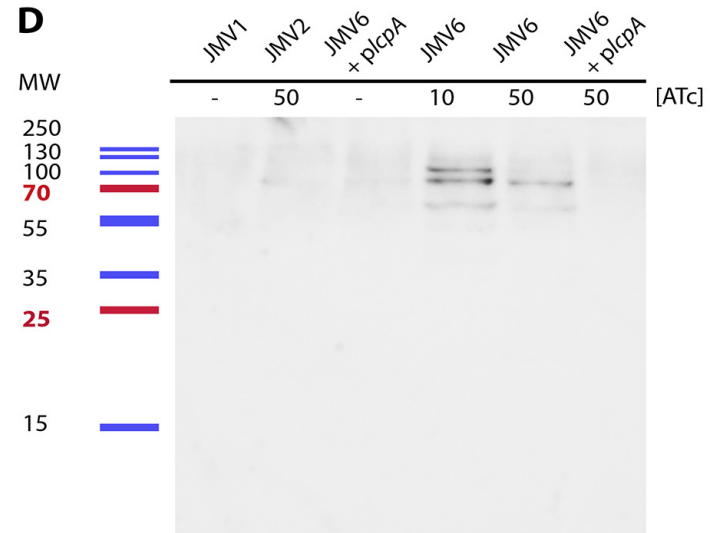
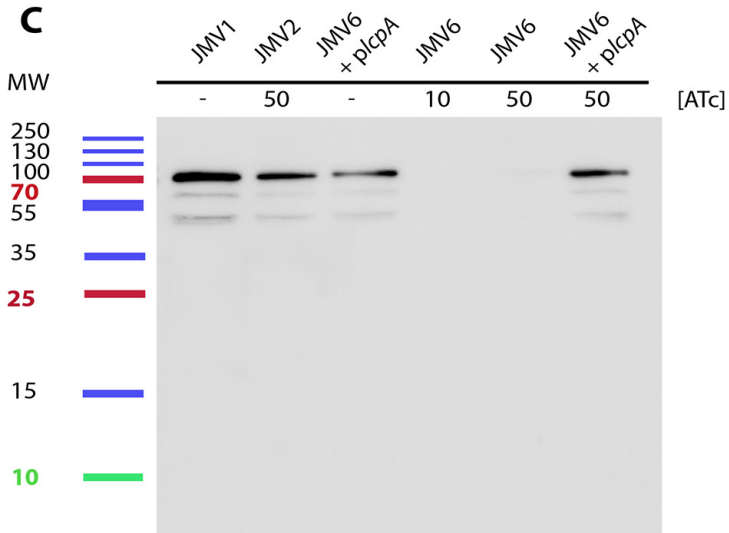
Cwp proteins extracts

Supernatant fraction

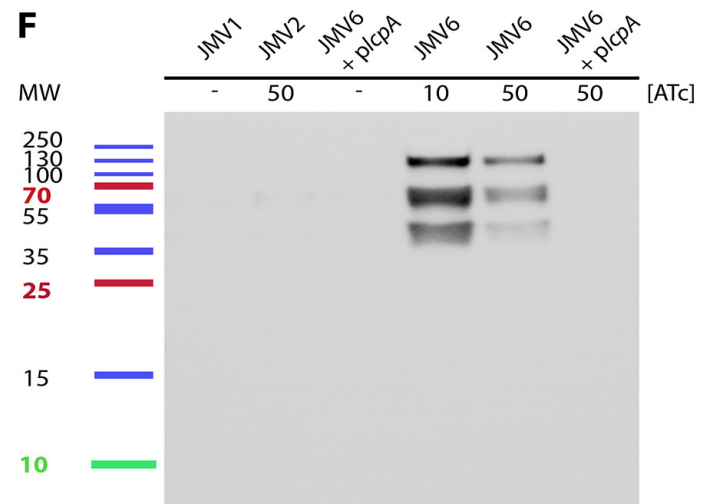
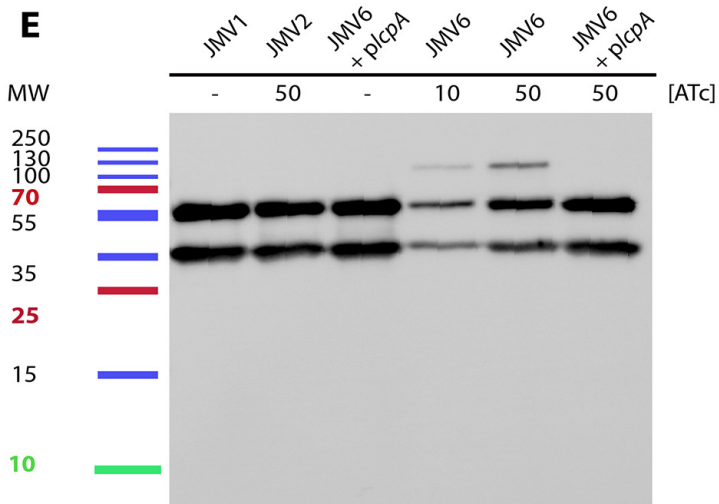
Coomassie blue staining

