

1 **ONLINE METHODS**

2

3 **Strains and culture conditions.**

4 Unless otherwise noted, bacterial cultures were grown at 37°C with Luria-Bertani (LB)
5 medium (Lennox) or Mueller-Hinton (MH) solid media supplemented when appropriate,
6 with the following antibiotics: 50 µg/ml kanamycin (Kan), 50 µg/ml chloramphenicol
7 (Cm), 100 µg/ml carbenicillin (Carb), 50 or 100 µg/ml spectinomycin (Sp) for *E. coli* and
8 100 µg/ml Sp for *Vibrio cholerae*. Selection of transconjugants was carried using 100
9 µg/ml Sp in all cases, except for *V. mimicus* and *V. vulnificus* where we used 50 µg/ml
10 Sp. Bacterial strains used in this study are listed in Supplementary Table 1. Other
11 molecules were added to the media with the following concentrations: 40 µg/ml 5-
12 bromo-4-chloro-3-indolyl-beta-D-galactopyranoside (Xgal), 0.3 mM Diaminopimelic acid
13 (DAP), 1% glucose and 0,2% arabinose.

14

15 **Plasmid construction.**

16 Plasmids are listed in Supplementary Table 1 and primers in Supplementary Table 6.

17 All plasmid sequences were verified through sequencing.

18 To generate the N and C plasmids for each toxin-intein fusion, the N- and C-terminal
19 toxin regions were amplified with primers F-toxin-EcoRI/R-toxin-intein and F-toxin-
20 intein/R-toxin-XbaI, respectively. N- and C-terminal intein regions were amplified with
21 primers F-intein-toxin/R-intein-XbaI and F-intein-EcoRI/R-intein-toxin, respectively. As
22 DNA templates for toxins we used chromosomal DNA from *V. cholerae* in all cases and
23 *V. fischeri* for *ccdB*. Intein amplification was done with chromosomal DNA from the
24 cyanobacteria *Nostoc punctiforme*. PCR products of N- and C-terminal regions were
25 fused by Gibson assembly³⁵. Each toxin-intein fusion was then digested with
26 EcoRI/XbaI (Thermo Fisher) and then cloned in EcoRI/XbaI digested pBAD43³⁶ and
27 pSU38³⁷ (or pSU18) plasmids, respectively (Supplementary Table 1). To generate the

28 mutated version of N-terminal plasmid (n*) whole plasmids were amplified using
29 primers F-Int-tox-mut/R-int-tox-mut.

30 To assemble the pU-BAD plasmid (Supplementary Fig. 5) we first cloned the C-
31 terminal CcdB-Npu fusion into a pBAD18 plasmid (EcoRI-XbaI). An *ompU* promoter
32 was inserted upstream the N-terminal ccdB/Npu fusion in N plasmid by PCR. The
33 *ompU* promoter region was amplified using F-PompU-1/R-PompU-dB (size=352 bp).
34 This promoter was chosen based on previous work²¹ that showed its high induction in
35 the presence of ToxR. A region containing the pSC101 origin was amplified using R-
36 BAD43-BAD18/F-4126 primers and the N-terminal CcdB-Npu plasmid as template. A
37 second region containing the N-terminal fusion was amplified using 4217/R-BAD43-
38 BAD18 primers and N-terminal plasmids also as templates. Other regions containing
39 the C-terminal fusion and Kan resistance gene were amplified using R-BAD18-
40 BAD43/F-BAD18-BAD43 primers and the C-terminal CcdB-Npu pBAD18 plasmid as
41 template. PCR products were then fused by Gibson assembly³⁵ producing the pU-BAD
42 plasmid.

43 To generate the pRS plasmid, (Supplementary Fig. 5) the *toxRS* operon from *V.*
44 *cholerae* O1 was amplified using F-toxR-SacI/R-toxS-XbaI primers, digested with SacI
45 and XbaI and ligated with SacI-XbaI digested plasmid pBAD30. The native RBS
46 sequence of *toxR* was kept.

