Collective protection against the type VI secretion system in bacteria

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ABSTRACT

Bacteria commonly face attacks from other strains via the type VI secretion system (T6SS), a molecular speargun that stabs and intoxicates competitors. Here we show how bacteria can work together to collectively defend themselves against these attacks. This project began with an outreach activity: while developing an online computer game of bacterial warfare, we noticed that one strategist ("Slimy") that made extracellular polymeric substances (EPS) was able to resist attacks from another strategist that employed the T6SS ("Stabby"). This observation motivated us to model this scenario more formally, using dedicated agent-based simulations. The model predicts that EPS production can serve as a collective defence mechanism, which protects both producing cells and neighbouring cells that do not make EPS. We then tested our model with a synthetic community that contains a T6SS-wielding attacker (*Acinetobacter baylyi*), and two T6SS-sensitive target strains (*Escherichia coli*) that either secrete EPS, or not. As predicted by our modelling, we find that the production of EPS leads to collective protection against T6SS attacks, where EPS producers can shield each other and nearby non-producers. Our work shows how EPS-producing bacteria can work together to defend themselves from attackers.

INTRODUCTION

Bacteria commonly live in densely-populated, multispecies communities where they must compete for limited space and nutrients (1–3). Life in these environments has driven the evolution of an array of bacterial weapon systems, used to inhibit or kill competing microbes (4, 5). One of the most widespread and sophisticated of these weapons is the type VI secretion system (T6SS), a contractile nanomachine that fires a needle into neighbouring bacteria to deliver toxic effector proteins (6).

Possession of the T6SS can confer a strong ecological advantage to bacteria cells (7–10). Conversely, being on the receiving end of a T6SS attack can be lethal. Defending against the T6SS, however, presents a unique set of problems for targeted cells, as—unlike many other weapon systems—the T6SS does not rely on the target cell's surface receptors or transport systems. Instead, it uses mechanical force to pierce the target cell's membrane and deliver its toxic cargo, which limits the potential range of mechanisms that can be employed in defence (11).

In the face of these challenges, here we show how bacteria can work together to protect themselves against T6SS attacks. Individual-level defence mechanisms are known, including immunity proteins, capsule formation, target modification, envelope stress responses, and the removal of susceptibility factors (12–16). However, some of the most powerful defences in bacteria come about when bacteria act as a collective, allowing groups of cells to take advantage of their large numbers (17–22).

This project began when we serendipitously identified a potential collective defence mechanism against the T6SS while developing a video game, as part of an outreach activity. The game—*Gut Wars*—uses an agent-based model developed by our group for research (17, 23–25) to illustrate different bacterial warfare strategies in the human gut microbiome. Running the game repeatedly, we noticed that "Slimy" strategists, which secrete extracellular polymeric substances (EPS), were particularly resistant against "Stabby" competitors armed with the T6SS. Secretion of EPS is widespread among bacteria and plays a key role in the formation of biofilms (26, 27). From observation of the game, we speculated that EPS released from the cell has the potential to protect both the cell that produces it and others around it, thereby functioning as a powerful collective defence mechanism. There is evidence that EPS has the potential to physically shield bacteria from T6SS attacks (12, 13, 15). Moreover, biofilm formation—involving EPS secretion—is known to reduce T6SS susceptibility (14), and is a response to bacterial competition via T6SSs

(28). We, therefore, decided to investigate whether EPS allows bacteria to work collectively in the face of T6SS attacks.

Here, we develop agent-based models of the competitions between T6SS attackers and EPS-producing target cells. As suggested by the computer game, these analyses predict that secreting EPS is a collective defence mechanism in which producer cells both protect each other, and also cross-protect nearby non-producing cells. We test our predictions using a synthetic community, in which T6SS-wielding *Acinetobacter baylyi* are competing with *Escherichia coli* strains secreting free (i.e. non-membrane-bound) EPS in amounts comparable to clinical *E. coli* isolates. These experiments revealed that EPS can indeed serve as a powerful collective defence against T6SS attacks. We identify two processes by which this collective defence can occur: i) EPS sharing between cells and ii) what we call “flank protection”, whereby groups of resistant cells shield non-producers. Interestingly, the latter process appears to be a very general route to collective defence, because it is predicted to occur whatever the underlying mechanism of protection against the T6SS.

RESULTS

Agent-based modelling predicts that EPS can protect against T6SS

Bacteria have evolved a wide repertoire of traits and strategies to increase their survival chances in densely-populated communities. We recently devised a simple browser-based computer game—*Gut Wars*—to showcase some of these competition strategies in a format accessible to children as well as adults. The game asks the user to select different characters representing distinct bacterial competition strategies, which are then pitted against each other in a simulated gut microbiome environment using agent-based modelling (Fig. 1A). Two of the available strategies are EPS production (“Slimy”) and T6SS firing (“Stabby”), both common traits in bacteria. While not originally implemented to fulfil this function, we noticed that i) “Slimy” bacteria were surprisingly resistant to T6SS attacks, and ii) the simulated EPS particles covered a large area around the producing cells. This led us to ask whether the secretion of loose (i.e. non-membrane-bound) EPS could protect cells from T6SS firing events, and so help EPS-producing bacteria survive when faced with a T6SS attacker.

To explore these questions, we implemented EPS secretion within an existing individual-based model of T6SS competition (24, 25). Following previous models (29–31), EPS production is

modelled as cells secreting loose, spherical particles into the environment, at a rate P_{EPS} (see Materials and Methods). As they grow, divide, and secrete EPS, producing cells create small pockets of EPS particles around themselves, which helps to separate cells from T6SS-wielding competitors (Fig. 1B). Note, we do not assume here that EPS can physically block T6SS needles, as this effect may not be universal (15). However, were this to occur, the expectation is that it will only increase the protection conferred to cells.

We performed simulation parameter sweeps to identify conditions where EPS production was most protective against T6SS attacks. Comparing simulations with and without EPS (respectively, P_{EPS} = 0.1, 0), we used a simple metric to quantify the benefit of EPS protection:

$$\textit{EPS benefit} = (N_{susc}(t_{end}) / N_{susc}(t_{start}))_{EPS+} - (N_{susc}(t_{end}) / N_{susc}(t_{start}))_{EPS-} ,$$

with $N_{susc}(t)$ the number of surviving susceptible cells present at time t. Varying the starting number of attacker and susceptible cells shows that EPS production always offers at least some T6SS protection (*EPS benefit* > *0*), and that production is most beneficial for intermediate attacker- and susceptible cell densities (Fig. 1C).

We performed additional simulations to test the robustness of EPS-mediated T6SS protection with respect to other simulation parameters (Fig. S1). Repeats of competition simulations with different EPS production rates showed that, as might be expected, susceptible survival decreases as the per-cell rate of EPS secretion is reduced (Fig. S1A); below a minimal secretion rate, survival is indistinguishable from that of a non-producing susceptible strain. We also tested a model in which EPS production is costly, such that susceptible cells suffer a growth penalty proportional to their EPS production rate,

$$\textit{Susceptible growth rate} = k_{grow}(1 - c_{EPS}\, P_{EPS}),$$

with k_{grow} the maximum cell growth rate, P_{EPS} the probability of EPS secretion per simulation timestep, and c_{EPS} the unit cost of EPS production. For various $c_{EPS} > 0$, costly EPS production remains net-beneficial to susceptible cells (Fig. S1B), such that the optimal secretion rate $P_{EPS}^* >$ 0. Predictably, EPS investment collapses for excessive costs (Fig. S1B), and is contingent on attacker presence (Fig. S1C). Overall, our simulations predict that production of loose, non-

membrane-bound EPS is an effective means for cells to protect themselves against the T6SS, even when costly.

