

1 **Adaptation to public goods cheats in *Pseudomonas aeruginosa***

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3 Siobhán O'Brien^{1*}, Adela M. Luján², Steve Paterson³, Michael A. Cant⁴ & Angus

4 Buckling⁵

5

6 ¹Center for Adaptation to a Changing Environment (ACE), ETH Zürich, 8092 Zürich,

7 Switzerland. siobhan.obrien@env.ethz.ch

8 ²College of Life and Environmental Sciences, University of Exeter, Penryn Campus.

9 Cornwall TR10 9FE, United Kingdom

10 ³Centro de Investigaciones en Química Biológica de Córdoba, CIQUIBIC, CONICET

11 and Departamento de Química Biológica, Facultad de Ciencias Químicas,

12 Universidad Nacional de Córdoba, Ciudad Universitaria, X5000HUA, Córdoba,

13 Argentina

14 ⁴Institute of Integrative Biology, University of Liverpool, Crown Street, Liverpool,

15 UK, L69 7ZB

16 ⁵Environment and Sustainability Institute, University of Exeter, Penryn Campus,

17 TR10 9FE, United Kingdom

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19 **Corresponding author*

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26 **Abstract**

27 Cooperation in nature is ubiquitous, but is susceptible to social cheats who pay little
28 or no cost of cooperation yet reap the benefits. The effect such cheats have on
29 reducing population productivity suggests that there is selection for cooperators to
30 mitigate the adverse effects of cheats. While mechanisms have been elucidated for
31 scenarios involving a direct association between producer and cooperative product, it
32 is less clear how cooperators may suppress cheating in an anonymous public goods
33 scenario, where cheats cannot be directly identified. Here, we investigate the real-time
34 evolutionary response of cooperators to cheats when cooperation is mediated by a
35 diffusible public good: the production of iron-scavenging siderophores by
36 *Pseudomonas aeruginosa*. We find that siderophore producers evolved in the
37 presence of a high frequency of non-producing cheats were fitter in the presence of
38 cheats, at no obvious cost to population productivity. A novel morphotype
39 independently evolved and reached higher frequencies in cheat-adapted versus control
40 populations, exhibiting reduced siderophore production but increased production of
41 pyocyanin - an extracellular toxin that can also increase the availability of soluble
42 iron. This suggests that cooperators may have mitigated the negative effects of cheats
43 by downregulating siderophore production and upregulating an alternative iron-
44 acquisition public good. More generally, the study emphasises that cooperating
45 organisms can rapidly adapt to the presence of anonymous cheats without necessarily
46 incurring fitness costs in the environment they evolve in.

47

48 **Keywords:** Siderophore; Public goods; Cooperation; Pseudomonas; Pyoverdine;
49 Experimental Evolution

50

51 **Background**

52 Cooperative behaviour (any action selected at least partly because of its beneficial
53 effect on another individual [1]) owes its ubiquity to incurring a direct or indirect
54 fitness benefit to individuals in cooperating groups. However, when cooperation
55 carries a cost it is associated with social cheats who pay little or no cost of
56 cooperation but reap the rewards. This fitness advantage facilitates their invasion of
57 cooperating groups, which can impose a large cost on the population as a whole, in a
58 ‘Tragedy of the Commons’ scenario [2,3]. However, cooperation persists at all levels
59 of biological organisation [4], suggesting that mechanisms have evolved that impede
60 the negative impact of cheats. Many organisms, including long-tailed tits [5], bumble
61 bees [6] and toads [7,8], preferentially direct help toward relatives, while tactics such
62 as punishing/policing cheats have been well documented, for example, in queenless
63 ants [9], honeybees [10] and humans [11,12].

64

65 Our understanding of how cooperators adapt to the presence of cheats has been
66 greatly enhanced by studies of microbes, due to their suitability for carrying out real-
67 time evolution experiments as well as identifying the genetic basis of behaviours.
68 Maintaining high relatedness between producer and beneficiary is paramount for
69 allowing cooperation to persist [13], so that directing the benefits of cooperation to
70 close kin or clone mates can mitigate the negative influence of cheats on population
71 growth [14]. Preferential interactions with close relative can be facilitated by a
72 spatially structured environment [15], but even in the absence of spatial structure
73 mechanisms such as ‘green beard’ genes [16,17] and antagonistic pleiotropy [18,19]
74 facilitate directing the benefits of cooperation to kin.