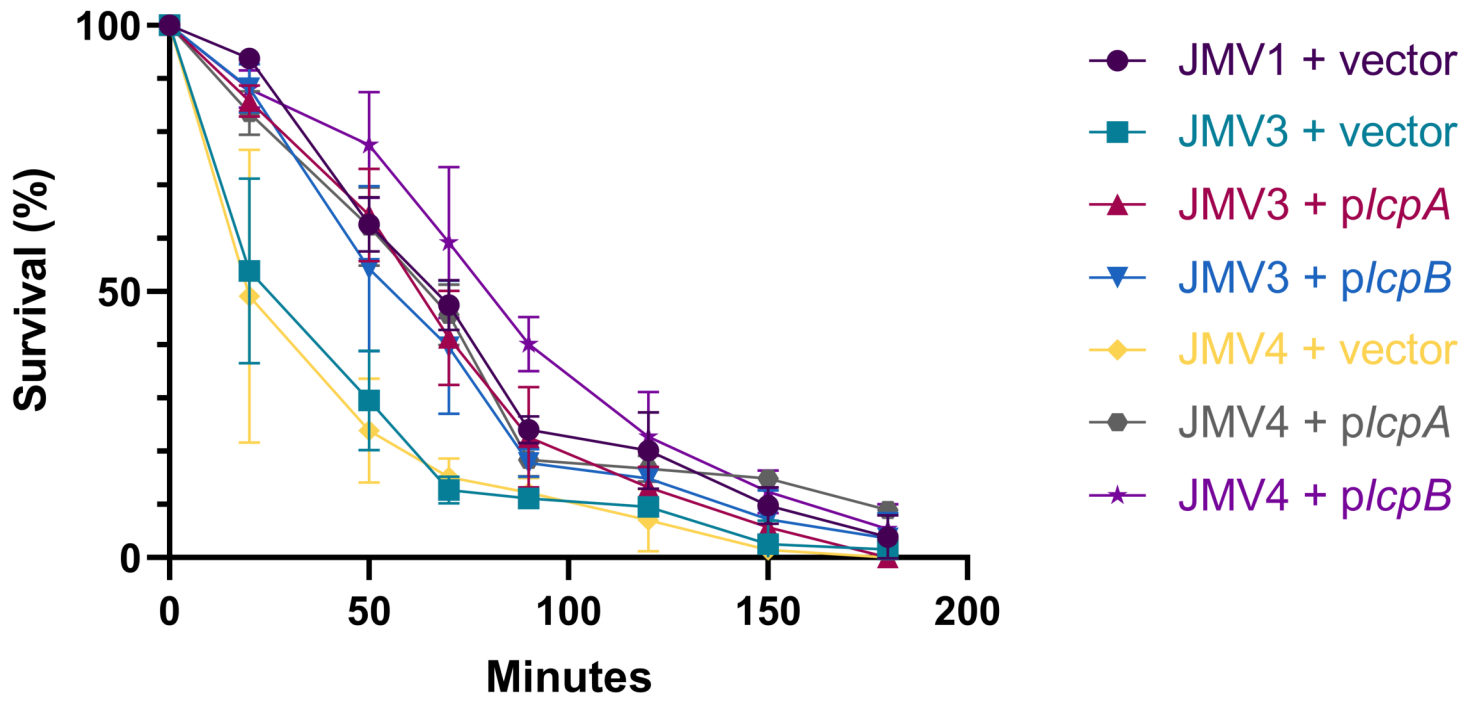
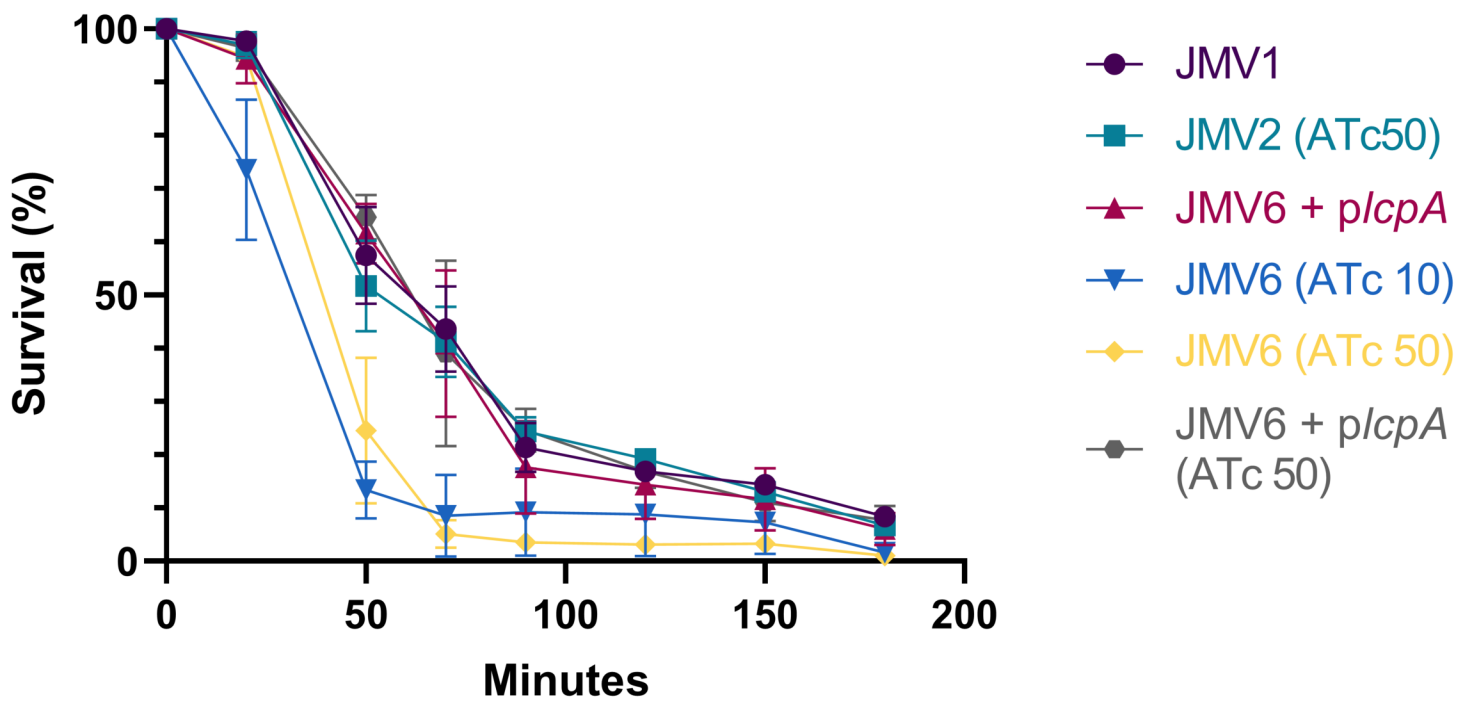