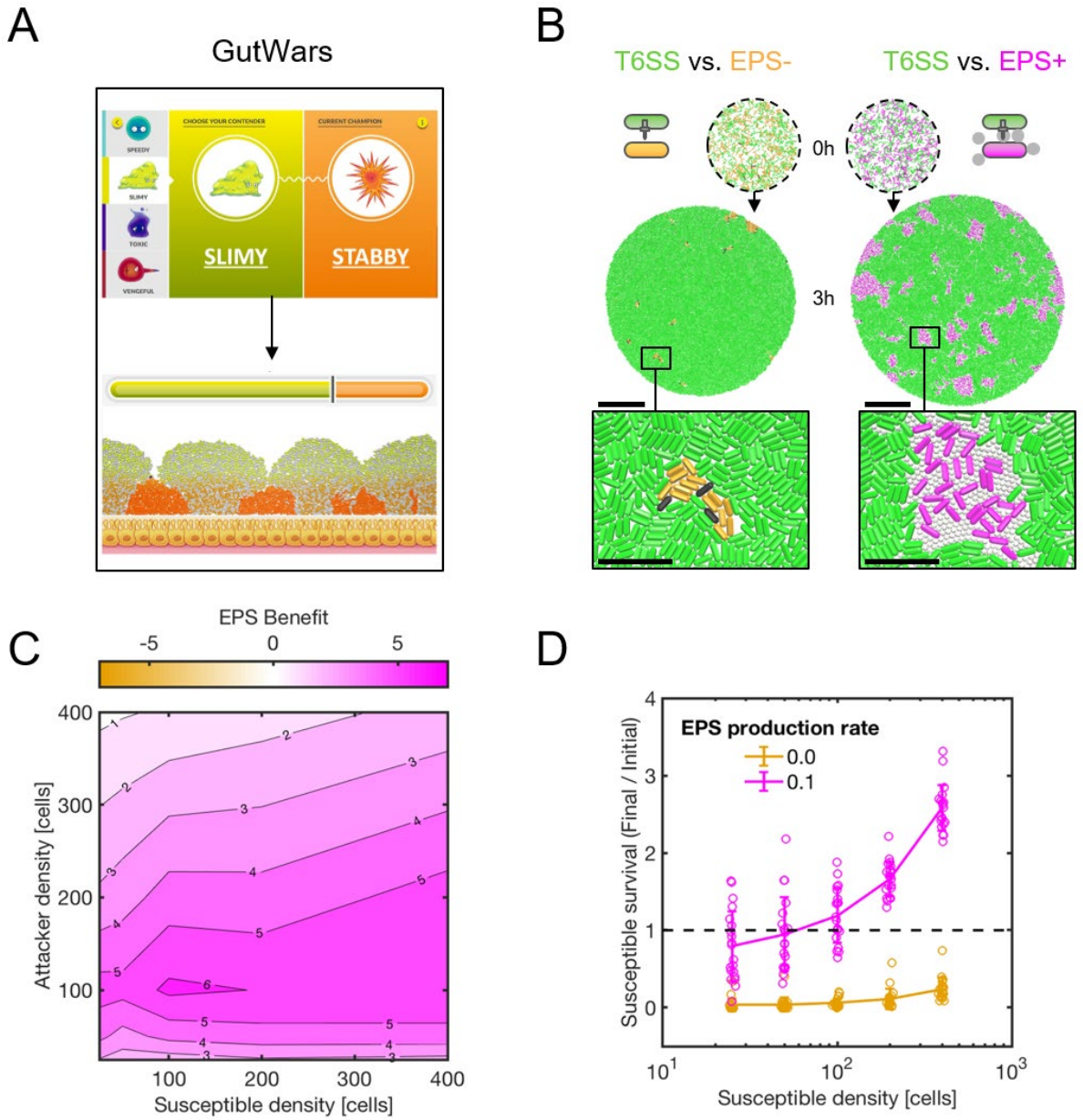

Fig. 1: Agent-based modelling of EPS secretion demonstrates collective defence against the T6SS. **(A)** Snapshots of our agent-based video game 'GutWars', showing EPS-producing 'Slimy' bacteria outcompeting T6SS-armed 'Stabby' rivals. **(B)** Agent-based simulations compete T6SS attackers (green) with EPS non-producing (EPS-, P_{EPS} = 0.0) and EPS-producing (EPS+, P_{EPS} = 0.1) susceptible cells (orange and magenta, right and left columns, respectively). Snapshots show i) initial cell seeding (0h), with 400 cells of each type scattered within a circular homeland, and ii) cell configuration after 3 hours' competition (3h). Scale bars: 50 µm. Zoomed sections highlight dead (black) susceptible cells and distribution of EPS particles. Inset scale bars: 10 µm. **(C)** Contour plot showing measurements of mean EPS benefit (see main text) as a function of initial attacker and susceptible cell density. N=20 simulation replicates per parameter combination. **(D)** Plot showing susceptible final:initial cell counts against initial susceptible density, exemplifying density-dependent benefit of EPS production (fixed attacker density of 400 cells). Individual data points are shown; lines and error bars correspond to data means and standard

deviations. Dashed line denotes Final:Initial susceptible ratio = 1, i.e. no net loss or gain of susceptible strain. N=20 simulation replicates per parameter combination; data replotted from (C).

124 **EPS protection is predicted to function as a collective trait**

125 We next used the simulations to more formally evaluate whether EPS protection is a collective
126 trait. A key feature of many collective traits is a positive relationship between the number of
127 individuals with the trait, and the benefit conferred (32). To look for this, we plotted the benefit of
128 EPS production against the starting number of susceptible (EPS producer) cells, which revealed
129 that the relationship is positive for many levels of EPS secretion (Fig. 1D, S2A, S2B). Note that
130 our metric controls for any density-dependent survival effects emerging solely from changes to
131 cell group size (33). That is, while survival is expected to generally increase with susceptible cell
132 number, this effect becomes much stronger when susceptible cells also produce EPS (Fig. 1D).
133
134 Next, we examined the extent to which the benefits from EPS production are shared among cells,
135 which is a second key feature of collective traits. Using the same competition protocol as before,
136 we ran simulations pitting T6SS attackers against susceptible EPS- cells, susceptible EPS+ cells,
137 or both together (Fig. 2A), for a range of initial cell densities. We then quantified the survival of
138 both the EPS+ cells and the EPS- cells when they grew either i) alone with the attacker or ii)
139 paired with the other susceptible cell type (Fig. 2B). As expected when the protective effect of
140 EPS is shared between cells, EPS- survival increased in the presence of EPS+ cells (Fig. 2B,
141 'rescue'), and, conversely, EPS+ survival decreased in the presence of EPS- cells (Fig. 2B,
142 'exploitation').
143

144 **A synthetic community demonstrates collective protection via EPS**

145 To test the model's predictions empirically, we turned to an established experimental system for
146 studying T6SS killing: competitions between a T6SS+ *A. baylyi* attacker strain and a T6SS-
147 susceptible *E. coli* strain (MG1655; (34)). Using their T6SS, *A. baylyi* cells can inject a cocktail of
148 different effector proteins into neighbouring cells which rapidly induce lysis in susceptible *E. coli*
149 (24). To compare the relative T6SS susceptibility of EPS-producing and non-producing *E. coli*,
150 we created *E. coli* MG1655 pRcsA2 (EPS+), a strain capable of undergoing IPTG-inducible
151 production of the exopolysaccharide colanic acid, which is a major component of natural *E. coli*
152 biofilms (35, 36). Colanic acid production is induced via plasmid-based expression of RcsA, the
153 major positive regulator of colanic acid biosynthesis in *E. coli* (37). Its plasmid-free parent
154 MG1655 serves as the non-EPS-producing control strain (EPS-), as MG1655 does not produce
155 significant amounts of colanic acid under the conditions used in this study (Fig. S3).