47 To assemble the toxin-intein N and C-terminal fusions as an operon (pToxInt plasmid),
48 N- and C-fusions were amplified using F-CcdB-EcoRI/R-Int-N-Int-C and F-Int-C-Int-
49 N/R-Int-XbaI primers and then ligated by Gibson assembly³⁵, digested with EcoRI/XbaI
50 and cloned into a pBAD43-EcoRI/XbaI digested plasmid. The fusion contains the
51 following sequence: 5' TGATAAGGAGGTAACATATG 3' between the N and C genes.
52 This sequence contains the RBS sequence necessary for translation of the C-terminal
53 fusion. The pTox plasmid was created by amplification of the *ccdB* toxin gene from *V.*
54 *fischeri* DNA with F-CcdB-EcoRI/R-CcdB-XbaI primers, EcoRI/XbaI digestion and
55 ligation into a pBAD43-EcoRI/XbaI digested plasmid. *E. coli* XL2blue strain that

56 contains F' plasmid integrated in the chromosome (containing the *ccdB/ccdA* TA
57 system and conferring resistance to CcdB), was used to transform with this ligation in
58 order to obtain positive clones.

59 To assemble the pPW genetic weapon, the *ompU* promoter was amplified as
60 previously described and ligated by Gibson assembly³⁵ with the product of pToxInt
61 plasmid PCR using F-dB-PompU/R-BAD-PU1 primers.

62 The pPLA plasmid was constructed first by amplifying by PCR the PL promoter³⁸ using
63 DNA from *V. cholerae* O139 and F-PL-plasmid/R-PL-*ccdA* as primers. Then, the *ccdA*
64 antitoxin gene was amplified using the F-*ccdA*-PL/R-*ccdA*-plasmid primers and *V.*
65 *fischeri* DNA. Finally, the pTox-Int plasmid was also amplified using F-plasmid-dA/R-
66 plasmid-PL primers. Ligation by Gibson assembly³⁵ of the three PCR products resulted
67 in the pPLA plasmid.

68 Mobilizable genetic weapons were created by amplifying the origin of transfer *oriT* RP4
69 using F-pSW23-BAD/R-*oriT*-BAD43 primers and the plasmid pSW23T³⁹ as template.
70 Then, the *oriT* PCR product was ligated through Gibson assembly³⁵ with the amplified
71 plasmid using F-BAD-pSW/R-BAD43-*oriT* primers and the weapon or control plasmids
72 as template.

73 To assemble the Final Weapon we the plasmid pFW (Figure 3) as follow. The *ompU*
74 promoter-1 was ligated into the pABRW plasmid as previously described for the pU-
75 BAD construction. In order to fine-tune the RBS of *ompU* in this plasmid as well as the
76 PL promoters,, PCRs were performed using F-*ccdB*-SD-OK/R-PU-SD-OK and F-PL-
77 SD-T/R-PL-SD-T primer pairs, respectively. Finally, to generate the pFW plasmid, an
78 operator O1 sequence (see ³⁸) was added into the PL promoter by PCR amplification of
79 the pFW2 plasmid using F-PL-O1/R-PL-O1 primers.

80 To generate the pPW-R6K, pFW-R6K and pNctrl-R6K plasmids we first amplified the
81 R6K replication origin using F-R6K-weapon/R-R6K-weapon primers and the pMP7⁴⁰
82 plasmid as template. Then, the pPW, pFW and pNctrl plasmids were amplified using F-

83 weapon-R6K/R-weapon-R6K primers. Finally, PCR fragments were ligated by Gibson
84 assembly³⁵.

85

86 ***ΔtoxRS* strain construction**

87 DNA regions 500 bp upstream and downstream of the *toxRS* operon were amplified
88 using F-toxRup-p7/R-toxRups and F-toxSdow/R-toxSdow-p7, respectively. The
89 amplified fragments were ligated by Gibson assembly³⁵ and then cloned into an R6K γ -
90 *ori*-based suicide vector, pSW7848⁴⁰ that encodes the *ccdB* toxin gene under the
91 control of an arabinose-inducible promoter, P_{BAD}. For conjugal transfer of plasmids into
92 *V. cholerae* strains, *E. coli* β 3914 was used as the donor. Clones where integration of
93 the entire plasmid in the chromosome by single crossover occurred were selected.
94 Elimination of the plasmid backbone resulting from a second recombination step was
95 selected as described ref 39.

96

97 **Transformation assays**

98 DH5 α chimiocompetent cells (Invitrogen) were transformed with 150 ng of pTox,
99 pToxInt or pN plasmids (Supplementary Fig. 1a). Transformants were then tested in Sp
100 containing media with glucose or arabinose to analyze toxin integrity. 10 to 12% of
101 pTox-transformed clones from were able to grow in the presence of arabinose. Four
102 independent clones were analyzed by sequencing and they all carried an insertion
103 sequence in the *ccdB* toxin gene. These clones were responsible for pTox
104 transformation rate decrease in comparison with the pToxInt and pN plasmids.