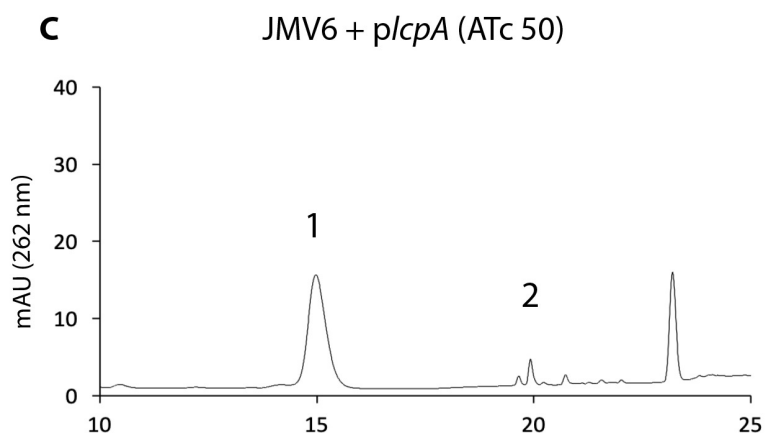
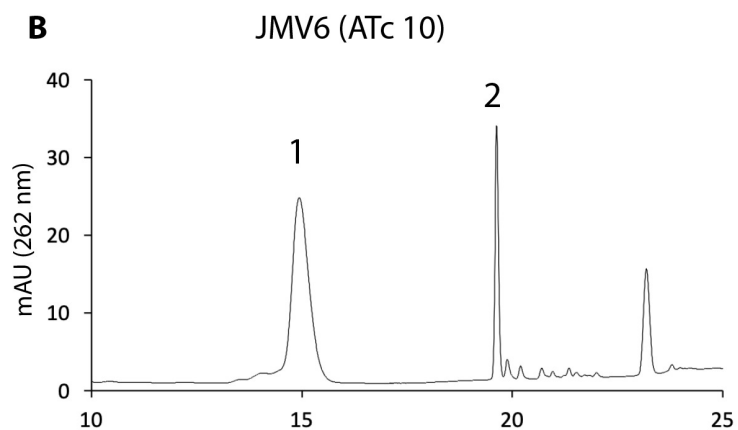
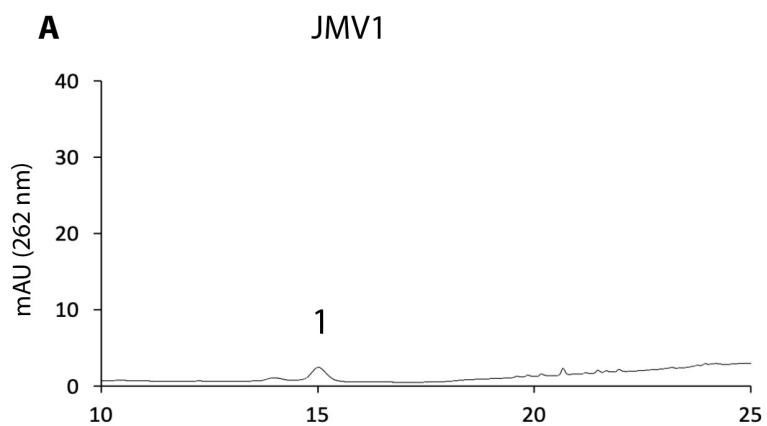
Anti-Cwp66 western



Anti-SlpA western



A**B**



D

Strain	Peak	Retention Time (min)	Area (mAU*min)	Area/OD _{600nm}
JM V1	1	15.0	0.8	0.5
	2	ND	ND	ND
JM V6 (ATc 10)	1	14.9	11.5	10.65
	2	19.6	3.2	3.0
JM V6 + <i>plcpA</i> (ATc 50)	1	15.0	6.9	3.0
	2	19.7	0.1	0.05

Peak 1 : UDP-MurNAc-pentapeptide

Peak 2 : amidated UDP-MurNAc-pentapeptide

SUPPLEMENTARY DATA

Tables

Table S1: Primers used for plasmid constructions

Name	Use: Construction of ...	5' Primer tail	Primer
JV54	pJV4	GGCTACTGCCAGAGACC	GGAAAAGATCCGGGGGATCGATCCTCTAG
JV55		GGCTACTTGCTGAGACC	TTAGCCTAATTGAGAGAAGTTTCTATAG
JV50	pJV5	GCAGATAAATAA	TGCCAGAGACCGGAAAAGATCCGGG
JV51		GTGTAACCTTCC	TTGCTGAGACCTTAGCCTAATTGAGAGAAG
JV52		AAGGTCTCAGCAA	GGAAAGTTACACGTTACTAAAGGGAATG
JV53		AGCTTGCATGTCTGCAGGCCT CGAG	CTTGTCGGTAGCTGTGGTATGGATTG
TC287	pJV6		GTTTAAACTCCTTTTTGATAATCTC
TC288			CGCTTATAATCCATAACAATCATCC
TC289		TATGGATTATAAGC	GCCGAAGCAAACCTAAGAGTGTG
TC290		AAAAGGAGTTTAAAC	AAACACATTCCCTTTAGTAACGTG
JV48	pJV8	AGATTGTAGTTCTTCGGATCCTCTA	GACTATGGAACGTACACTTTTGCGG
JV49		CCGGTCTCTGGCA	TTATTTATCTGCGTAATCACTGTTTTAGTC
JV58	pJV11 (<i>lcpA</i> deletion plasmid)	CGATAGGGTCTCGTTGC	GTCACCAAATACCATAGTTTCTT
JV59		CGATAGGGTCTCG	CATTAATATCCCCTACTTTCTAAATTTTTTAAT
JV60		CGATAGGGTCTCC	AATGGTATTTGAAAAAATTGATAAAAATAGT
JV61		CGATAGGGTCTCC	TAACATTTATCAATTCCTGCAATTC
JV62		CGATAGGGTCTCG	GTAAAAAATTCCAAAACAAACCAATAATTTG
JV63		CGATAGGGTCTCG	TGCCTTAAGTCGCCATTTTTAAAC
JV64	pJV12 (<i>lcpB</i> deletion plasmid)	AGTACCGGTCTC	CTTGCCTATTGATAATAAAAATAAAAGTCTTAAGC T
JV65		AGTACCGGTCTC	CCATAAGTACCCCTTCTTTCTTCTT
JV66		AGTACCGGTCTCC	TATGGTATTTGAAAAAATTGATAAAAATAGT
JV67		AGTACCGGTCTCC	TAACATTTATCAATTCCTGCAATTC
JV68		AGTACCGGTCTCC	GTAAAAAATTCAACATAAAGTTTATTA AAAAGTA TAAGA
JV69		AGTACCGGTCTC	CTGCCTTGATGGTATAACATCAACACC
JV70	pJV13 (<i>lcpAB</i> deletion plasmid)	TTCCTGGGTCTCCCC	TAATATCCCCTACTTTCTAAATTTTTTAAT
JV71		TTCCTGGGTCTCC	TAGGCCGGCCAAGTGGGCAA
JV72		TTCCTGGGTCTCCTTCT	TAGGGTAACAAAAAACACCGTATTTCTACGATGT
JV73		TTCCTGGGTCTCC	AGAAAATTCAACATAAAGTTTATTA AAAAGTATAA GATTAATACT
TC381	pMEZ5		CTTTTTGATAATCTCATGACC
TC382			GAAATGCAAGTTTCTAACTAAC
TC383			TAGTTAGAACTTGCATTTCACTTGCAT TTCGGCCGGCCGAAGC
TC384			GTCATGAGATTATCAAAAAGACACATT CCCTTTAGTAACGTGTAACCTTC
TC403		GGCTACGGTCTCTTTGC	ACATTTCTCCCCAAATTATTAATTTATAAT TATTTTTTATAATTTTTATC