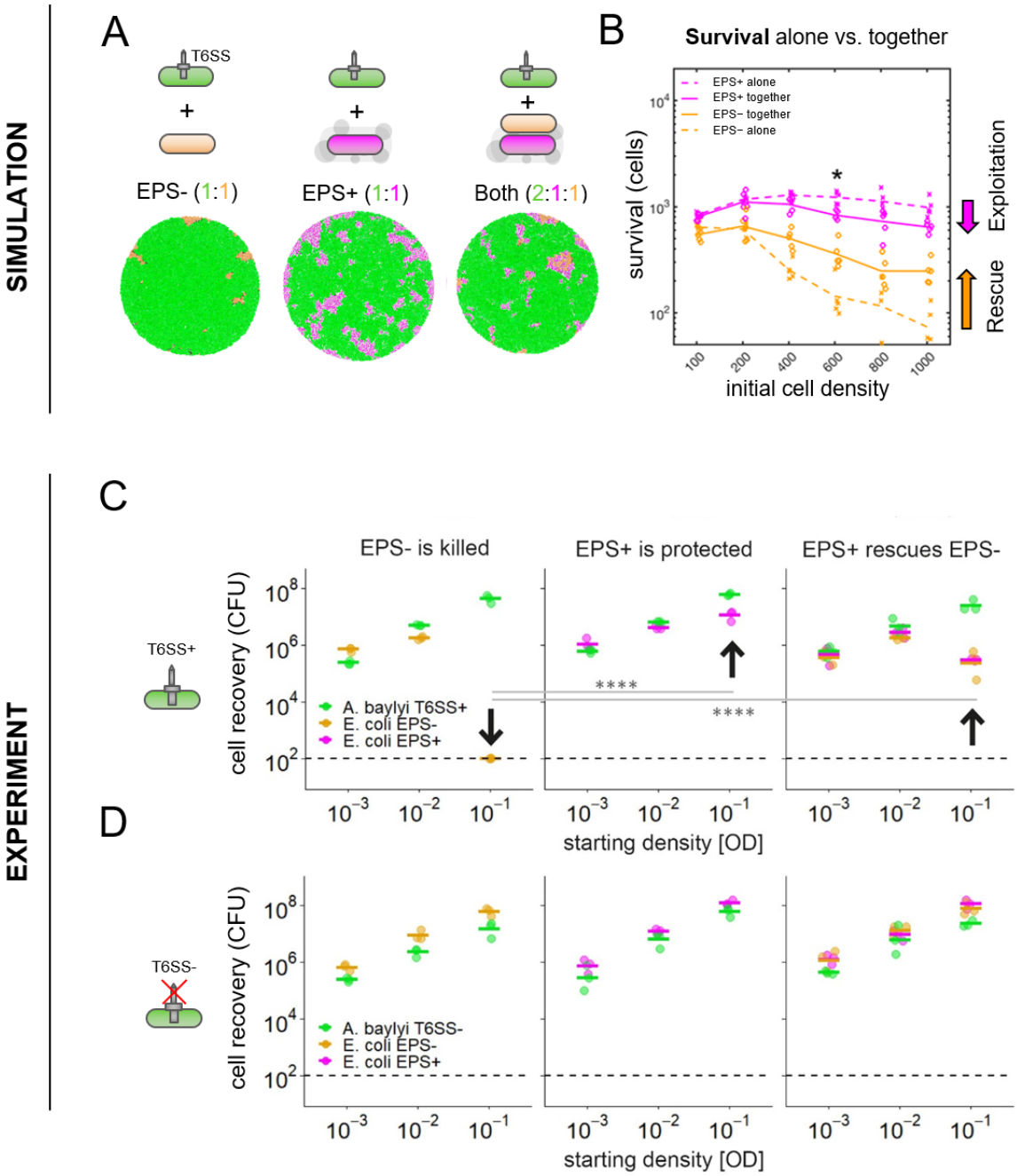

Fig. 2: Modelling and experiments show that EPS secretion protects both producer and non-producer *E. coli* from T6SS attacks. (A) End-state snapshots of agent-based simulations competing T6SS attackers (green) with EPS- or EPS+ (orange, magenta) strains, or both strains at once. **(B)** Survival of each susceptible strain (EPS+, magenta; EPS-, orange) growing alone against T6SS attackers (dashed lines), or together with the other susceptible strain type (solid lines). * denotes the scenario depicted in (A). **(C+D)** We conducted analogous competition assays *in vitro* between three bacterial strains: *A. baylyi* ADP1 (T6SS attacker), *E. coli* MG1655 Gen^R (EPS-), and *E. coli* MG1655 pRcsA2 (EPS+; colanic acid overproducer). For each strain, cell recovery (CFU) after 6h of co-culturing at different starting cell densities (optical density; OD) is shown. Individual data points (n=3) and their means are shown as dots and lines, respectively. Arrows highlight key comparisons. **(C)** Survival of *E. coli* EPS- (left), EPS+ (centre) or a 1:1 mix of EPS- and EPS+ (right), when competed against T6SS+ *A.*

baylyi. At high seeding density (OD = 10^{-1}), EPS+ cells survive pairwise competitions against a T6SS attacker better than EPS- cells (middle and left; $p < 0.0001$). When co-cultured with EPS+ and competing against the attacker (right), survival of EPS- cells is strongly increased relative to when they face the attacker alone (left; $p < 0.0001$). When EPS+ cells are co-cultured with EPS- and compete against the attacker (right), EPS+ survival is reduced compared to when they face the attacker alone (left; $p < 0.0001$). **(D)** Repeat of (C) with *A. baylyi* lacking a functional T6SS. When competed against a T6SS- attacker in pairwise competitions, no difference in cell recovery between EPS+ and EPS- cells was detected ($p = 0.66$). For both (C) and (D), competitions were analysed per strain combination and seeding density, with statistical analyses on log-transformed data via two-way ANOVA ($\alpha = 0.01$) with Tukey post-hoc tests (****: $p < 0.0001$).

