



Mordue, J., O'Boyle, N., Gadegaard, N. and Roe, A. J. (2021) The force awakens: the dark side of mechanosensing in bacterial pathogens. *Cellular Signalling*, 78, 109867. (doi: [10.1016/j.cellsig.2020.109867](https://doi.org/10.1016/j.cellsig.2020.109867)).

This is the author's final accepted version.

There may be differences between this version and the published version. You are advised to consult the publisher's version if you wish to cite from it.

<http://eprints.gla.ac.uk/226598/>

Deposited on: 02 December 2020

Enlighten – Research publications by members of the University of Glasgow
<http://eprints.gla.ac.uk>

1 **The Force Awakens: the dark side of mechanosensing in bacterial pathogens**

2 Authors: James Mordue¹, Nicky O'Boyle¹, Nikolaj Gadegaard², Andrew J Roe^{1*}

3 ¹Institute of Infection, Immunity and Inflammation, University of Glasgow, Glasgow, G12 8TA, UK

4 ² School of Engineering, Rankine Building, University of Glasgow, Glasgow G12 8LT, UK

5 *Correspondence: Andrew.Roe@glasgow.ac.uk (AJR)

6 **Abstract**

7 For many bacteria, the ability to sense physical stimuli such as contact with a surface or a potential
8 host cell is vital for survival and proliferation. This ability, and subsequent attachment, confers a wide
9 range of benefits to bacteria and many species have evolved to take advantage of this. Despite the
10 impressive diversity of bacterial pathogens and their virulence factors, mechanosensory mechanisms
11 are often conserved. These include sensing impedance of flagellar rotation and resistance to type IV
12 pili retraction. There are additional mechanisms that rely on the use of specific membrane-bound
13 adhesins to sense either surface proximity or shear forces. This review aims to examine these
14 mechanosensors, and how they are used by pathogenic bacteria to sense physical features in their
15 environment. We will explore how these sensors generate and transmit signals which can trigger
16 modulation of virulence-associated gene expression in some of the most common bacterial pathogens:
17 *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Escherichia coli* and *Vibrio* species.

18

19 **Introduction**

20 Most bacteria live in communities that are associated with a surface, and attachment has a wide range
21 of benefits to the survival and spread of many species [1], [2]. It allows bacteria access to nutrients
22 which settle or adsorb on surfaces in higher concentrations than the surrounding environment,
23 allowing bacteria growth in low nutrient environments [3], [4]. This makes surface sensing and

24 attachment extremely important to both pathogenic and non-pathogenic bacteria. For pathogens
25 within a host organism, attachment provides resistance to removal by fluid flow, while close contact
26 to host cells ensures access to the host's resources and enables injection of virulence factors [5]–[7].
27 Adhesion to a surface helps protect against antibiotics by reducing the net negative charge on the
28 bacterial cells [8] and by enhancing the stability of the plasma membrane [9]. Attachment also allows
29 for localised increases in bacterial cell concentration and for specialization of cells and other
30 cooperative behaviours within that community [10].

31 Adhesion is the initial stage in the development of biofilms, bacterial communities suspended in an
32 extracellular matrix. This matrix is composed of a mixture of polysaccharides, proteins and
33 extracellular DNA to form a three-dimensional structure [11]. Biofilms are manufactured by bacteria
34 to improve their survival and proliferation by conferring a series of benefits such as improved
35 protection from mechanical removal (shear force of fluid flow or abrasion) and attack by chemical
36 (such as antibiotics) and biological agents (such as phage or predators). Bacterial attachment can
37 however be seriously detrimental to human interests, health in the case of pathogens or industrial
38 output in the case of biofouling organisms attached to industrial surfaces [12], [13].

39 Bacteria can respond to a wide range of environmental cues such as nutritional gradients [14],
40 osmolarity [15], [16] and the presence of host molecules [17]. They feed this information into complex
41 regulatory pathways that control gene expression. In addition to chemical signals, bacteria can
42 respond to physical cues in their environment. The ability to perceive when they are in contact with a
43 surface is vital for the transition from a free-living planktonic lifestyle to a sedentary one comprising
44 adhesion to a surface. This is an even more important consideration when bacteria need to survive
45 within a host. Accordingly, the numerous environmental niches present within a host often require
46 pathogens to use special tools to survive and prosper. These tools, or virulence factors, are highly
47 diverse in their forms and functions.