TC404	pMEZ12 (<i>p/cpA</i>)	GGCTACGGTCTCTTGCC	CTAATCTTCAACCATAATATCTTTAAATATGA AATC
JV101	pJV21 (<i>p/cpB</i>)	GGCTACGGTCTCA	TTGCTTTCTACTGAAAATGGTAGAAAAATAG
JV102		GGCTACGGTCTC	CTGCCTTATTGTTTAAACTCTATGTCATTAAT ATAAATC
JV136	pJV27 (insertion of P_{tet} - <i>lcpB</i> in the chromosome)	GGCTACGGTCTCTTGCC	TAAAATAAGAAGCCTGCATTTGC
JV137		GGCTACGGTCTCT	TCCTTTACTGCAGGAGCTC
JV138		GGCTACGGTCTCTAGGAGAAA ATT	TTTTGTCAAATTAAGAAATTTGTTATAC
JV139		GGCTACGGTCTCCTTGC	TTATTGTTTAAACTCTATGTCATTAATATAAA ATC

Table S2: primers used for PCR check of mutants

Name	Use : PCR check of ...	Primer
JV85	<i>lcp</i> ORF replacement by <i>catP</i> (JMV3, JMV4, and JMV6)	GCACTTTTCATCATTTCCACATCATTTAAC
JV86		GAATTCATCATCAATAGGAAATTCAAATTGC
JV87		CAAATTCAGATACAGTAGTATTAGTAAATG
JV88		CTATACAAGATGATAGTATAAATACAGAGGC
JV90		GTACAAGGTACACTTGCAAAGTAGTGGTC
JV91		CAAGTTCATCACGCAGTATGTGACGG
JV99		P_{tet} - <i>lcpB</i> insertion in <i>erm</i> locus (JMV2 and JMV6)
JV100	CGGTCACGGTGTAATCTTCTGTGACTGCC	
TC153	GAATATTACTACCAAGAAAGCCAGTAG	
TC154	GACATATTACAGATTTTATATTTAATGAC	

Figures

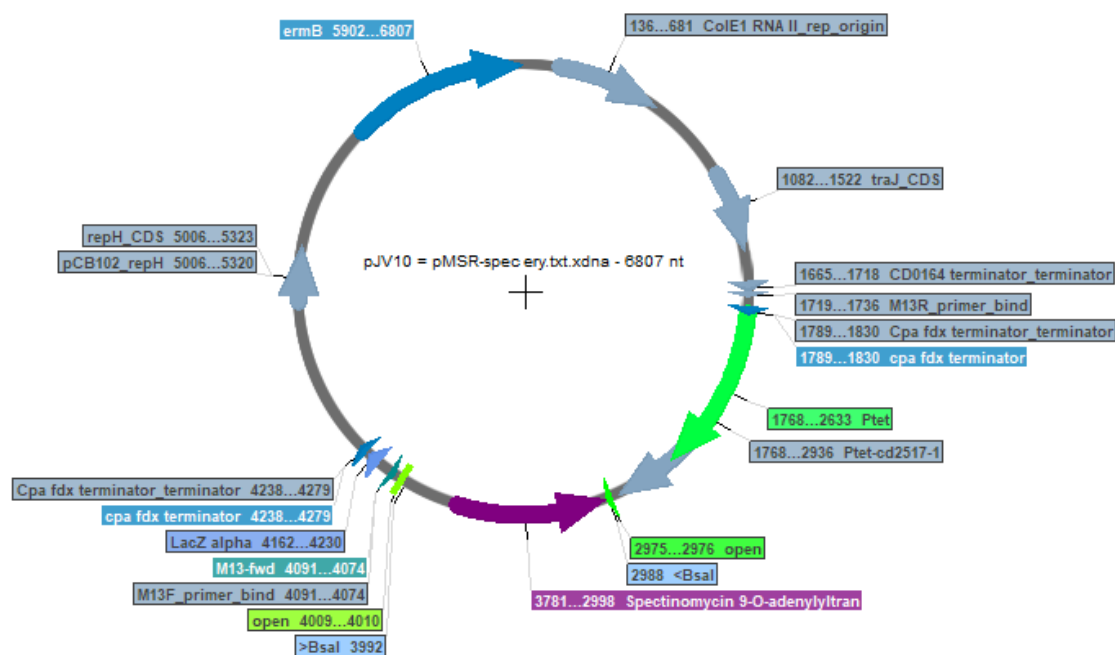


Figure S1

Graphic map of the pJV10 plasmid used to construct deletion plasmids of the *lcp*

On this graphic map of the pJV10 plasmid, created by Serial Cloner, the spectinomycin resistance gene flanked by Bsal sites to allow Golden Gate assembly, an erythromycin resistance gene, and the P_{tet} -CD2517 (Toxin) from the pMSR to facilitate counterselection during the allelic exchange are shown.