105 DH5 α cells (Invitrogen) were co-transformed with two plasmids simultaneously. Both
106 plasmids were then simultaneously selected (Supplementary Fig.4).

107 Transformation of the donor strain β 3914 was performed in the presence of DAP.

108

109 **Growth tests**

110 Eighteen independent clones from DH5 α transformation were inoculated in p96
111 microplates containing LB media with Sp and glucose. The TECAN Infinite 200
112 microplate reader (TECAN, Männedorf, Germany) was used to determine growth
113 curves, with absorbance (620nm) taken at 6-minute intervals for a period of 12 h. The
114 obtained OD values were plotted as seen on Supplementary Fig. 1b.

115 In Supplementary Fig. 2 for analysis of bactericide effect of CcdB toxin: *V. cholerae*
116 O139 was co-transformed with antitoxin-*ccdA* (pBAD24-*ccdA*) and pPW plasmids in
117 the presence of arabinose allowing the antitoxin to be expressed. pPW plasmid
118 contains the toxin-intein under the control of *ompU* promoter, which is always active in
119 *V. cholerae*. Bacteria culture supplemented with antibiotics for maintaining both
120 plasmids and arabinose, were diluted at OD=0.5 (time 0h). Then bacteria were washed
121 three times with MH media with antibiotics and glucose, in order to switch off antitoxin
122 expression, and incubated for 4h at 37°C. Total bacteria were calculated by the CFU/ml
123 at time 0h and 4h present in MH media with antibiotics and with glucose (1%) or
124 arabinose (0,2%). Data numbers were calculated from four independent experiments
125 (n=4).

126

127 **Conjugation assays.**

128 Overnight cultures of donor and recipient strains were diluted 1:100 in culture media
129 with antibiotic and grown at 37°C for 2-3 hours. Then, cultures were diluted to an OD₆₀₀
130 = 0.5. The different conjugation experiments were performed by a filter mating
131 procedure described previously⁴¹ with a donor/recipient ratio of 1::1. When the
132 recipients were composed of a mixed population the donor/mixed-recipient ratio was
133 1::0.5-0.5. Before mixing the different bacteria, cultures were washed three times with
134 fresh media to remove antibiotics. In Supplementary Table 2 bacteria were mixed in
135 different proportions (2:1 and 3:1) to test whether this would impact conjugation
136 efficiency. Conjugation was performed during 4h at 37°C on filter in MH plates

137 supplemented with DAP (and containing NaCl until 332mM final concentration in the
138 case of *V. vulnificus*).

139

140 ***In vivo* conjugation in zebrafish larvae and *Artemia salina***

141 All animal experiments described in the present study were conducted at the Institut
142 Pasteur according to European Union guidelines for handling of laboratory animals
143 (http://ec.europa.eu/environment/chemicals/lab_animals/home_en.htm) and were
144 approved by the Institut Pasteur Animal Care and Use Committee and the Direction
145 Sanitaire et Veterinaire de Paris under permit #A-75-1061. Conjugative killing was
146 assessed as follow. Four-day-postfertilization zebrafish larvae were exposed to water
147 containing 10⁴ CFU/ml of *V. cholerae* O139 for 2 hours at 27°C (Figure 4a) or a 1::1
148 mixed population containing 10⁵ CFU/ml *V. cholerae* O139 + *V. cholerae* O1 (Figure
149 5a, mix *Vibrio*) for 2 hours at 27°C. Then, larvae were washed in sterile water three
150 times and then placed into a well containing 10⁷ or 10⁶ CFU/ml (Figure 4a, *V. cholerae*
151 O139 and mix *Vibrio*, respectively) of the *E. coli* β3914-Δdap donor strain containing
152 either the pN_{ctrl} or pFW plasmid for 24 hours at 27°C. In Supplementary Fig. 11b and
153 11c, infection dose for *Vibrio* was the same than for Fig. 4a. Larvae were transferred to
154 bacteria-free wells, washed in sterile water three times and then placed into a well
155 containing Tricaine (Sigma-Aldrich #E10521) at 200 mg/ml to euthanize them. Finally,
156 they were transferred to a tube containing calibrated glass beads (acid washed, 425
157 um to 600 um, Sigma-Aldrich #G8722) and 500 µl of water. Five larvae were mashed
158 using FastPrep® Cell Disrupter (BIO101/FP120 QBioGene) for 45 seconds at
159 maximum speed (6,5 m/sec) to analyze their microbiota (Supplementary Fig. 11) in MH
160 Media + X-gal or TCBS media for selection of *V. cholerae*. Blue bacteria corresponding
161 to *V. cholerae* O139 were detected in MH media. Transconjugants selection was done
162 into MH Media + X-gal and Sp and then, replication of these MH plates were done on
163 TCBS media to specific identify *V. cholerae*. Strain identity was confirmed through