75

76 Several studies have demonstrated real-time evolution of cheat resistance in
77 cooperator populations. *Pseudomonas fluorescens* biofilms can be invaded by non-
78 contributing cheats, compromising the integrity of the biofilm. Coevolution between
79 these two phenotypes gives rise to increasingly efficient cheats and more resistant
80 cooperators [20]. Moreover, cooperators have been found to evolve ways of opposing
81 productivity of cheats who fail to contribute to dead-end stalk cells in *Myxococcus*
82 *xanthus* [21], and *D. discoideum* [22]. However, the exact mechanism of cheat
83 resistance in these cases is unclear.

84

85 While such examples involve direct physical association between producer and
86 cooperative trait, it is less clear if and how adaptation may occur in an anonymous
87 public good scenario, where there is usually no clear physical link between producer
88 and product. Hence, directly targeting cheats for punishment/policing or directing
89 benefits of cooperation toward kin is problematic. Moreover, simple point mutations
90 often lead to the rapid production of cheats, making pleiotropy unlikely as an anti-
91 cheating mechanism [23]. Several recent studies have suggested novel ways by which
92 bacteria can fine-tune their cooperative output to ensure beneficiaries are highly
93 related. For instance, quorum sensing can be used by bacteria to infer when they are
94 surrounded by clone mates, allowing them to tune their investment into cooperative
95 traits depending on the genotype of surrounding cells [24,25]. Similarly, *Escherichia*
96 *coli* plasmid donors can bias altruistic transfer of beneficial plasmids only to other
97 cells that share the donation alleles [26]. However, this requires a degree of
98 population structuring or an association between transfer and discrimination alleles.

99

100 Here, we investigate the real time evolutionary response of cooperators to cheats
101 when cooperation is mediated by a public good that is individually costly and carries a
102 group-level benefit: the production of iron-scavenging siderophores by *Pseudomonas*
103 *aeruginosa*. Cheats evolve rapidly in this system, avoiding the cost of siderophore
104 production while still retaining the correct receptor for uptake of the siderophore-iron
105 complex [1, 27]. **Two** recent studies coevolved siderophore producers and cheats
106 together, and reported the evolution of reduced siderophore production in producer
107 populations [28,29]. However, in these studies either the fitness consequences of
108 altered siderophore production were not assessed [28] or the experimental design did
109 not impose selection for cooperation, so that cheating, rather than resistance to
110 cheating, was selected for [29]. As such, these studies did not determine whether or
111 not coeprators can adapt to cheats. Here, we evolve *P. aeruginosa* in the presence or
112 absence of cheats, under conditions where there is selection for cooperation: patches
113 within a metapopulation are mixed and single co-operator clones from this mixture
114 used to inoculate new patches. Mixing patches means that genotypes from the most
115 productive patches, i.e. in which cooperators are less exploited by cheats, are
116 overrepresented in subsequent generations, while those from less productive patches
117 are underrepresented. Inoculating new patches with single clones resulted in high
118 relatedness, and hence stronger selection for cooperation [30].

119

120 **Materials and methods**

121 *Strains and growth media*

122 The *P. aeruginosa* strain PAO1 was used as the siderophore-producing wildtype. A
123 gentamicin-resistant PAO1 (PAO1^R) and gentamicin-resistant PAO1 with a *lacZ*
124 reporter gene insertion (PAO1^R*lacZ*) were engineered by integrating a gentamicin

125 resistance cassette (Tn7-gm) and a *lacZ* gene (with a gentamicin resistance cassette;
126 Tn7-gm-*lacZ*), respectively at the *att::Tn7* locus in *P. aeruginosa* PAO1 [31].
127 PAO1 Δ *pvdD* Δ *pchEF* is a gentamicin-susceptible isogenic mutant strain of PAO1 with
128 genes encoding both primary and secondary siderophores, pyoverdine and pyochelin
129 knocked out [32]. Experiments were carried out in Kings Medium B (KB) [33]: (10 g
130 glycerol, 20 g proteose peptone no. 3, 1.5 g K₂HPO₄·3H₂O, 1.5 g MgSO₄·7H₂O per
131 litre). Where stated, KB medium was made iron-limited by the addition of freshly
132 made filter-sterilised 100 μ g/ml human apotransferrin and 20mM NaHCO₃ to KB
133 medium immediately before use. Since siderophore production is repressed when
134 there is an excess of Fe²⁺ [34]; iron-limitation ensures that siderophores are essential
135 for growth and stimulates their production. Gentamicin was used at a concentration of
136 30 μ g/ml and 5-Bromo-4-chloro-3-indolyl- β -D-galactopyranoside (X-gal) at 90 μ
137 g/ml. Bacteria were grown at 37°C shaken at 180rpm unless stated otherwise.