48 Following the sensing of surface attachment, or indeed appropriate niche-specific metabolic cues,
49 alteration in protein expression is facilitated through modulation of gene expression by transcription
50 factors (TFs) [18]. Bacteria encode hundreds of diverse TFs to cope with the immense diversity of
51 environmental signals that require modulation of gene expression [19]. These predominantly take the
52 form of either two-component sensor kinase regulators that operate phospho-relay signal
53 transduction pathways [20], or cytosolic TFs such as LysR and AraC type transcriptional regulators [20],
54 [21]. Typically, a specific helix turn helix motif within the DNA-binding domain of TFs facilitate direct
55 interaction with a consensus sequence upstream of the coding region of the target genes [21].
56 Through modulation of DNA topology and interaction with RNA polymerase and other TFs, expression
57 levels of the target genes can be manipulated [22]. In the case of cytosolic TFs, further selectivity and
58 specificity is conferred by the binding of small molecules that are often niche-specific metabolites and
59 serve as cofactors for TF activity [23].

60 It is important to understand the interaction between bacterial surface sensing systems and the
61 regulation of virulence factors in order to develop a complete picture of pathogen behaviour within
62 the host. Improved understanding of this has the potential to improve treatments of numerous
63 infections and ultimately improve patient outcomes. Many of the mechanisms by which bacteria
64 attach to surfaces, both living and inanimate, are relatively well studied [24]–[26]. Furthermore, the
65 study of how proximity to surfaces is sensed and interpreted via signal transduction to allow for the
66 appropriate expression of virulence factors is a rapidly evolving area with considerable recent
67 advancements. In this review, we will discuss the colonisation factors mediating these attachment
68 events, the signal transduction pathways that allow for interpretation of the surface signal, the
69 regulatory proteins that mediate a change in virulence factor expression and the specific virulence
70 factors reported to be regulated by these processes in specific pathogenic bacteria.

71

72 **Non-pathogenic mechanosensing**

73 While this review focuses on the mechanosory mechanisms of pathogenic bacteria it is important to
74 highlight that these and other mechanisms are not limited to pathogens. One of the best studied
75 examples is *Caulibacter crescentus* which possesses a tight adherence (Tad) pilus that shares a number
76 of common features to the type IV pilus. Ellison et al. observed that the Tad pilus appeared to perform
77 a similar mechanosensory function to the type IV pilus, with the Tad pilus undergoing cyclical extension
78 and retraction [27]. Upon contact with a surface the Tad pilus attaches resulting in resistance to pilus
79 retraction. After attachment extension and retraction cycles stopped and synthesis of the holdfast
80 adhesin (an important factor in the attachment process) increased. It is thought that retraction of the
81 Tad pilus is used as a mechanosensory mechanism to initiate changes in attachment related gene
82 expression allowing *C. crescentus* to react dynamically to its physical environment [27]. This and other
83 examples of mechanosensing in non pathogens have recently been covered, hence the focus of this
84 review are specific mechanisms used by pathogens [28].

85

86 **Colonisation factors with roles in surface sensing**

87 **Flagella**

88 The sensing of physical cues by mechanical sensory systems forms an important part of environmental
89 recognition. These mechanosensors allow bacteria to respond to shear forces exerted by flow [29],
90 [30], gravity [31] and the physical interaction with surfaces and other objects in their environment
91 [32]. For pathogenic bacteria, the sensing of physical interactions with surfaces is vital for their survival
92 and success within the host. Flagella are whip-like organelles, ranging from 1-9 μm in length [33],
93 anchored to the bacterial cell surface and used primarily for cell motility [34]. Despite their central
94 role in motility, flagella of many bacterial species have been shown to play roles in surface sensing,
95 adhesion and biofilm formation [32], [34]–[36]. Bacterial surface sensing can be mediated by the
96 interference in the rotation of the bacterial flagella by a proximal surface [37]. This interference is
97 often termed flagella impedance. Flagella have been observed to function as mechanosensors capable

98 of detecting surface contact in several organisms including *Vibrio parahaemolyticus* [38], *P.*
99 *aeruginosa* [39] and *Bacillus subtilis* [40].