156 We first sought to measure the amount of colanic acid secreted by the EPS+ strain, as well as
157 test where it is localised with respect to the cell membrane. Across *E. coli* strains, colanic acid
158 can be secreted both as a capsule tethered to the producing cell membrane, as well as in
159 untethered, loose form (38). The difference between these two states is likely to strongly influence
160 the role of colanic acid in collective protection from external assaults. To benchmark our colanic
161 acid quantification and localization assays, we compared the EPS+ and EPS- strains to six clinical
162 *E. coli* isolates (Table S2). As for the majority of the clinical isolates, phase-contrast microscopy
163 showed that our EPS+ strain has no visible membrane-bound capsule. This observation is
164 consistent with colanic acid being untethered to producing cells and released into the extracellular
165 environment (Fig. S3A). This conclusion was further supported by colanic acid quantification
166 assays where we measured the amount of colanic acid found in total cell extracts vs. supernatant
167 fractions of cultures harvested from agar plates. For the EPS+ strain, the entirety of the detected
168 colanic acid was recovered in the supernatant (Fig. S3B). This same assay also revealed that the
169 amount of loose colanic acid secreted by EPS+ is comparable to that secreted by two clinical
170 isolates (#0172 and #0993, Fig. S3B). The EPS+ *E. coli* strain, therefore, secretes loose colanic
171 acid at rates comparable to naturally occurring *E. coli,* allowing for a direct test of the role of EPS
172 in T6SS-mediated competitions.
173
174 Next, we compared the EPS+ and EPS- *E. coli* strains in competition against a T6SS-wielding *A.*
175 *baylyi* (ADP1; T6SS+) and a T6SS-deficient mutant (ADP1 Δ*tssM*; T6SS-). We seeded a 1:1
176 mixture of *A. baylyi* with either EPS+ or EPS- *E. coli* at various densities on agar plates and
177 measured strain recovery after 6h of co-culture using selective plating (Fig. 2C). At low seeding
178 densities, the T6SS is less efficient because it relies on cell-cell-contact for killing (24, 33). At high
179 seeding densities, we expect the T6SS to be maximally effective; this was confirmed in our
180 competition assays, as the EPS- control strain suffered maximal killing at high densities (Fig. 2C,
181 left). In contrast, the EPS+ strain survived much better at high densities (Fig. 2C, middle), with a
182 10^5-fold increase in survival against T6SS+ *A. baylyi* compared to EPS-. This advantage was

183 dependent on T6SS-activity, as there was no detectable difference in recovery between EPS+
184 and EPS- after pairwise competition with the T6SS- *A. baylyi* (Δ*tssM*) mutant (Fig. 2D). To test
185 whether the presence of EPS in the environment alters T6SS activity, we measured firing rates in
186 hundreds of T6SS+ *A. baylyi* cells exposed to cell-free supernatants with and without EPS, and
187 were unable to detect a difference (Fig. S4). These results strongly support our model's prediction
188 that non-membrane-bound EPS can protect susceptible cells from killing by the T6SS.
189
190 We then examined the potential for a producer strain to cross-protect a non-producer, as expected
191 for a collective defence mechanism. We conducted 3-way competitions between T6SS+ *A. baylyi*
192 and both the EPS+ and EPS- *E. coli* (2:1:1 ratio of *A. baylyi* : EPS+ : EPS-) and quantified strain
193 recovery as above. At high seeding densities, as predicted by the model, the survival of EPS-
194 increased 1000-fold in the presence of EPS+ (Fig. 2C, right) compared to when they faced the
195 T6SS attacker alone (Fig. 2C, left), indicating that the presence of secreted EPS can rescue
196 otherwise susceptible cells from T6SS attacks even if they do not produce EPS themselves.
197 Further consistent with the modelling, we observed that relative survival of the EPS+ strain
198 decreased in presence of EPS- (Fig. 2C, right) compared to when grown alone with the T6SS
199 attacker (Fig. 2C, left) suggesting that the presence of non-producing cells partially compromises
200 the protective effects of EPS production.
201
202 **Cross-protection can emerge from flank protection**
203 Our modelling and experiments show that EPS can function as a collective defence, whose
204 benefit is shared among cells in a colony or biofilm. We next sought to understand the
205 mechanism(s) underpinning this collective property. We initially reasoned that loose EPS would
206 be shared between cells, resulting in the protection of non-producing cells seen in both modelling
207 and experiments. To test this hypothesis, we modified our model so that EPS+ cells no longer
208 secreted loose EPS particles, but instead became intrinsically resistant to T6SS attacks (requiring
209 2 hits to kill instead of 1), as has been demonstrated in capsule-forming bacteria (15). The goal
210 of this model was to remove the possibility of EPS sharing between cells, so that we could test
211 whether sharing was necessary for the cross-protection of non-producer cells (Fig. 3).

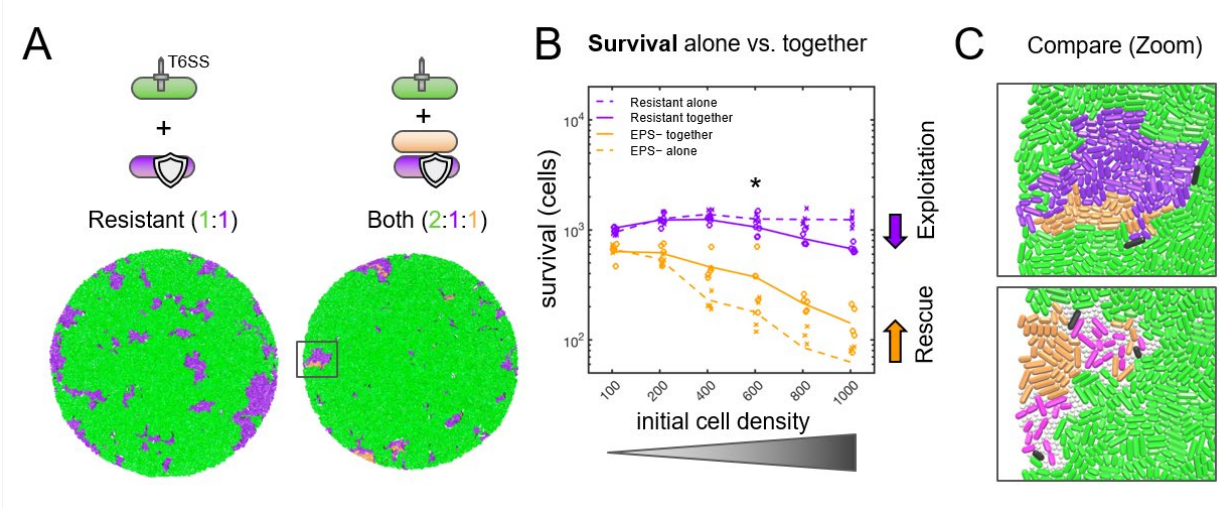

Fig. 3. Modelling shows that cross protection can occur without EPS sharing (A) End-state snapshots of agent-based simulations competing T6SS attackers (green) with an EPS- strain (orange), a T6SS-resistant strain (purple) that secretes no EPS particles, or both strains at once. Box corresponds to zoomed section in (C). **(B)** Survival of Resistant strain (purple) and the EPS- susceptible strain (orange) growing alone against T6SS attackers (dashed lines), or together with the other strain type (solid lines). N=5 simulations per parameter combination; lines denote mean survival. **(C)** Magnified views showing Resistant strain shielding EPS- from the attacker (top), similar to where protection occurs via secretion of loose EPS (bottom).