138

139 *Costs and benefits of siderophore production*

140 We firstly confirmed that siderophore production carries a cost, and is exploitable by
141 non-producing cheats in our experimental context: 6ml iron-limited shaken KB
142 medium. We established six PAO1 populations (cooperator), six PAO1 Δ *pvdD* Δ *pchEF*
143 populations (cheat) and six populations in 1:1 co-culture, quantifying relative fitness
144 of cheats after 24h. Proportions of bacteria were inoculated so that the density of
145 bacteria added to each microcosm was $\sim 10^7$ CFU's ml⁻¹ (colony forming units).
146 Bacterial densities were assessed by plating appropriate dilutions on KB agar after
147 24h growth.

148

149 *Evolution Experiment*

150 We evolved cooperators (PAO1^R) in the presence and absence of a high frequency
151 (90%) of siderophore-negative cheats (PAO1 Δ pvdD Δ pchEF) (figure A1). This high
152 frequency of cheats ensures there is selection for cooperators to adapt to mitigate the
153 adverse effects of cheats on population productivity. Our design comprised of 6
154 replicate populations for each treatment (+/- cheats), with each population consisting
155 of 6 'patches'. Patches were initiated with a single cooperator colony; 10⁷ CFU's ml⁻¹
156 for the control treatment and 10⁶ CFU's ml⁻¹ for the 90% cheat treatment. 9x10⁶
157 CFU's ml⁻¹ PAO1 Δ pvdD Δ pchEF were also added to the 90% cheat treatment so that
158 the final inoculated bacterial density was also 10⁷ CFU's ml⁻¹. After 24h growth,
159 100 μ l was combined from each patch and plated on KB agar + gentamicin
160 (facilitating cheat removal). Single colonies were then selected at random to inoculate
161 new patches, and cheats were re-added to the appropriate treatment, using the same
162 number of CFU's as before. This design (global competition and high relatedness)
163 selected for subpopulations with high productivity, since genotypes from the most
164 productive subpopulations were overrepresented in the mixture (see [18]) This
165 process of enforcing global competition was repeated 18 times (~190 generations),
166 but cultures were allowed to grow for 96 hours (rather than 24h) between the
167 enforcement of the final 4 rounds of global competition, transferring 1% of the cells
168 to fresh media every 24h. This was to accelerate evolutionary change which we
169 speculated was being constrained by daily bottlenecking of cultures.

170

171 *Quantifying fitness of evolved populations: competition experiments*

172 Fitness of each of our 12 evolved populations was assessed relative to their ancestor
173 in both selective environments: in the presence and absence of cheats. Six replicates
174 were established per population in 6ml Fe-limited medium, totalling 144 fitness

175 assays. Half of the tubes were inoculated with $\sim 5 \times 10^5$ CFU's ml^{-1} ancestral
176 PAO1^R*lacZ* (gentamicin-resistant and *lacZ* insertion strain), $\sim 5 \times 10^5$ CFU's ml^{-1} of the
177 appropriate evolved population and $\sim 9 \times 10^6$ CFU's ml^{-1} of PAO1 Δ *pvdD* Δ *pchEF*, so
178 that cheat strains represented a high proportion ($\sim 90\%$) of the total bacterial density in
179 each microcosm, and the total inoculated density was 10^7 CFU's ml^{-1} . A further 72
180 microcosms (cheat-free competitions) were inoculated with $\sim 5 \times 10^6$ CFU's ml^{-1}
181 ancestral PAO1^R*lacZ* and $\sim 5 \times 10^6$ CFU's ml^{-1} of the appropriate evolved population,
182 so the total inoculum was 10^7 CFU's ml^{-1} . Microcosms were grown for 24h, after
183 which densities were assessed by plating liquid cultures on KB agar supplemented
184 with 30 $\mu\text{g/ml}$ gentamicin and 90 $\mu\text{g/ml}$ Xgal, and counting viable colonies.
185 Gentamicin facilitated the removal of cheats at the counting stage, which otherwise
186 would have dominated the plates and resulted in very low cooperator counts. Evolved
187 and ancestral cooperator strains were distinguished by a dark blue appearance of the
188 ancestral strain on Xgal-supplemented agar. Finally, the neutrality of the *lacZ*
189 insertion in the ancestral strain under these growth conditions was confirmed by
190 competing PAO1^R*lacZ* with PAO1^R at 1:1 in Fe-limited KB media.