164 yellow color development in TCBS *Vibrio* specific media. The amoeba *Tetrahymena*
165 *thermophila* (*T. thermophila*) was added to feed larvae during the experiment.

166

167 Groups of 225±15 larvae of *Artemia salina* stage nauplii suspended in 1ml volume of
168 seawater were washed using sterile cell strainer Nylon filters 100 µm pore size
169 (Falcon) and three times with the same volume (3x1ml) of sterile PBS (D8537, Sigma).

170 Nauplii were suspended in 1ml PBS and then infected with 10⁷ *V. cholerae* O1 or a mix
171 of 10⁷ *V. cholerae* O1 and O139 for 2 hours in agitation at 27°C. Then nauplii were
172 washed as previously described and exposed to 10⁷ of β3914 - Δ*dap* bacteria with

173 pN_{ctrl} or pFW plasmid for 4 hours at 27°C. These experiments were repeated four times
174 independently. The microbiota from 1ml containing 225±15 nauplii were analyzed as

175 previously described for zebrafish. In the case of *Artemia*, we have used M63B1
176 minimal media where *Artemia* feel asleep and then put them on ice, previous the use of

177 fast-prep (FastPrep® Cell Disrupter (BIO101/FP120 QBioGene) for 45 seconds at
178 maximum speed (6,5 m/sec)). Transconjugants were selected from 225±15 nauplii

179 after pN_{ctrl} or pFW conjugation treatment into MH media with Sp and X-gal
180 (Supplementary Fig. 12a,b). For the identification of *V. cholerae* in the mix of both

181 serogroups (Fig. 4b and Supplementary Fig. 12b), replication of these MH plates were
182 done into TCBS media to specifically identify *V. cholerae*. Strain identity was confirmed

183 through yellow color development in TCBS *Vibrio* specific media.

184

185 **Co-localization of *E. coli* and *V. cholerae* in the zebrafish larvae and *A. salina* by**
186 **Microscopy.**

187 Co-localization of *E. coli* and *V. cholerae* in the zebrafish larvae was assessed as
188 follow. Four-day-postfertilization zebrafish larvae were exposed to water containing 10⁶

189 CFU/ml *V. cholerae* O1-GFP for 2 hours at 27°C. Then washed in sterile water three
190 times and then placed into a well containing 10⁷ CFU/ml of *E. coli*-RFP for 24 hours at

191 27°C. Larvae were removed from the well and then placed into a well containing

192 Tricaine for euthanize them. Infected and non-infected larvae were visualized by
193 fluorescence microscopy (EVOS FL microscope-Life technologies) using appropriate
194 wavelength conditions enabling or not the visualization of GFP and RFP. Fluorescence
195 was only detected in infected larvae and more precisely into the gut where both
196 bacteria are co-localized.

197 In the case of *A. salina* stage nauplii the microscopy experiment was done using 10^7 *V.*
198 *cholerae*-GFP for 2 hours in agitation at 27°C. Then nauplii were washed as previously
199 described and exposed to 10^7 of *E. coli*-RFP strain for 2 hours. Microscopy conditions
200 were performed as for zebrafish experiment.

201

202 **Statistics**

203 In Supplementary Fig. 9, one-way ANOVA with Dunnett's Multiple Comparison Test
204 was performed. PNcontrol-R6K vs pPW-R6K, Mean Diff. = 2.383e+008, q = 4.183,
205 **P<0.05, 95% CI of diff = (8.937e+007 to 3.871e+008). PNcontrol-R6K vs pFW-R6K,
206 Mean Diff. = 2.308e+008, q = 4.227, **P<0.05, 95% CI of diff = (9.187e+007 to
207 3.896e+008).

208 In Supplementary Fig. 13, one-sided t-test Mann Withney was performed. *E. coli* SXT
209 vs *E. coli* MG1655. P value = 0.0143. *P < 0.05.

210

211 **References**

212

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