212 We then competed the resistant cell type against T6SS attackers as before, either in the presence
213 or absence of the EPS- susceptible cell type (Fig. 3A). To our surprise, this again lead to collective
214 T6SS defence, which displayed both cross-protection and the same density-dependence seen
215 for loose EPS (Fig. 3B). Close inspection of simulations revealed that resistant cells act as
216 barriers, protecting the flanks of susceptible cell groups by physically separating them from T6SS
217 attackers (Fig. 3C). We therefore term this mechanism 'flank protection'. Because we see cross
218 protection, flank protection is also a collective effect, but one that can be provided by a purely
219 private resistance mechanism, as well as by loose EPS.
220

221 **Time-lapse microscopy demonstrates cross-protection involves EPS sharing**

222 Our modelling shows that EPS-producing bacteria can collectively defend themselves against
223 T6SS attacks via flank protection, without sharing of EPS between cells. However, an important
224 simplification of the model is that it represents EPS as small solid spheres. This limits the ability
225 of EPS to flow past and around cells in a manner that may not always reflect the behaviour of real
226 EPS (39). Given this potential limitation of the model, we decided to investigate whether our
227 original hypothesis of EPS sharing was important in the experimental data, even if it was not
228 necessary for collective defence in the model. To do this, we turned to time-lapse confocal
229 microscopy, which enables direct observation of cells over time (Fig 4). We competed fluorescent

230 protein-expressing strains of *A. baylyi* (*vipA-sfGFP*, green) with EPS+ *E. coli* (*mScarlet*, magenta)
231 and EPS- *E. coli* (*BFP*, orange) and performed competitions on agar pads as before, except we
232 imaged different locations in the competition area hourly, using confocal microscopy. End-state
233 images of the competition area (Fig. 4A) provided visual confirmation of i) improved survival of
234 EPS+ relative to EPS-, and ii) improved survival of EPS- in the presence of EPS+. Surviving EPS-
235 cells also tended to co-localise with EPS+ cells (bottom right), similar to behaviour observed in
236 our model.
237
238 To look for signatures of EPS-mediated cross-protection in our time-lapse data, we examined
239 T6SS-mediated killing at boundaries between *A. baylyi* and *E. coli* cell groups (Fig. 4B) using
240 automated analysis of confocal time-lapse images. We reasoned that, if cross-protection occurred
241 via the association of loose EPS with EPS- cells, then an EPS- cell group should be able to
242 withstand the T6SS attacker better when EPS+ producers were also present. Specifically, the
243 boundaries between the T6SS attacker and EPS- cells should shift less in the favour of the T6SS
244 attacker, if EPS+ cells are also present nearby. Accordingly, we measured the rate of *A. baylyi*
245 encroachment into EPS+ and EPS- cell groups (Fig. 4B, “Invasion”), normalising this by the total
246 length of interface between *A. baylyi* and each individual susceptible strain (Fig. 4B, “Boundary”).
247 The resulting metric, which we term the normalised invasion rate, provides an estimate of how
248 susceptible each *E. coli* strain is to T6SS attack. Crucially, since the normalised invasion rate
249 examines *A. baylyi*–EPS+ and *A. baylyi*–EPS- strain interactions separately, it excludes any
250 possible effects of flank protection.
251
252 Our measurements of normalised invasion rates over time showed that the EPS- strain was
253 indeed invaded less rapidly when grown together with the EPS+ strain, vs. when grown alone
254 (Fig. 4C, left). This improvement was most pronounced between hours 3 and 4 of competition.
255 Meanwhile, the EPS+ strain was invaded at a consistently lower rate (Fig. 4C right) than the EPS-
256 strain, with normalised invasion rates largely unchanged by the presence / absence of the EPS-
257 strain (i.e., no significant exploitation effect detected). These effects are summarised in Fig. 4D:
258 integrating over all time points, the EPS- cell groups suffered significantly more invasion when
259 the EPS+ strain was absent. Importantly, this variation was contingent on T6SS activity: control
260 experiments showed minimal variation in EPS- strain invasion with EPS+ strain presence when
261 attackers lacked a functional T6SS (Fig. 4E, right). Note that these data do not exclude a role for
262 flank protection in the experiments, but they do provide evidence that EPS+ cells increase survival

263 of EPS- cells *at a distance*. This result is consistent with collective protection being mediated—at
264 least in part—by shared EPS.