100 **Type IV pili**

101 The use of motility organelles as mechanosensors does not appear to be unique to flagella. Type IV
102 pili are long (1-4 μm), thin (50–80 Å) [41], membrane-bound filamentous structures utilised by a wide
103 range of organisms for a variety of functional purposes including roles in motility and attachment [42]–
104 [44]. They are extended via polymerisation by an assembly ATPase, can attach to a surface and retract
105 via depolymerisation powered by a retraction ATPase [45]. This gives rise to what is known as
106 twitching motility [46] and allows bacteria that employ it to spread swiftly across surfaces [47]–[49].
107 Twitching motility has been observed in several bacterial species and is particularly well studied in *P.*
108 *aeruginosa* [50]. While acting as virulence factors in their own right, like flagella, type IV pili play an
109 important role as mechanosensors.

110

111 **Molecular mechanisms of surface sensing and virulence regulation in bacterial pathogens**

112 ***Pseudomonas aeruginosa***

113 *P. aeruginosa* is an opportunistic pathogen causing both chronic and acute infections in a wide range
114 of hosts and at many different sites within the body. In humans, acute disease caused by *P. aeruginosa*
115 is often characterised by cytotoxicity, invasion of host tissue and can progress to systemic infection
116 and sepsis. This pattern of pathogenesis is the results from expression of numerous proteases, toxins
117 and type III secretion system (a needle-like complex that allows injection of specific effectors into a
118 host cell [51], [52]) activity. This can be manifested by infection of burn injuries on the skin and
119 ventilator-associated pneumonia. Chronic infection on the other hand is noncytotoxic, far less invasive
120 and does not typically lead to systemic infection. This pattern of pathogenesis is commonly seen in
121 patients with cystic fibrosis where *P. aeruginosa* forms a biofilm that cannot be cleared and results in

122 damaging long-term inflammation in the lungs [53]–[56]. The diversity of these infections is
123 orchestrated by accurate sensing of the environment and the production of an appropriate virulence
124 response.

125 The polar flagellum of *P. aeruginosa* has been shown to play a central role in the attachment process
126 as a part of a mechanosensory system. *P. aeruginosa* cells have been observed to initially attach to a
127 surface, often only temporarily, with many cells quickly detaching. However, those that remain
128 attached, bind irreversibly to the surface rapidly halting the rotation of their polar flagella [57], [58].
129 Impedance of rotation occurs via the interaction of the signal recognition particle (SRP)-type
130 guanosine triphosphatase (GTPase) FlhF with FliG (a component of the flagellar motor machinery) and
131 FimV, (a peptidoglycan binding protein which forms part of the structural complex of the *P. aeruginosa*
132 type IV pilus and has been shown to increase the production of cyclic adenosine monophosphate
133 [cAMP]) [39]. This interaction triggers an increase in intracellular cAMP which activates further
134 downstream regulatory events, altering flagellar rotation [39]. FlhF is a known regulator of flagellar
135 positioning, is conserved between other bacterial species with polar flagella [59] and, when deleted,
136 results in flagella being positioned in areas other than the cell pole [60]. Schniederberend et al. [39]
137 found that the flagella of *P. aeruginosa* $\Delta flhf$ mutants continued to spin even after flagellar attachment
138 but could have the wild-type phenotype restored by 23 independent suppressor mutations which
139 were mapped to the cAMP-dependent transcriptional regulator Vfr.

140 Vfr has been shown to control the expression of over 200 *P. aeruginosa* virulence genes [61], [62].
141 These Vfr regulated genes include surface localised virulence factors such as the type II and type III
142 secretion systems [61] (T2SS and T3SS), the former of which is used by *P. aeruginosa* to transport
143 virulence molecules such as proteases, the latter can inject specific effectors that modulate their
144 eukaryotic hosts to promote bacterial survival and proliferation [51], [52]. Additionally, Vfr positively
145 regulates the production of proteases, toxins and the type IV pilus, a motility organelle and major
146 surface adhesin [61], [63]–[65], while downregulating flagellar genes [66]. These virulence factors are

147 primarily associated with acute *P. aeruginosa* infection phenotypes as opposed to the chronic
148 infection phenotype commonly seen in the lungs of cystic fibrosis (CF) patients [67].