191

192 *Measuring public goods production*

193 After ~ 190 generations, each replicate was diluted and cultured on KB agar to
194 measure: i) colony morphotypic variation; ii) *per capita* siderophore production; iii)
195 production of the most costly and efficient iron-siderophore, pyoverdine [35-37]; iv)
196 the toxin pyocyanin, which can generate soluble iron.

197

198 Thirty randomly selected colonies from each population were statically grown in
199 200 μl iron-limited KB medium (siderophore-stimulating conditions). *Per capita* total

200 siderophore production was quantified by combining 50 μ l from each of the 30 single
201 colony cultures, centrifuging to pellet cells and performing a 50% Chrome azurol S
202 (CAS) assay on the supernatant, measuring A_{630} of cultures as well as the cell-free
203 supernatant (reference culture) [38,39]. A measure of iron chelator activity relative to
204 the reference culture in each population was given by $[1-(A_{pop}/A_{ref})]$, standardised by
205 the optical density (A_{600}) of the relevant culture. *Per capita* pyoverdine was quantified
206 for each of our 30 isolated colonies per population using a pyoverdine-specific
207 emission assay [40]. Briefly, fluorescence of each culture was measured at 460nm
208 following excitation at 400nm, using a Biotek Synergy 2 Spectrophotometer. Optical
209 density (OD) was measured at 600nm, and the ratio RFU/OD was employed as a
210 quantitative measure of *per capita* pyoverdine production. Finally, evolved
211 populations were analysed for production of the toxin pyocyanin, which can promote
212 soluble ferrous iron [41]. Briefly, all evolved populations were plated on gentamicin-
213 supplemented agar to remove cheats. Wildtype cells (with gentamicin resistance)
214 were washed from plates using 6ml KB broth, and grown overnight in 30ml glass
215 tubes. After 24h, cells were centrifuged, and A_{691} was measured for each population,
216 standardised by A_{600} . Ancestral wildtype, cheat and uninoculated KB broth were
217 included in all of our assays as controls.

218

219 *Quantifying evolved population productivity*

220 To investigate whether any adaptation to cheats in treatment populations sacrificed
221 population productivity, the relative growth rate of each evolved population was
222 assessed by growing each evolved population for 24h in Fe-limited KB media. Final
223 densities were quantified by plating liquid cultures on KB agar and counting viable
224 colonies.

225

226 *Addition of exogenous pyocyanin*

227 We investigated whether pyocyanin could rescue the poor fitness of siderophore
228 cheats in an iron-limited environment. We tested the effect of 10 μ M, 30 μ M and
229 50 μ M pyocyanin on the growth of both PAO1 (cooperator) and siderophore negative
230 cheat PAO1 Δ pvdD Δ pchEF, relative to a pyocyanin-free control. 10⁷ CFU's ml⁻¹ of
231 cooperator or cheat was inoculated into 6ml iron-limited pyocyanin-supplemented KB
232 and grown for 24h. Final densities were assessed by plating on KB agar.

233

234 *Resequencing methods and bioinformatic analysis.*

235 The Wizard® Genomic DNA Purification kit (Promega) was used to isolated genomic
236 DNA from overnight cultures, according to manufacturer's instructions. The quality of
237 the isolated gDNA was assessed using Nanodrop (Thermo Scientific). Four smooth
238 and four novel morphotypes from end point cheat-adapted populations were selected
239 for sequencing. TruSeq PCR-free genomic libraries were prepared at the Centre for
240 Genomic Research, University of Liverpool and 2x 250bp paired-end reads generated
241 on an Illumina MiSeq platform. See S1 for further details on sequence data
242 preparation.

243

244 *Statistical analyses*

245 All data were analysed using R version 2.15.1 [42]. We determined population
246 Malthusian growth rate (m) as $\ln(\text{final density}/\text{start density})$ [43]. Relative fitness of
247 strain x compared with strain y ($W(x)$) was calculated in co-culture as $m(\text{strain}$
248 $x)/m(\text{strain } y)$, and in monoculture as $m(\text{strain } x)/\text{mean}(m(\text{strain } y))$. When $W(x) = 1$,
249 fitness of strain $x = \text{strain } y$. Following an F-test to compare variances, and a Shapiro-

250 Wilk normality test, we used Student's t -tests and Wilcoxon rank-sum tests to
251 compare m values in monoculture, or W values between treatments. To assess whether
252 ($W(x)$) was significantly different from 1, we used 1-sample t -tests or Wilcoxon
253 signed-rank tests.