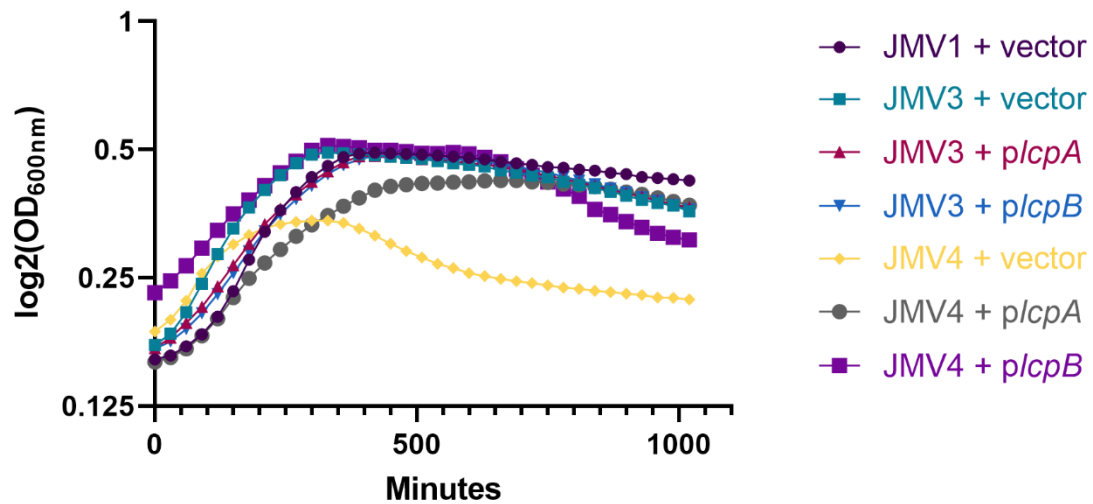
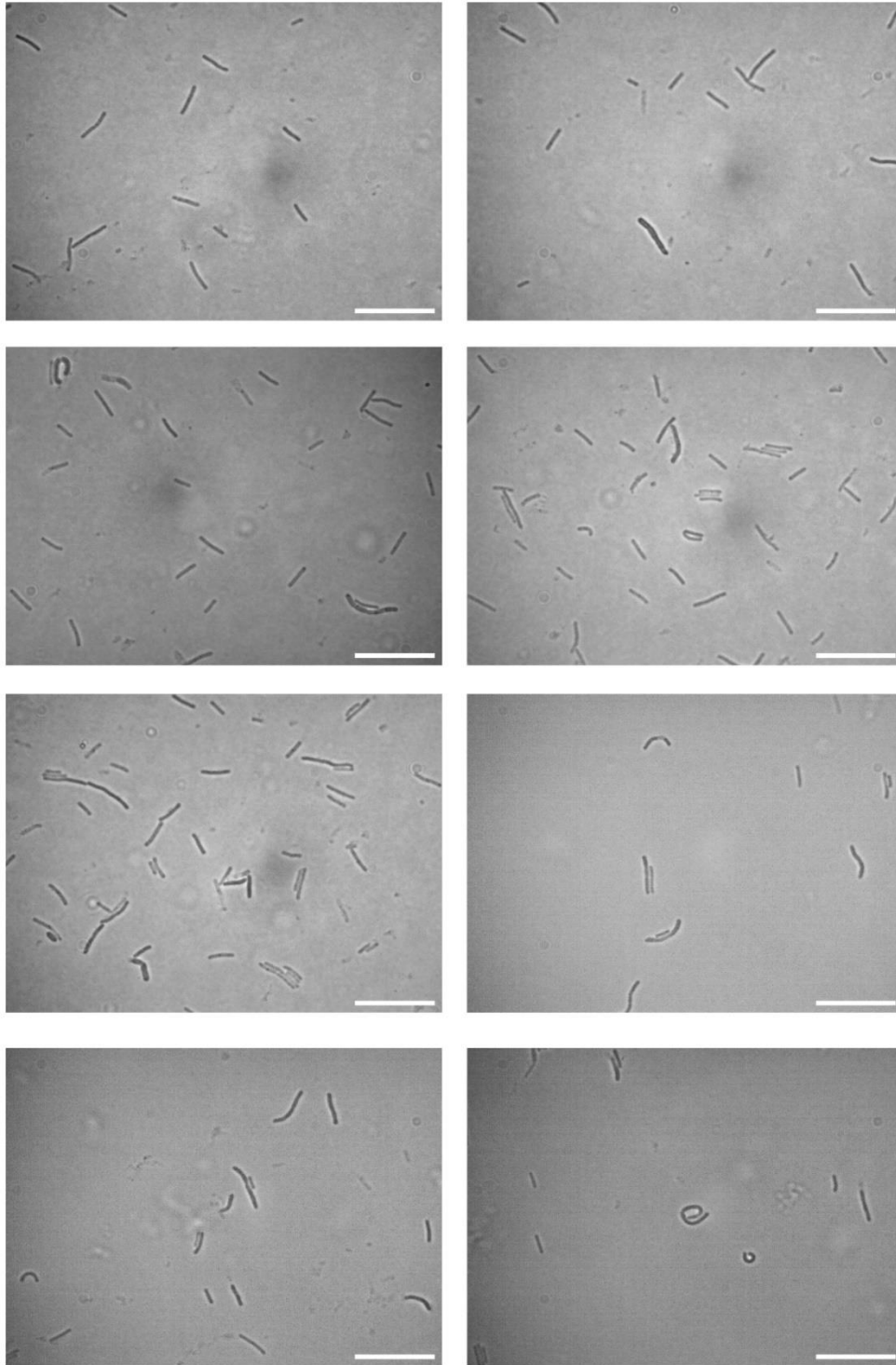


Figure S2

The Δ *lcpB* strain presents an altered growth

Growth curve of single mutant strains of *lcpA* (JMV3) and *lcpB* (JMV4), harboring either the pMTL84222, or the *p*lcpA or *p*lcpB plasmid. The growth was observed in BHI medium for 17 hours (1020 minutes). The graph represents the mean of 3 independent experiments.



Scale bar : 20 μm

Figure S3

The ΔlcpB mutant (JMV4) is thicker, curved, or inflated in liquid culture.

These panels present additional pictures of the JMV4 strain observed in optic microscopy. The scale bar represents 20 μm .