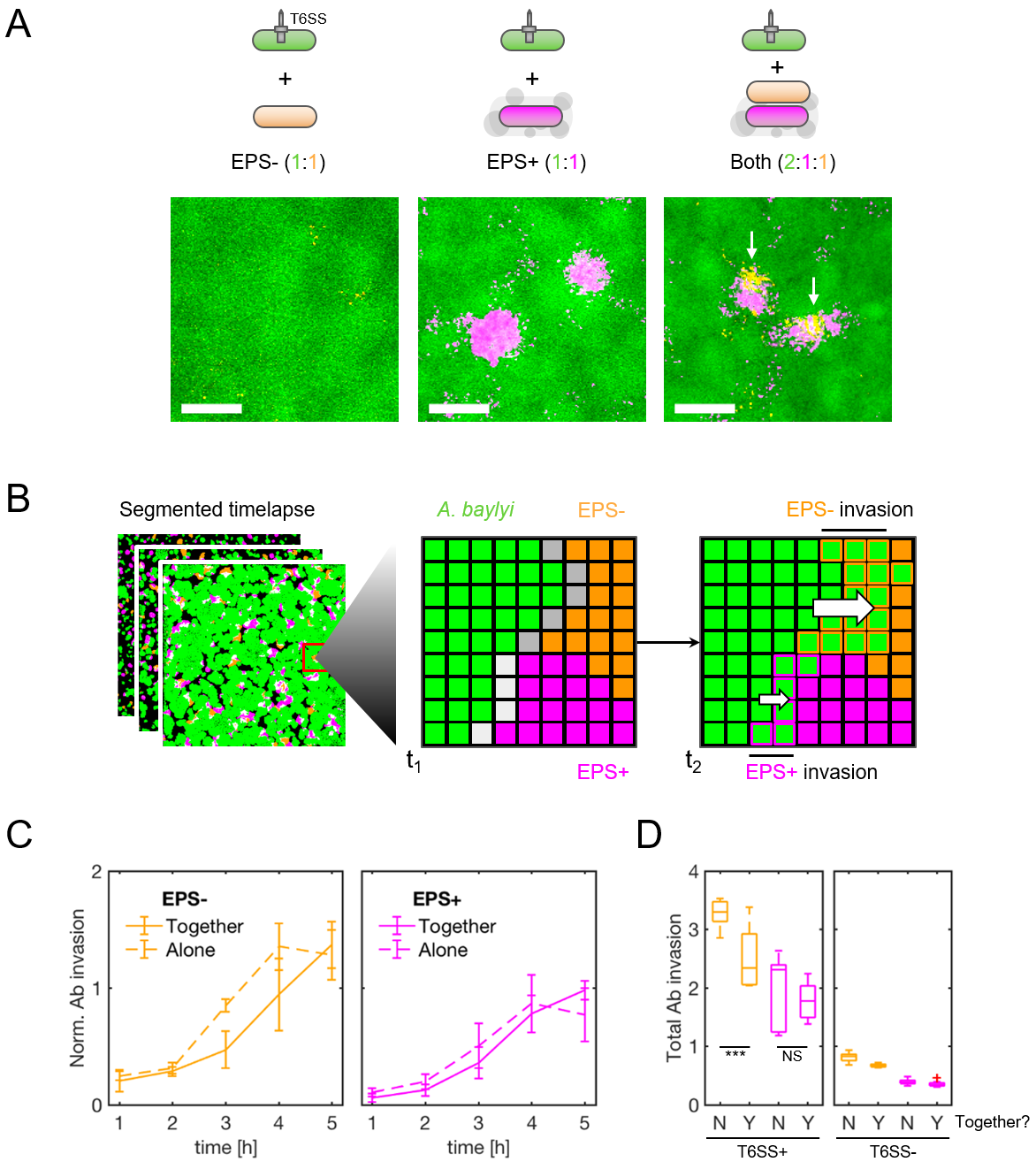

Fig. 4: *A. baylyi* invades EPS- *E. coli* cell groups less rapidly in the presence of EPS+ strain, supporting ranged protection via EPS sharing. (A) Attacker (green), EPS- (orange) and EPS+ (magenta) strains expressing fluorescent proteins were mixed and co-cultured as before (Fig. 2C,D), this time analysing competition dynamics using confocal microscopy. Colonies were imaged for 7h at 1h intervals, across five 470 x 470 µm frames spanning the colony edge (position 1) to its centre (position 5). Example images shown are zoomed-in areas of interest from position 4 (t = 6h); scale bars: 50 µm. **(B)** Automated image analysis for measuring rate of *A. baylyi* invasion into *E. coli* cell groups. We used segmented time-lapse images to identify i) boundaries between *A. baylyi* and EPS-, EPS+ *E. coli* cell groups (grey pixels), and ii) the rates at which *A. baylyi* expanded into EPS-, EPS+ *E. coli* groups

(orange- and magenta-edged pixels). **(C)** Measurements of *A. baylyi* invasion rates, normalised by boundary length, comparing invasion of EPS- (left) and EPS+ (right) cell groups, grown alone (dashed lines) or together (solid lines). Lines connect data means, and error bars denote standard deviations. Time-lapse data aggregated over colony positions 2-5; Position 1 was excluded for analysis since cells quickly grew beyond a monolayer, confounding our 2-D analysis. N=3 biological replicates; 12 data points per time point. (**D**) Comparison of total normalised invasion (area under curves in (D)) across all strain pairings, including T6SS- controls. Red cross denotes outlier data point (> Q3 + 1.5 * IQR). Significance assessed using one-sample Kruskal-Wallis tests; *** denotes p = 0.0004; N.S., non-significant.

DISCUSSION

Our modelling shows how EPS can serve as a highly protective, collective defence strategy against T6SS attacks, and one that can also mediate cross-protection of neighbouring, non-producing cells. Moreover, an experimental test of our model revealed that EPS dramatically increases *E. coli* survival in competition with T6SS-wielding *A. baylyi*. Here, colanic acid is secreted into the extracellular environment and we find evidence that it has the potential to protect cells other than the producer. Secretion of colanic acid is widespread in *Enterobacteriaceae* such as *E. coli*, *Klebsiella*, *Salmonella* and *Enterobacter* (40, 41), where it plays an important role in biofilm formation (35, 36, 42), and confers protection against various environmental stressors such as desiccation, osmotic stress, and oxidative stress (43, 44). Moreover, elevated EPS production (mucoidy) readily evolves in *E. coli* and other species in response to predation by phages (45–47), and membrane-anchored capsules can protect pathogenic bacteria from attacks by the immune system (48–50). EPS-mediated protection from T6SS attacks could therefore also evolve as a by-product of adaptation to other types of stressors, as well as a direct response to T6SS attacks itself.

With both modelling and experiments, we also found that EPS non-producing cells are able to survive T6SS attacks better when co-cultured with EPS producers. Additionally, our simulations identified a mechanism of cross-protection that we call flank protection, whereby groups of T6SS-resistant producers reduce the exposure of non-producers to attackers. However, in the experiments, we find evidence for a second, perhaps more intuitive, mechanism whereby loose EPS covers non-producers and directly shields them. Specifically, our microscopy experiments support the presence of direct protection via EPS sharing, as evidenced by a reduction in attacker invasion at the edges of non-producer cell groups. This implies that secreted EPS can shield non-producing cells, at a range spanning multiple cell lengths.

As discussed, our analyses do not exclude flank protection as a contributor to cross-protection in our experiments; we expect it to occur in parallel with EPS sharing. Indeed, flank protection has

294 the potential to be highly general: it is predicted to emerge whenever sensitive cell groups
295 interface with resistant cell groups, without assuming anything about the underlying resistance
296 mechanism. Collective resistance, therefore, may emerge widely, including in cases where EPS
297 is not shared between cells (15). More generally, flank protection has the potential to be mediated
298 by other mechanisms of T6SS resistance, such as envelope stress responses, or the production
299 of immunity proteins. In principle, it could generate unexpected collective protection against any
300 contact-dependent weapon, including via the T4SS, T7SS, and Cdi systems (4), adding further
301 complexity to interbacterial interactions.
302
303 T6SS-wielding bacteria are increasingly being considered as potential biotherapeutics, capable
304 of delivering toxins into pathogenic bacteria (51, 52). Our work cautions that many species have
305 the potential to resist such attacks due to the widespread ability of bacteria to work as collectives.
306 Consistent with this, bacteria are already known to display collective defences against antibiotics
307 (17, 19, 22), predators (53) and phage (20), and biofilm formation continues to be a major issue
308 in industry and medicine (54–57). Strategies that seek to remove problem strains, therefore,
309 needs to consider the ability of bacteria to work both as individuals and as groups.
310

311 ## MATERIALS AND METHODS

312 ### Agent-based modelling

313 We ran agent-based model simulations using the open-source modelling software Cellmodeller
314 (58). To simulate T6SS-mediated interactions and EPS particle secretion, we devised additional
315 code modules, available for download at https://github.com/WilliamPJSmith/CellModeller. The
316 key processes incorporated in our model are summarised here.

317 Model description

318 *Cell growth and division*. Bacterial cells are modelled as exponentially-growing rigid elastic rods
319 with fixed radius R, which push on one another as they elongate and divide (after doubling their
320 initial volume V_0, plus a small random noise term η_{div}). All cells are assumed to have equal access
321 to growth-limiting nutrients. Generally, cells pay no growth penalty for using either T6SS needles
322 or EPS secretion, and so a cell's volume V increases over time as $\Delta V = k_{grow} V \Delta t$, with k_{grow} the
323 maximum specific growth rate, and Δt the simulation timestep. However, we also explored
324 scenarios in which EPS secretion carried a range of growth costs proportional to the EPS
325 secretion rate (see Fig. S2B,C). Immediately after cell growth, an energy penalty method is
326 applied each timestep to compute cell movements necessary to minimise total cell-cell overlap,

subject to viscous drag forces acting on each cell. This process, described previously in detail (23, 58), approximates the elastic repulsion forces acting between cells in physical contact.

EPS secretion. Similar to previous work, we model agglomerations of EPS polymers as inert, pseudospherical particles (29–31). EPS+ cells secrete these particles from randomly chosen points on their surface. These particles have radius 0.4 μm, rod segment length 0.01 μm, and are assumed mechanically identical to bacterial cells. The secretion probability per time step, P_{EPS}, is at most 0.1, such that the max secretion rate is capped at 1 particle per timestep. EPS particles persist indefinitely, and completely ignore the effects of T6SS toxin injection (see below).

T6SS interactions. Each time step, T6SS+ cells can fire needles of length *R/2,* projecting orthogonally from randomly chosen sites on their cell surface. The number of firings per cell per unit time is drawn from a Poisson distribution, whose mean is k_{fire}. After firing, each needle is checked to determine if it comes into contact with any other cell in the population (line-segment method). Subsequent to this contact finding, each cell's state is updated to indicate the number of T6SS needle hits it sustained. Cells die (cease growing) after being struck N_{hits} times in this way, and lyse (disappear) following a fixed delay of $1 / k_{lysis}$. Each T6SS needle can deliver its toxin payload to at most one cell. T6SS+ cells are assumed completely immune to their own T6SS toxins, such that they effectively ignore all collateral fire from clone-mates. EPS particles do not obstruct T6SS needles, and so EPS particles can only protect bacterial cells from T6SS attacks by enforcing spatial separation of attacker and susceptible cells.