149 In addition to the flagella, *P. aeruginosa* can sense contact with surfaces using their type IV pili [29],
150 [68], [69]. Persat et al. [69] and Inclan et al. [70] demonstrated that once type IV pili have attached, a
151 signal is generated when the organelle attempts to retract. This resistance to retraction triggers the
152 Pil-Chp chemosensory system, leading to increased production of cAMP which in turn activates the
153 expression of virulence-related genes. This signal transduction happens via an accessory protein FimL,
154 which is part of the Pil-Chp system, interacting with FimV. As mentioned earlier FimV is a type IV
155 structural protein shown to increase the production of cAMP. It is thought that FimL, along with PilG,
156 localises at the cell poles via FimV. This allows PilG to be phosphorylated, activating the Pil-Chp system
157 which regulates the membrane-bound adenylate cyclase CyaB [71], [72]. CyaB is a major source of
158 cAMP which, similar to the mechanosensing pathway activated by the flagella, binds to the Vfr
159 virulence regulator and increases expression of proteins associated with acute virulence [61]. The
160 surface sensing signal generated by the type IV pili in *P. aeruginosa* is relatively short-lived but results
161 in further promotion of type IV pilus activity, giving rise to a positive feedback loop which promotes a
162 stronger signal for activation of virulence and biofilm pathways [69]. Phylogenetic comparison
163 between *P. aeruginosa* and other gamma-proteobacteria show that the components of this system
164 (FimL and FimV) are conserved in species that encode type IV pili and a Chp-like sensory system,
165 suggesting that this mechanosensory mechanism might be a common approach utilised in other
166 organisms of that group like *Acinetobacter baumannii*, *Vibrio cholerae* and *Vibrio vulnificus* [70].

167 In addition to flagellar impedance and interference with type IV pili retraction, *P. aeruginosa* is also
168 thought to possess a third surface sensing mechanism which acts upon contact with a host cell surface.
169 This system is thought to utilise the product of the *pilY1* gene, which encodes a putative
170 mechanosensory protein and adhesin [73] that is a stimulator of virulence and biofilm formation in
171 response to surface attachment. PilY1 is normally expressed on the cell surface and upregulated

172 during surface contact and attachment [74]. Siryporn et al. [74] found that $\Delta pilY1$ mutants and
173 mutants in genes encoding minor pilin proteins PilW and PilX showed poor virulence phenotypes in a
174 eukaryotic amoeba infection model (*Dictyostelium discoideum*). This effect was shown to be
175 independent of the loss of the type IV pilus as mutants in genes encoding other pilin proteins, such as
176 $\Delta pilB$ and $\Delta pilC$, which failed to produce a functional type IV pilus filament still retained their virulence
177 phenotypes. Virulence modulation through PilY1, PilW and PilX took place despite a weakened
178 attachment phenotype in mutants that lacked the ability to produce type IV pili and appears to
179 operate separately to the other functions of the pilus filament. The Pil-Chp pathway also involves the
180 physical interaction of PilJ and FimS in response to surface-associated signals. FimS acts together with
181 AlgR as a two-component system and is a transmembrane sensor kinase [75]. The FimS-AlgR system
182 (its own expression promoted by cAMP-Vfr) upregulates *pilY1* gene expression. PilY1 along with the
183 PilVWX minor pilins localize at the inner cell membrane and act via FimS-AlgR, PilJ and Vfr to
184 autoregulate their expression [68]. PilY1 contains a mechanosensing Von Willebrand factor A domain
185 similar to those produced by human endothelial cells to facilitate platelet aggregation [76]. This
186 domain is stretched when exposed to shear force [77] and mutation can result in constitutive
187 activation of *P. aeruginosa* virulence without surface attachment [74]. It is thought that PilY1 signals
188 through the type IV pilus PilMNOP alignment complex and the diguanylate cyclase SadC, both localised
189 at the inner membrane [68], [78]. This activates cyclic dimeric GMP (c-di-GMP) production and in
190 addition to the aforementioned virulence against amoeba has been shown to influence swarming
191 motility and early-stage biofilm formation [79]. In *P. aeruginosa* this surface sensing mechanism is
192 important for attachment, colonisation and appropriate triggering of virulence in several host
193 organisms, ranging from mammalian models to single-celled amoebae [80], [81].