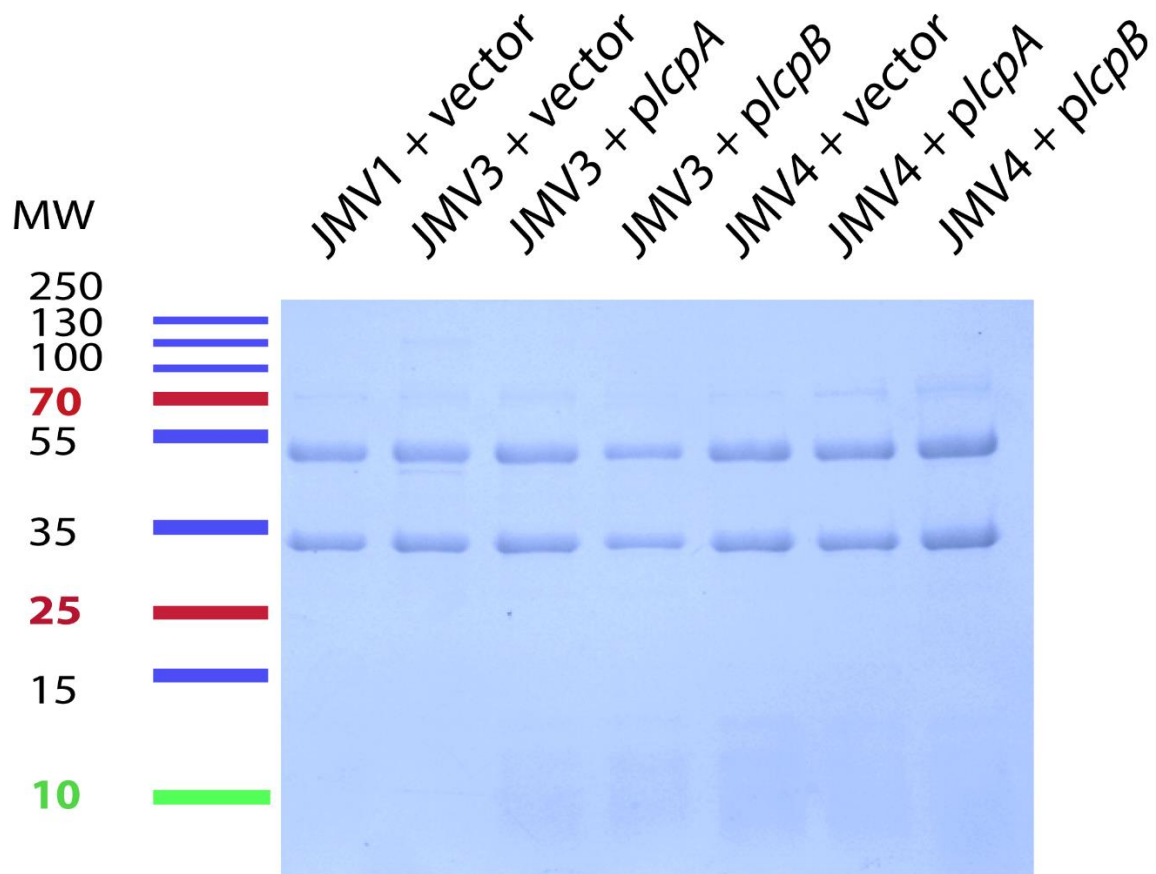


Figure S4

The single *lcp* mutants JMV3 and JMV4 exhibit a normal S-layer content

This Coomassie staining of Cwp protein extractions shows that the Cwp content of the S-layer of JMV1, JMV3 and JMV4 harboring either pMTL84222 (vector), *plcpA* or *plcpB* plasmid. The protein ladder is graduated in kg Dalton (kDa). MW: molecular weight.

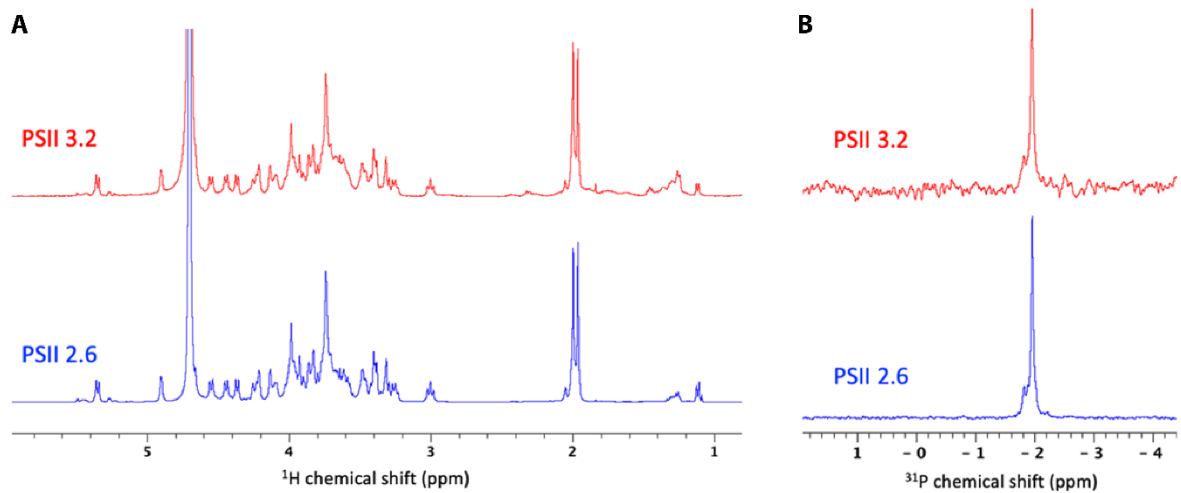


Figure S5

The PSII was obtained and the absence of contamination with LTA was confirmed by NMR.

^1H (A) and ^{31}P (B) NMR spectra of the PSII extracted from culture pellets of the 630 strain. Two samples were sent for analysis, named PSII 3.2 and PSII 2.6. Both were confirmed to contain PSII. The chemical shift is measured in part-per-million (ppm).