Computation and post-processing

All agent-based simulations were run using a 2017 Apple MacBook Pro laptop computer, with concurrent simulations distributed between an Intel 3.1 GHz quadcore i7-7920HQ CPU, an Intel HD 630 Graphics card, and an AMD Radeon Pro 560 Compute Engine. Simulation data were visualised using Paraview software, and analysed using custom Matlab and R scripts.

Simulation protocols

All simulations were initialised by randomly scattering different combinations of cells on a flat surface, within a circular 'homeland' of radius 50 μm. At simulation time $t = 0$, all cells lie flat on the surface, but have randomised orientations. All simulations were run for 130 time steps (Δt = 0.025h), totalling 3.25h of simulated time. Depending on conditions (most crucially, the number of EPS particles present), most simulations had a runtime of between 10 and 30 minutes (approximately 10 simulations per hour after concurrency).

359 **Bacterial growth conditions**

360 All strains were routinely grown overnight in 5 ml LB medium (per L: 10g Tryptone, 10g NaCl, 5g
361 Yeast Extract) in 15 mL polypropylene tubes with agitation (220 rpm). Where necessary, the
362 medium was supplemented with streptomycin (50 µg/mL), ampicillin (100 µg/mL), carbenicillin
363 (100 µg/mL) or gentamycin (15 µg/mL). Routine culturing was carried out on 1.5% w/v LB Agar
364 at 37°C (*E. coli*) or 30°C (*A. baylyi*). All pre-cultures and experiments were carried out at 30°C on
365 0.8% w/v LB Agar, unless indicated otherwise. Optical density (OD) of liquid cultures was
366 measured at 600 nm. For time-lapse microscopy experiments, samples were kept at 30°C
367 throughout the duration of the experiment using a custom-built incubation chamber.

368

369 **Strain construction**

370 For the generation of MG1655 *mScarlet-I*::Tn7 and MG1655 *mTagBFP2*::Tn7, MG1655 cells were
371 transformed with either pGRG25-P*max*::*mScarlet-I* or pGRG25-P*max*::*mTagBFP2* via
372 electroporation and selected on ampicillin at 30°C. The resulting transformants were cultured for
373 16 h at 30°C in liquid LB medium supplemented with ampicillin and arabinose (0.5% w/v). A small
374 volume (appr. 5 µL) of these cultures was streaked onto 1.5% w/v LB agar supplemented with
375 arabinose (0.5% w/v) and incubated at 42°C for 12 h. For each construct, three fluorescent
376 colonies were then selected, streaked onto 1.5% w/v LB agar and incubated at 42°C for 12 h.
377 Resulting colonies were tested for ampicillin sensitivity. For the generation of *E. coli* MG1655
378 *mScarlet-I*::Tn7 pRcsA2, MG1655 *mScarlet-I*::Tn7 cells were transformed with pRcsA2 (37) via
379 electroporation and selected on 100 µg/mL carbenicillin at 37°C. All plasmids and strains used in
380 this study are listed in Table S2.

381

382 **Competition assays**

383 To monitor survival of different *E. coli* strains in competition with *A. baylyi* strains, overnight
384 cultures of *A. baylyi* and *E. coli* were diluted (*A. baylyi* 1:10; *E. coli* 1:100) into 5 mL of fresh LB
385 medium supplemented with appropriate antibiotics (Table S2) and 0.5 mM IPTG to induce
386 production of colanic acid. We used *vipA-sfGFP*-labelled *A. baylyi* ADP1 as the T6SS-positive
387 competitor, whereas an isogenic *tssM* deletion mutant was used as T6SS-negative control
388 competitor. Cultures were then grown for 3 h with agitation, washed twice with LB medium, and
389 resuspended and normalized in LB medium to an optical density at 600 nm (OD600) of 0.1. An
390 *A. baylyi* strain was then mixed with an *E. coli* strain at a ratio of 1:1 (100 µL : 100 µL), and for

391 each strain combination 5 µL were spotted in triplicates in 24-well plates pre-filled with LB agar
392 supplemented with 0.5 mM IPTG (1 mL per well). For experiments at different seeding densities
393 (Fig. 2), the initial 1:1 mix was further diluted 10-fold (for OD = 0.01) or 100-fold (for OD = 0.001)
394 before being spotted on LB agar. For experiments with three competitors (Fig. 2), one *A. baylyi*
395 strain and two *E. coli* strains were normalized to OD = 0.1, mixed at a ratio of 2:1:1 (*A. baylyi* : *E.*
396 *coli* : *E. coli*), and further diluted if required before being spotted on LB agar. Plates were then
397 dried in a laminar flow at room temperature for approximately 20 min to allow droplet drying,
398 before being incubated at 30°C for 6 h. After incubation, competition spots were washed off with
399 500 µL NaCl (0.8%) each and subjected to seven rounds of 10-fold serial dilution. Colony-forming
400 units (CFUs) of *A. baylyi* and *E. coli* strains were determined by plating on streptomycin (100
401 µg/mL; selecting for *A. baylyi*), ampicillin/carbenicillin (100 µg/mL; selecting for *E. coli* MG1655
402 pRcsA2) or gentamycin (15 µg/mL; selecting for *E. coli* MG1655 Gen^R) media, incubated at 30°C
403 (*A. baylyi*) or 37°C (*E. coli*).
404

405 **Determination of T6SS firing rate**

406 To determine T6SS firing rate in *A. baylyi* cells exposed to EPS produced by *E. coli* (Fig. S4A),
407 cells of *E. coli* EPS+ and EPS- were grown overnight for 16 hours at 37°C, and 1 mL of bacterial
408 suspension was centrifuged for 5 min at 17000 g to sediment cells. The resulting supernatants
409 were sterile-filtered using 0.2 µm syringe filters (Sartorius), and 5 µL were each pipetted onto
410 separate cut-outs (ca. 5 mm x 5 mm) of 1% w/v LB agarose and left to dry for 20 min at room
411 temperature. In parallel, cells of the focal strain (*A. baylyi* T6SS+ *clpV-mCherry2*) were grown to
412 exponential phase in liquid culture (OD600 ~ 0.8-1.0) before spotting 1 µL of culture onto the
413 agarose pads treated with supernatant, and leaving them to dry for 5 min at room temperature.
414 Pads were then inverted onto a 5-cm diameter glass bottom Petri dish with a 3-cm diameter
415 uncoated n° 1.5 glass window (MatTek Corporation), so that the cells were sandwiched between
416 the agarose and the glass. The sample was then moved to the microscope and imaged
417 immediately. Time-lapse fluorescence microscopy was performed using a Zeiss Axio Observer
418 inverted microscope with a Zeiss Plan-Apochromat 63x oil immersion objective (NA = 1.4) and
419 ZEN Blue software (version 1.1.2.0). Time-lapse images were recorded for 3 minutes at a 10-
420 second interval. Exposure times were 1.05 ms for brightfield and 500 ms for mCherry2 (ex:
421 589 nm | em: 610 nm). The rate of T6SS firing was measured in a total of n = 916 *A. baylyi* cells
422 via detection of ClpV (*mCherry*) fluorescent foci (24). Each new ClpV focus was assumed to mark
423 one T6SS contraction event in a focal cell. Three separate fields of view at different locations on