194 The chemotaxis-like Wsp system has also been implicated in surface sensing. Signals are generated by
195 growth on a surface and thought to be recognized by the membrane bound receptor WspA. While the
196 exact nature of the signal remains unknown, it is believed to be the result of physical changes to the
197 periplasmic environment, caused by either the mechanical strain of surface contact or the

198 physiological changes that accompany the transition to a biofilm state. This signal is transitted via the
199 other components of the Wsp system (WspBCDEF), present in the cell cytoplasm, resulting in
200 phosphorylation of WspR. Phosphorlyated WspR then synthesises c-di-GMP, activating biofilm
201 formation, virulence gene expression and supressing motility [82].

202 Surface contact-induced virulence activation has been further explored by assaying virulence against
203 *D. discoideum* following attachment of bacteria to a variety of surfaces of varying composition,
204 including plastics, glass, polyacrylamide and agar [74]. It was found that the activation of virulence
205 was similar on all surfaces and therefore appeared to require the physically rigid surface rather than
206 any specific chemical surface composition. Siryaporn et al. [74] hypothesize that non-specific virulence
207 activation, could allow *P. aeruginosa* to infect a wide range of host species despite differences in their
208 individual surface receptors and tissue chemistries. Similar results were observed in mouse
209 macrophages to those seen in *D. discoideum*, with surface-attached *P. aeruginosa* shown to be more
210 virulent than planktonic bacteria as measured host cells lysis. Siryaporn et al. [74] also found that
211 when bacteria were allowed to attach to the surface of the plant species *Epipremnum aureum* and
212 grown in the presence of *D. discoideum* it resulted in secretion of virulence factors toxic to *D.*
213 *discoideum*, further suggesting activation of virulence in response to non-specific surface attachment.

214 It has been proposed that regulation of surface sensing is integrated into other regulatory networks
215 such as quorum sensing. Siryaporn et al. [74] grew bacteria to different growth phases, allowed them
216 to attach to surfaces, exposed them to *D. discoideum* and measured host killing. Virulence was
217 drastically increased between mid and late exponential phase. This suggested that increased cell
218 density could be activating quorum sensing and in turn affecting virulence factor expression. Quorum
219 sensing in *P. aeruginosa* is primarily regulated by the transcriptional activator LasR [83]. Siryaporn et
220 al. [74] observed that *lasR* mutants showed a disrupted virulence phenotype. However, neither high-
221 density planktonic *P. aeruginosa* cells nor over-expression of LasR quorum sensing in planktonic
222 bacteria resulted in lysis of eukaryotic cells. From this the authors conclude that quorum sensing alone

223 is not sufficient for optimum virulence and that mechanosensing is also of crucial importance. As such,
224 this indicates that PLY1 mechanosensing and LasR dependent quorum sensing act in concert to ensure
225 appropriate virulence regulation in *P. aeruginosa*. This non-specific mechanosensing behaviour is
226 believed to allow *P. aeruginosa* to infect a broad range of host species while maintaining carefully
227 regulated virulence mechanisms.

228

229 ***Proteus mirabilis***

230 *Proteus mirabilis* is a pathogen associated with infections of the urinary tract. On contact with a
231 surface *P. mirabilis* can undergo a phenotypic change from small swimmer cells, adapted to life in
232 liquid, into longer swarmer cells expressing high numbers of flagella that promote persistence within
233 the host [84]–[86]. This differentiation is a metabolically costly process and involves the expression of
234 50 genes, including several known to encode virulence factors which improve *P. mirabilis* survival and
235 mediate damage to the host [87].

236 It has been shown that, like *P. aeruginosa*, *P. mirabilis* uses flagellar impedance as a signal of surface
237 contact [88]. Inhibition of the rotation of the flagellar motor can result from several different physical
238 interactions. These include contact with solid surfaces, high viscosity liquids and the binding of
239 flagellar components by specific antibodies [89]. Belas et al. [89] found that mutations in many
240 flagellar genes resulted in *P. mirabilis* losing the ability to switch to a swarming phenotype. Surprisingly,
241 it was also found that mutation of genes that encode for the flagellar basal structure (*fliF*, *fliG* and *fliL*)
242 resulted in differentiation into swarmer-like cells in non-inducing liquid media and hyper-elongated
243 swarmer cells when grown on solid agar. The constitutive activation of this swarmer differentiation
244 pathway via specific flagellar components further reinforces the role of the flagella as a
245 mechanosensory organelle capable of detecting proximity to a surface [90]. Activation of the flagellar
246 sensory pathway via these mutations was shown to up-regulate the expression of *zapA* which encodes
247 a metalloprotease, an enzyme that can degrade antibacterial peptides, such as LL-37 and β -defensin,