254

255 1 and 2-sample t -tests were used to compare *per capita* total siderophore production
256 between evolved populations and between evolved populations and the ancestor
257 (using mean ancestral siderophore production as the alternative value in 1-sample
258 tests), and a Kolmogorov-Smirnov test for non-parametric data with unequal
259 variances was employed to compare the frequency of a novel morphotype in control
260 and treatment populations. A 1-sample t -test, and Wilcoxon signed-rank was used to
261 assess whether evolved pyoverdine production in control and treatment populations
262 differed significantly from that of the ancestor. To compare *per capita* pyoverdine
263 between evolved populations, we used a linear mixed effects revised (LMER) model,
264 assigning condition (treatment/control) as a fixed factor and population as a random
265 factor, controlling for the presence of 30 datapoints for each of 12 populations. To
266 determine fitness of evolved populations relative to ancestor in the presence/absence
267 of cheats, a LMER model was employed to account for non-independent datapoints (6
268 replicates per population), assigning 'population' as a random factor and both
269 condition (treatment/control) and cheats (present/absent) as fixed explanatory factors
270 (including interaction). A general linear model (GLM) was used to investigate
271 whether pyocyanin production is affected by evolution condition (control/treatment
272 lines). The relationship between the proportion of novel morphotypes and *per capita*
273 production of pyoverdine and pyocyanin was examined using separate generalised
274 linear models with a quasibinomial error structure. Finally, the effect of exogenous

275 pyocyanin on growth rate was calculated as the change in growth relative to the
276 control at each pyocyanin concentration using selection coefficient (r): $m(\text{strain } x) -$
277 $\text{mean}(m(\text{strain } y))$. Using a GLM, the effect of pyocyanin concentration (continuous
278 numeric variable) and strain identity (cooperator or cheat) on promoting growth was
279 investigated (including the interaction). To ensure the effect of adding 10 μ M
280 pyocyanin was accounted for, the control treatment relative selection coefficient was
281 included and standardized to zero.

282

283 **Results**

284 *Costs and benefits of siderophore production*

285 As with previous studies in iron-limited minimal media [30,44], monocultures of
286 cooperators exhibited a higher growth rate compared with cheat monocultures
287 (Wilcoxon rank-sum test: $W=34, p<0.05$), however this effect was reversed in 1:1 co-
288 culture, where cheats had a growth rate advantage over cooperators (1-sample t-test of
289 relative fitness against 1: $t_5=2.74, p<0.05$, figure A2). Thus, while siderophore
290 production carries a group-level fitness benefit, is individually costly in this context.

291

292 *Quantifying fitness against ancestor and productivity of evolved populations*

293 To determine adaptation to cheats, we competed evolved lines against the ancestor in
294 the presence and absence of 90% cheats: the same conditions as the selective
295 environments. Populations evolved with cheats had a higher fitness than populations
296 evolved in the absence of cheats, but only when cheats were present (LMER treatment
297 x cheat interaction; $X^2_{1,5}=24.04, p<0.0001$, figure 2).

298

299 Given that our experimental design also selected for high within-population yields, we
300 measured the mean growth rate of evolved populations as monocultures under the
301 selective (iron-limited) conditions, finding no difference in mean growth rate between
302 control and treatment lines (Student's t-test, $t_{10}=0.03$, $p=0.98$, figure A3). Finally, we
303 verified that the use of an ancestor possessing a *lacZ* genetic marker in this
304 experiment did not alter relative fitness: in direct 1:1 competition with non-*lacZ*
305 ancestor, $W(lacZ)$ did not differ from 1 (1-sample t-test (alt=1), $t_5=-1.57$, $p=0.18$).

306

307 *Public goods production following evolution*

308 After ~ 190 generations of growth, populations grown in the presence of cheats
309 exhibited reduced per capita total siderophore production compared with ancestor (1-
310 sample t-test (alt=0.7), $t_5=3.41$, $p<0.05$, figure 1A) and cheat-free control populations
311 (Student's t-test, $t_{10}=2.77$, $p<0.05$, figure 1A). Testing for pyoverdine specifically,
312 treatment populations showed decreased pyoverdine output compared with ancestor
313 (1-sided Wilcoxon signed-rank test, alternative = 7876.51, $V=4$, $p<0.0001$, figure 1B)
314 and control populations (LMER: $X^2_{1,3}=9.79$, $p<0.01$, figure 1B). Control populations
315 did not differ from ancestral total per capita siderophore production (1-sample t-test
316 (alt=0.7) $t_5=0.7$, $p=0.51$, figure 1A), but per capita pyoverdine output was reduced
317 over the course of the experiment (1-sample t-test, alternative = 7876.51, $t_{179}=18.63$,
318 $p<0.0001$, figure 1B).