424 the same agarose pad were monitored for each treatment. Image analysis was performed using
425 FIJI 2.1.0/1.53c (59). For each field of view, total number of cells and ClpV foci were determined
426 each minute via thresholding, segmentation and object counting in the brightfield channel, and
427 the FIJI built-in “Find maxima” function in the mCherry fluorescence channel, respectively

428

429 **Colanic acid quantification**

430 To quantify the amount of colanic acid (CA) produced by different *E. coli* strains (Fig. S2), 1 mL
431 of overnight cultures were washed once with fresh LB medium and density-adjusted to an OD of
432 1.0. For each strain, 50 µL were then spotted in triplicates in 24-well plates pre-filled with LB agar
433 supplemented with 0.5 mM IPTG (1 mL per well). Plates were then dried in a laminar flow at room
434 temperature for approximately 20 min to allow droplet evaporation, before being incubated at
435 30°C for 6h. Cell material was then harvested by adding 1 mL of sterile ddH_2O to the well and
436 pipetting up and down until all material was suspended, and then transferred to a sterile 1.5 mL
437 tube. Tubes were vortexed for 5-7 seconds, and the OD600 was determined for all replicates. Of
438 these volumes, twice 400 µL were then transferred to two separate reaction tubes pre-filled with
439 600 µL ddH_2O: one for quantification of total CA, and one for quantification of CA secreted into
440 the extracellular environment. For quantification of total CA (Fig. S3), samples were boiled for 20
441 min at 95°C, centrifuged at 17’000 g for 20 min, and 1 mL of supernatant was used for further
442 processing. For quantification of CA in the extracellular environment (Fig. S3), samples were
443 centrifuged at 17’000 g for 20 min, and 1 mL of supernatant was used for further processing. To
444 test whether sterile-filtering removes EPS from supernatants (Fig. S4B), *E. coli* MG1655 pRcsA2
445 (EPS+) and MG1655 Gen^R (EPS-) strains were grown overnight for 16 hours at 37°C, and 1 mL
446 of bacterial suspension was centrifuged for 5 min at 17000 g to sediment cells. The resulting
447 supernatants were either sterile-filtered using 0.2 µm syringe filters (Sartorius) or left unfiltered,
448 and 900uL of supernatant was used for further processing. Relative CA production was then
449 determined through the quantification of L-Fucose (60). Briefly, samples were boiled with 4.5 mL
450 $H_2SO_4 \cdot H_2O$ (6:1 H_2SO_4 and H_2O) for 20 min and cooled to room temperature. Then, 900 µL of
451 each sample was transferred to a spectrophotometer cuvette and absorbance was measured at
452 396 nm (A_{396}) and 427 nm (A_{427}). To each cuvette was then added 100 µL of freshly prepared L-
453 cysteine hydrochloride (1M), mixed by pipetting, and absorbance was again measured at 396 nm
454 ($A\text{-}cy_{396}$) and 427 nm ($A\text{-}cy_{427}$). The concentration of L-Fucose was then determined by calculating

455 $(A\text{-}cy_{396} - A_{396}) - (A\text{-}cy_{427} - (A_{427})$ and applying a previously generated L-Fucose standard
456 curve (0-100 µg/mL).
457
458 **Confocal microscopy**
459 To image competition dynamics, fluorescently tagged versions of all relevant strains (Table S2)
460 were pre-cultured and density-adjusted to OD600 = 0.1 as described in "Competition assays".
461 For each strain combination, 5 µL were then spotted onto a glass bottom Petri dish filled with 8
462 mL 0.8% w/v LB agar supplemented with 0.5 mM IPTG. After drying for ten minutes at room
463 temperature, the plate was inverted to allow for immediate imaging of the competition area
464 through air. Time-lapse confocal imaging was then carried out using a Zeiss Plan-Apochromat
465 10x objective (NA = 0.45) on a Zeiss LSM880 confocal laser scanning unit using ZEN Black
466 software (version 14.0.18.201). Images (each covering an area of 472.33 µm x 472.33 µm) were
467 acquired hourly for 7 h, over 5 different colony positions, spanning in total the entire radius of the
468 competition area (edge to centre). Three biological replicates were carried out for each strain
469 combination.
470
471 **Confocal image analysis**
472 *Image segmentation and stabilization.* Following acquisition, raw confocal image data were
473 analyzed using FIJI (59). Multichannel images were split into individual channels, with each
474 channel subjected to separate background subtraction (rolling ball radius 50 px) and conversion
475 to binary image data via user-defined thresholds. To maximise the accuracy of cell group
476 boundary tracking, we stabilised images using the FIJI 'StackReg' plugin (61), applied to the GFP
477 (*A. baylyi*) channel. This stabilisation made it necessary to exclude later time points (t=6,7h) as
478 these were typically confluent, confounding accurate registration of images. We also excluded
479 colony position 1 (colony edge); here, coffee-ring effects (62) consistently led to the formation of
480 3-D cell groups as early as 2h into the competition. As our image analysis is limited to 2-D, we
481 were unable to accurately track inter-strain boundaries at this position. For visualization purposes,
482 mtagBFP2 fluorescence is false-coloured orange in all images throughout the manuscript.
483
484 *Normalised invasion rates*. To estimate T6SS killing rates at interstrain boundaries (Fig. 4), we
485 tracked changes in strain occupancy at each pixel across consecutive time-lapse images, using

custom MATLAB scripts. We compared consecutive time points (t-1, t; t=1,2,3,4,5h) in each stablised time lapse. Any pixel where EPS+ channel signal was lost, and replaced with new *A. baylyi* signal, was marked as being 'invaded' by *A. baylyi*, giving a measure of EPS+ cell killing by the attacker. EPS+ invasion pixel counts were normalised by the amount of Ab-EPS+ contact found in the t-1 image. We measured Ab-EPS+ contact by dilating *Ab* cell group images (MATLAB *imdilate* method; 3 pixel spherical structuring element) and computing their overlap (in pixels) with EPS+ cell groups. Performing this procedure in reverse (dilate EPS+ onto *Ab*) yielded similar boundary pixel counts. EPS- invasion was calculated and normalised in the same way.

Statistical Analysis

Statistical analysis and data visualization were performed using RStudio version 1.2.5033 (63) and packages dplyr (64), Rmisc (65), ggplot2 (66), and cowplot (67); as well as Matlab version 2017b (9.3.0.713579). For all statistical tests, the significance level α was set to 0.05. To test whether cell recovery differed between competitions (Fig. 2), two-way ANOVA of log-transformed CFU values with a post-hoc Tukey's HSD test was performed. To test whether colanic acid production differed between strains (Fig. S3B), and whether firing rate differed when cells were exposed to EPS (Fig. S4A), a two-sided Wilcoxon rank sum test was performed. To test whether filtering removed EPS from supernatants (Fig. S4B), a two-sided, paired samples Wilcoxon signed rank test was performed. To test whether total normalised invasion of the EPS- strain changed when grown alongside the EPS+ strain (or vice versa; Fig. 4), we used one-sample Kruskal-Wallis tests. Statistical details (sample size, test values, p-values) for each experiment are provided in the respective Figure legends.

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