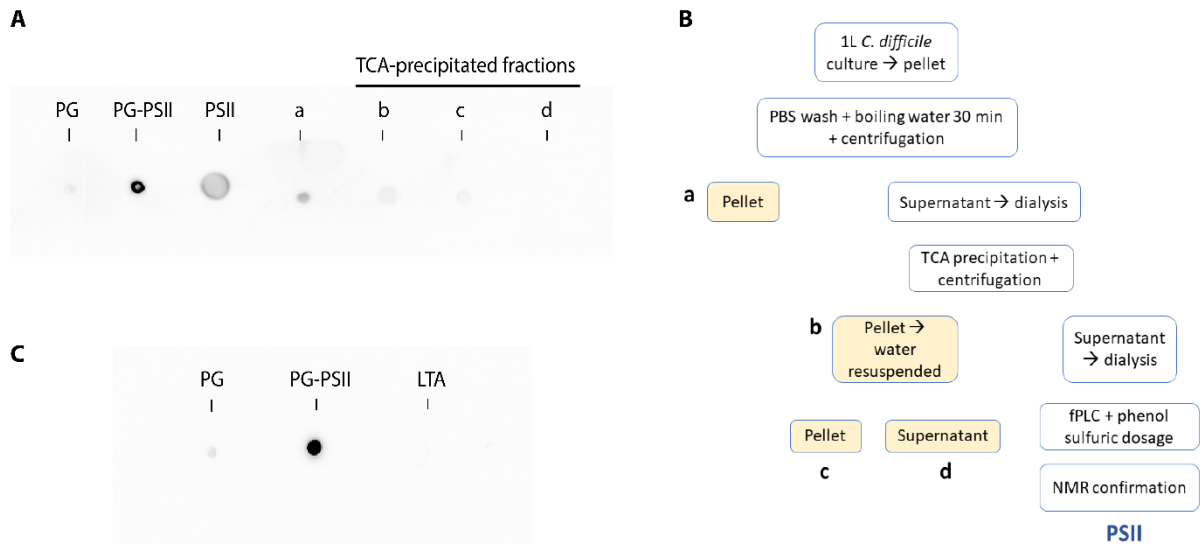
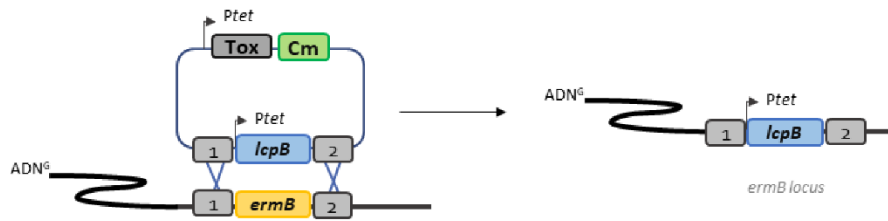


Figure S6

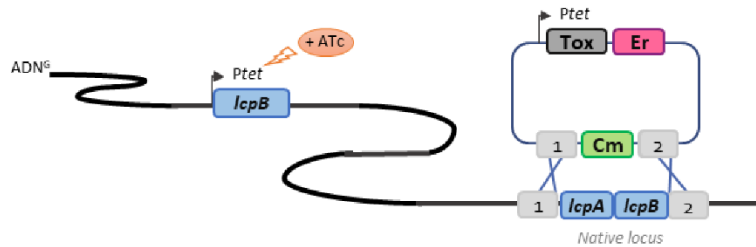
The immunization led to antibodies production and these antibodies showed good specificity for the PSII

This dot blot assay shows that the antibodies produced by the rabbits recognize well the RMN-verified PSII (**A**) of *C. difficile* and the PG linked PSII (PG-PSII) (**A** and **C**) and do not cross-react with peptidoglycan (**A** and **C**) or lipoteichoic acid (LTA) (**C**) of *C. difficile*. Moreover, different samples at different stages of the purification process were tested (**B**). Briefly, PSII purification protocol was performed as followed (white boxes, steps of PSII purification, yellow boxes, potential contaminant molecules) : 1 litter of *C. difficile* culture was pelleted. Pellet was washed in PBS and boiled in water for 30 minutes. After centrifugation, pellet (a) was tested to know whether some PSII were not recovered. The supernatant was further used for purification and a TCA precipitation was performed. After centrifugation, pellet (b) was tested to know whether some PSII was not recovered; it was resuspended in water and centrifuged again, giving pellet (c). The supernatant (d) was dialyzed and applied on fPLC. PSII was recovered, dosage was performed by phenol sulfuric method and PSII was analyzed by NMR.

Step 1 : insert the supplementary copy into the *ermB* region of the chromosome by ACE and verify by PCR



Step 2 : induce the additional copy with ATc and delete the gene in the native locus



Step 3 : modulate the expression of *lcpB* by modifying ATc concentration in culture medium

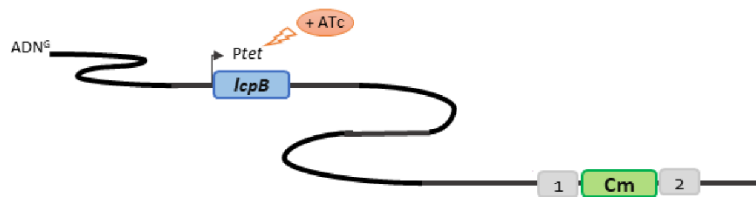
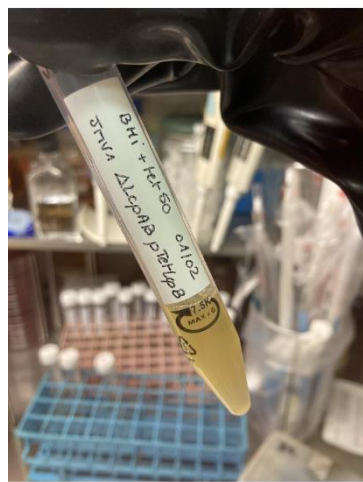


Figure S7

A new strategy designed to construct a conditional-lethal mutant in *C. difficile*

Schematic representation of the strategy used to create a conditional-lethal mutant of *C. difficile* *lcpA* and *lcpB* genes. The strategy consists in three major steps: first the insertion of an inducible copy of *lcpB* in the *erm* locus of the chromosome (under control of P_{tet}), then the deletion of both *lcpA* and *lcpB* by replacing the ORFs with a *catP* gene, and finally the control of the *l* expression of *lcpB* thanks to ATc induction.