319

320 *Novel morphotypes*

321 We recorded the appearance of a novel morphotype with a slightly raised surface and
322 reduced surface area in evolved populations (Figure A4, Table A1). After ~190
323 generations, not only was the frequency of this morphotype significantly higher in our

324 treatment than control populations (Kolmogorov- Smirnov test, $D=0.83$, $p<0.05$), it
325 went to fixation in 3 out of 6 treatment populations (Table A1). The proportion of
326 evolved novel morphotypes within a population was positively correlated with
327 pyocyanin production (GLM, $F_{1,10}=21.22$, $p<0.001$, Table A1), and negatively
328 associated with pyoverdine production (GLM, $F_{1,10}=35.64$, $p<0.001$, Table A1).
329 Notably, population level pyocyanin production was only elevated relative to control
330 when the proportion of novel morphotypes in a population reached fixation, and this
331 variation between populations meant that we did not detect significant differences in
332 total pyocyanin between populations (GLM, $F_{1,10}=3.03$, $p=0.11$, Table A1). We
333 confirmed that the novel morphotype showed elevated pyocyanin and reduced
334 pyoverdine production relative to ancestral-like colonies, by performing individual
335 assays (replicated thrice) on the eight colonies subsequently selected for sequencing
336 (see below) (pyoverdine: LMER, $X^2_{1,4}=3.94$, $p<0.05$; pyocyanin: LMER, $X^2_{1,4}=26.51$,
337 $p<0.0001$).

338

339 To identify the mutation(s) that might confer this wrinkly pyocyanin-overproducing
340 phenotype, the genomes of the ancestral, four smooth (isolated from treatment
341 populations T1, T6 and T3) and four novel morphotypes (isolated from treatment
342 populations T2, T4, T5 and T6) were sequenced and subjected to comparative
343 genomic analysis. We observed deletions of 38.33Kb (on average) in the novel
344 phenotypes compare to the smooth and ancestral strains (Fig A5, Table A2, A3).
345 Bioinformatic analysis revealed that the deleted genomic fragments contain 19 genes
346 common to all novel morphotypes, including *lasR* and *rsaL* genes encoding a
347 regulator and a repressor of quorum sensing (QS) regulated factors, respectively
348 (Table A3). These genes were not mutated in any sequenced smooth colonies. Among

349 the four smooth colonies, three in-frame deletions were observed in three different
350 colonies: in *fha1* (2/3) and *ftsY* (1/3) - neither of which are associated with iron-
351 acquisition.

352

353 *Addition of exogenous pyocyanin*

354 The addition of exogenous pyocyanin was beneficial for both siderophore-producing
355 and non-producing strains; however, the effect of increasing pyocyanin concentration
356 on growth rate was greatest for non-producing strains (GLM, strain identity x
357 pyocyanin concentration interaction, $F_{1, 44}=12.02$, $p=0.001$, figure 3).

358

359 **Discussion**

360 Here, we investigated whether populations of the bacterium *P. aeruginosa* under
361 selection for high productivity were capable of adapting to the presence of public
362 goods cheats, where public goods in this case are iron-scavenging siderophores. We
363 found that after ~190 generations, cheat-adapted populations manifested greater
364 fitness in the presence of cheats compared with control populations, while displaying
365 no apparent growth rate cost when grown in the absence of cheats. While evolved
366 populations had significantly reduced pyoverdine production relative to the ancestor
367 (adaptation to growth conditions), cheat-adapted populations further reduced their
368 production of pyoverdine compared with control populations. Novel morphotypes
369 appeared in 5/6 cheat-adapted populations, characterised by deletions in *lasR* and *rsaL*
370 genes. The morphotype showed elevated pyocyanin and reduced siderophore
371 production, and its presence resulted in population-level reductions in pyoverdine,
372 while fixation of the morphotype in 3/6 cheat-adapted populations resulted in
373 increased pyocyanin production. Taken together, these data suggest that one way

374 cooperators may have adapted at least in part to the presence of siderophore cheats is
375 by down-regulating siderophore production while up-regulating an alternative means
376 to obtain iron (pyocyanin).

377

378 Our work has some parallels with recent work by Kümmerli *et al* [29] whereby
379 coevolution between *P. aeruginosa* siderophore cooperators and cheats drove reduced
380 pyoverdine output by cooperators and blockage of the costly *pvdS* signalling pathway
381 by coevolving cheats. However, the evolution of reduced pyoverdine in this study and
382 that observed by Kummerli *et al* is likely to have been driven by different selection
383 pressures. Notably, Kummerli *et al* performed experimental coevolution by
384 transferring 1% of each culture to new media daily. This design facilitates local
385 competition and low relatedness, which reduces pyoverdine production *per se*,
386 because cheating is favoured [30]. Conversely, the metapopulation design established
387 in our study ensures that any reduction in cooperative output is a direct consequence
388 of adapting to resist the impact of cheats rather than selection for cheating. In line
389 with this, Harrison [28] found that coevolving *P. aeruginosa* cooperators and cheats
390 in metapopulations that impose selection for cooperation reduced pyoverdine
391 production. However, in this case consequences of lowered pyoverdine for cooperator
392 fitness were not determined, and the coevolutionary design made it difficult to
393 disentangle the effects of altered relatedness and cheating [45].

394

395 We have speculated that reductions in pyoverdine and elevated pyocyanin in the novel
396 morphotype may have contributed to the observed adaptation to siderophore cheats in
397 some populations. Reduced pyoverdine production will presumably mitigate some of
398 the fitness costs imposed by pyoverdine cheats [37]. The resulting reduction in iron

399 acquisition may be compensated for by up-regulation of pyocyanin, whose canonical
400 function is a toxin [46]. Pyocyanin is a potent reducing agent that converts insoluble
401 ferric (Fe^{3+}) to ferrous (Fe^{2+}) iron [41], which can diffuse into cells via cell-surface
402 porins (eliminating the requirement of a siderophore-specific receptor). Accordingly,
403 we found that the addition of exogenous pyocyanin had a stronger effect in enhancing
404 growth of siderophore-negative cheats compared with cooperators, suggesting it can
405 compensate for lack of siderophore production. Moreover, recent studies investigating
406 adaptation of *P. aeruginosa* to the antimicrobial gallium nitrate show that cells
407 become resistant by downregulating pyoverdine (which acts in this case as a gallium
408 transporter) and upregulating pyocyanin [47,48]. However, while populations with
409 high frequencies of novel morphotypes may have benefitted from this increase in
410 pyocyanin, the remaining populations are likely to have evolved alternative, unknown
411 strategies to cope with reduced pyoverdine production. One possibility is that prudent
412 regulation of cooperative traits can impede the spread of cheats, by only cooperating
413 when the costs of doing so are minimal. For example, the diffusible *P. aeruginosa*
414 carbon-rich rhamnolipid is expressed only when growth is limited by another nutrient
415 source [49]. However, in our experiment the costs of cooperating were consistently
416 high, based on our finding that cheats invaded cooperators when competed at 1:1.

417

418 The novel morphotype characterised by reduced pyoverdine and increased pyocyanin
419 production, carried deletions in *lasR* and *rsaL* genes. LasR and RsaL are two
420 transcriptional regulators that positively and negatively regulate the expression of QS
421 regulated virulence factors, respectively [50-52]. Pyoverdine production is under
422 positive control of the Las system and its inactivation has been reported to reduce the
423 production of this siderophore [53]. LasR also regulates pyocyanin production,

424 however the pyocyanin biosynthetic operon *phzA-G1* is under direct repression of
425 RsaL and it has been shown that cells that lack *rsaL* overexpress pyocyanin [54]. It
426 therefore seems likely that these deletions play a role in the observed phenotypic
427 changes in the novel morphotype, although we can't rule out that other gene deletions
428 in this novel morphotype may have contributed to changes in siderophore and
429 pyocyanin production, as well as adaptation more generally.

430

431 Our finding that that the growth rate of siderophore cheats in iron-limited media can
432 be rescued by the addition of exogenous pyocyanin suggests that like siderophores,
433 pyocyanin may also act as a public good. This is further supported by studies in
434 animal models demonstrating reduced growth and virulence of pyocyanin negative
435 mutants compared with wildtype [55,56] but that mutant growth is enhanced by the
436 presence of wildtype producers in mixed infections, or the addition of exogenous
437 pyocyanin [56]. Note that in this case, pyocyanin is probably not linked to iron
438 scavenging, as non-producers had intact siderophores, and pyocyanin has a range of
439 additional *in vivo* activities such as apoptosis of neutrophils that could enhance
440 growth. This then begs the question: why weren't pyocyanin overproducers in our
441 evolved cheat-adapted populations exploited by individuals making less pyocyanin?
442 The most likely explanation is that pyocyanin over-production imposes a small
443 metabolic cost (relative to siderophores), at least under these experimental conditions;
444 hence pyocyanin non-producers would have little, if any, fitness advantage.
445 However, our results do not rule out the possibility that pyocyanin producers could
446 ultimately be exploited by the evolution of pyocyanin cheats in this or other
447 environments.