BHI broth + **ATc 50**



BHI agar

No ATc



BHI agar

+ **ATc 50**

Figure S8

The anchoring of PSII is essential for *C. difficile* growth

The conditional-lethal mutant pre-cultured overnight in liquid BHI in the presence of 50 ng.mL⁻¹ATc is not able to grow on a BHI plate without ATc but grows correctly in the presence of ATc at 50 ng.mL⁻¹.

Texts

Text S1: construction of plasmids for the study

The plasmids used in this study were constructed using either the Gibson assembly protocol from NEB (23) or the Golden Gate assembly from NEB (24, 25) cloning technique. For Golden Gate assembly, the primers were designed using the NEB Builder® assembly tool.

Construction of deletion plasmid for the *ermB* locus

pJV4: the spectinomycin cassette was amplified from pAT28 and flanked with BsaI sites using JV54/JV55 primers. The PCR product was inserted in the pBLUNT cloning vector by blunt-end DNA cloning to give pJV4.

pJV5: the spectinomycin cassette flanked with BsaI sites was amplified from pAT28 using JV50/JV51 primers, and the downstream region of *ermB* locus was amplified from genomic DNA of 630 strain using JV52/53 primers. Both PCR products were assembled using the Gibson assembly protocol (NEB Biolabs) to give pJV5.

pJV7: the spectinomycin cassette flanked with BsaI sites was extracted from pJV4 using restriction digestion with XhoI and BamHI. The pMSR was opened by restriction digestion with XhoI and BamHI. The spectinomycin cassette was then cloned into the linearized pMSR plasmid by a classical ligation process.

pJV8: the upstream region of the *ermB* locus was amplified from genomic DNA of 630 strain using JV48/JV49 primers, and the spectinomycin + downstream region of *ermB* locus fragment was amplified from pJV5 using JV50/JV53 primers, and the pMSR plasmid was amplified using JV46/JV47 primers. The three PCR products were assembled using the Gibson assembly protocol (NEB Biolabs) to give pJV8.

Constructing deletion plasmids for *lcpA*, *lcpB* and the conditional-lethal deletion of both

lcp

pJV6: the *ermB* cassette was amplified from pMTL84222 using TC289/TC290 primers, and pMTL83151 was amplified using TC287/TC288 primers. Both PCR products were assembled using the Gibson assembly protocol (NEB Biolabs) to give pJV6. pJV10: this plasmid results from the subcloning of pJV7 (fragment with the spectinomycin resistance cassette flanked by BsaI sites and P_{ter}-CD2517 toxin) into pJV6 (Erm^R) using the restriction enzymes SacII and XhoI.

pJV11: the upstream and downstream regions of *lcpA* were amplified from genomic DNA of 630 strain using respectively JV58/59 and JV62/JV63 primers. The *catP* cassette was amplified from the pMSR plasmid using JV60/JV61 primers. The three PCR products were inserted in the pJV10 using the Golden Gate assembly protocol (NEB Biolabs) to give pJV11.

pJV12: the upstream and downstream regions of *lcpB* were amplified from genomic DNA of 630 strain using respectively JV64/65 and JV68/JV69 primers. The *catP* cassette was amplified from the pMSR plasmid using JV66/JV67 primers. The three PCR products were inserted in the pJV10 using the Golden Gate assembly protocol (NEB Biolabs) to give pJV11.

pJV13: the upstream region of *lcpA* and the downstream region of *lcpB* were amplified from genomic DNA of 630 strain using respectively JV58/JV70 and JV73/JV69 primers. The *catP* cassette was amplified with its promoter from the pMSR plasmid using JV71/JV72 primers. The three PCR products were inserted in the pJV10 using the Golden Gate assembly protocol (NEB Biolabs) to give pJV11.

Constructing complementation plasmids for *lcpA* and *lcpB*

pTC131: pJV4 was digested using BamHI/XhoI restriction enzymes, and the DNA fragment Spec of approximately 1kb was ligated pMTL84151 previously digested by BamHI/XhoI restriction enzymes.

pMEZ5: The *ermB* cassette from pMTL-84222 was amplified using TC383/TC384 primers, and pTC131 was amplified using TC381 and TC382 primers. Both PCR products were assembled using the Gibson assembly protocol (NEB Biolabs) to give pMEZ5.

pMEZ12: P_{lcpA} -*lcpA* was amplified from genomic DNA of 630 strain using TC403/TC404 primers and inserted in pMEZ5 using the Golden Gate assembly protocol (NEB Biolabs) to give pMEZ12.

pJV20: P_{lcpB} -*lcpB* was amplified from genomic DNA of 630 strain using JV101/JV102 and inserted in pTC131 using the Golden Gate assembly protocol (NEB Biolabs) to give pJV20.

pJV21: pJV20 was digested using StuI and KpnI restriction enzymes, and the DNA fragment of approximately 1,5kb was ligated with pMTL84222 (Erm^R) previously digested by StuI and KpnI restriction enzymes.

pJV27: the P_{tet} was amplified from pRPF185 using JV136/JV137 primers, and the *lcpB* was amplified from genomic DNA of 630 strain using JV138/JV139 primers. Both PCR products were inserted in pJV8 using the Gibson assembly protocol (NEB Biolabs) to give pJV27.

Cloning *gusA* reporter plasmids

pMDR1: Kanamycin cassette flanked with BsmBI restriction enzyme sites was amplified from pJV4 using TC393/TC394 primers. *gusA* was amplified from pRPF185 using TC395/TC396 primers. Both PCR DNA fragments were inserted into pTC131 using the Golden Gate assembly protocol to give pMDR1.

pMDR2: Spectinomycin cassette was amplified from pAT28 using TC397/TC398 and inserted into pMDR1 to give pMDR2.

pMDR8: P_{icpA} was amplified from genomic DNA of 630 strain using TC409/TC410 and inserted into pMDR2 to give pMDR8. P_{icpB} was amplified from genomic DNA of 630 strain using TC411/TC412 and inserted into pMDR2 to give pMDR5.