448

449 One counterintuitive result was the loss of fitness through time in evolved
450 populations: competing ancestral against evolved cooperator populations in the
451 presence and absence of cheats demonstrated that evolved control populations were
452 consistently outcompeted by the ancestor, while evolved treatment populations
453 managed to negate this only in the presence of cheats. The inherent disadvantage of
454 evolved populations could not be attributed to differences in growth between
455 PAO1^R*lacZ* and PAO1^R, and was potentially a consequence of population
456 bottlenecks resulting from transfer of single clones, which may have resulted in the
457 fixation of deleterious mutations [57].

458

459 It is always debatable whether *in vitro* results are relevant to the real world. While
460 siderophore mutants are present in natural populations [58,59] and can have a
461 selective advantage when rare [15] it is unclear if a) they act as cheats in this context
462 and b) if selection has acted in ways that mitigate their exploitation, as observed here.
463 Pyocyanin over-producing genotypes are associated with exacerbated cystic fibrosis
464 infections [60] and while it can be speculated that these phenotypes represent an
465 alternative mechanism of iron-acquisition, these correlational data can of course be
466 open to different interpretations. Nonetheless, the evolutionary impact of altered
467 social interactions between microbes should be carefully considered in all cases,
468 particularly in light of the development of novel therapeutics aimed at disrupting
469 microbial social interactions [56, 69]. Given that pyocyanin directly harms host cells,
470 kills competitors, and results in more virulent infections [54, 64, 68], investigation
471 into whether pyocyanin contributes significantly as an iron-uptake mechanism in
472 natural populations is warranted.

473

474 **Data, code and materials**

475 The datasets supporting this article have been uploaded as part of the supplementary
476 material.

477

478 **Competing Interests**

479 The authors declare no conflict of interest

480

481 **Authors Contributions**

482 SOB carried out experimental work and statistical analysis, as well as designing the
483 study and drafting the manuscript. SP performed genome sequencing and SP and AL
484 interpreted genome sequences. MC and AB conceived the study, and AB also
485 coordinated the study and helped draft the manuscript. All authors gave final approval
486 for publication.

487

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491

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740 **Figure Captions**

741 **Figure 1:** Total siderophore **(A)** and pyoverdine **(B)** production by evolved control
742 populations (Ctrl.), treatment populations (Trt.; evolved in the presence of 90%
743 cheats) and the ancestral clonal PAO1 (Anc.). After ~190 generations, treatment
744 populations exhibited reduced per capita total siderophore production (1-sample t-test

745 (alt=0.70672), $t_5=3.4056$, $p < 0.05$) and pyoverdine production (1-sided Wilcoxon
746 signed-rank test, alternative = 7876.512, $V=4$, $p < 0.0001$), relative to the ancestor. For
747 **A**, data are means of 6 evolved populations for each treatment \pm SEM, and the single
748 population of ancestral PAO1. For **A**, data are means of pyoverdine production for 30
749 colonies for each evolved population (6 evolved populations each for control and
750 treatment condition), and the single ancestral PAO1.

751

752 **Figure 2:** Relative fitness of evolved populations in a 1:1 co-culture with ancestral
753 wildtype PAO1, in both the presence and absence of cheats, in iron-limited KB media.
754 Evolved populations were generally less fit than their ancestor, with the exception of
755 treatment populations when competed under the same conditions as which they had
756 evolved in (in the presence of 90% cheats). (LMER treatment x cheat interaction:
757 $X^2_{1,5}=24.044$, $p < 0.0001$). Data are means of 6 replicates per each of 12 evolved
758 populations \pm SEM.

759

760 **Figure 3:** Effect of the addition of exogenous pyocyanin to PAO1 (cooperator; circles
761 and dashed line) and PAO1 Δ pvdD Δ pchEF (cheat; triangles and solid line)
762 populations. Selection coefficient is calculated relative to a control cooperator or
763 cheat population to which no pyocyanin was added. The effect increasing pyocyanin
764 has on relative fitness (r) is greatest in cheat populations (GLM, strain identity x
765 pyocyanin concentration, $F_{1,44}=12.018$, $p=0.001$). Fitness (r) relative to control
766 population (no pyocyanin added) was calculated as $m(\text{strain } x) - \text{mean}(m(\text{strain } y))$.
767 Lines are plotted based on predictions from minimal GLM model. Data are means of
768 6 replicates per treatment \pm SEM.

769