248 that are used by the immune system to help fight bacterial infection [87], [91]. Sensory pathway
249 activation was also shown to up-regulate the expression of *hpmB* [89], the first gene in the *hpmBA*
250 operon. This operon also encodes the HpmA hemolysin which is a major cytotoxin used by many
251 clinical *P. mirabilis* strains to cause tissue damage and facilitate cellular invasion by the bacteria [87].
252 Mechanosensing of surfaces via the flagella allows *P. mirabilis* to carefully regulate the differentiation
253 process from swimmer to swarmer cells and so to more efficiently regulate the production of virulence
254 factors needed for colonisation and persistence within its host.

255

256 ***Escherichia coli***

257 *Escherichia coli* are an extremely diverse species of commensal and pathogenic bacteria found in the
258 GI tract of many organisms. Many *E. coli* strains are not harmful to their hosts, but certain strains can
259 cause infections at various sites in the body including infections of the urinary and GI tract [92]. In
260 addition to using numerous chemical sensory systems, *E. coli* has also been shown to regulate its
261 virulence through the use of mechanosensors [30].

262 *Enterohemorrhagic E. coli* (EHEC) strain O157:H7 is a problematic pathogen that causes haemorrhagic
263 colitis, and in more severe cases kidney damage in the form of haemolytic uremic syndrome (HUS).
264 The development of HUS is linked with high morbidity and mortality [93]. EHEC infections are typically
265 acquired by ingestion of foods contaminated by faecal material. EHEC uses a T3SS, several adhesins
266 and Shiga toxins as virulence factors to mediate disease [94]–[96]. The T3SS is encoded on a
267 horizontally acquired pathogenicity island, designated as the locus of enterocyte effacement (LEE) and
268 consists of 4 polycistronic operons (LEE1-5), activated by the first of these (LEE1). LEE1 contains a
269 critically important activator of the LEE, known as Ler, or LEE-encoded regulator [97]. The T3SS allows
270 EHEC to inject effector proteins into the host cells that line the large intestine, remodelling the actin
271 cytoskeleton to form pedestals on which the bacteria adhere tightly. These pedestals are known as
272 attaching and effacing (A/E) lesions, are highly characteristic of EHEC infection and are very effective

273 at promoting their persistence in the intestinal environment [98], [99]. Expression of the LEE in EHEC
274 is controlled by both chemical signals and physical forces acting on mechanosensory apparatus. The
275 LEE has been shown to be induced by several environmental cues including temperature shifts as the
276 bacteria travels through the gastrointestinal (GI) tract, neutral pH after exit from the stomach, reduced
277 oxygen concentrations, quorum sensing molecules, bicarbonate, glucose and hormone signals from
278 the host [100]–[104].

279 Alsharif et al. [30] showed that the LEE is only weakly induced by chemical environmental signals alone.
280 Alsharif et al. [30] infected HeLa epithelial cells with EHEC and monitored LEE1 promoter activity using
281 fluorescence microscopy and GFP producing reporter strains. Bacteria that attached to host cells
282 displayed strong activation of *ler* and formation of the characteristic A/E lesions. However, bacterial
283 cells that attached to glass rather than the host cell surface showed comparatively weak LEE activation
284 even in Dulbecco's Modified Eagle Medium (DMEM) which has been previously shown to be an
285 activator of *Ler* [105]. *Ler* is activated by GrlA (itself encoded on the LEE pathogenicity island) and in
286 Δ *grlA* strains LEE1 was not strongly induced on host-attached nor unattached bacteria and significantly
287 reduced formation of A/E lesions was observed. A recent paper by Sirisaengtaksin et al. [106] has
288 shown that GrlA is also required to transition from the inner membrane of planktonic cells to the
289 cytoplasm to efficiently activate virulence genes. Bacteria expressing GrlA-GFP fusion proteins were
290 adhered to polylysine coated microfluidic channels before applying fluid shear. GrlA is a membrane-
291 bound transcription factor under normal conditions but when shear forces are encountered by EHEC,
292 GrlA is released into the cytoplasm. Here it binds and activates the LEE1 promoter triggering the
293 expression of the LEE operon [106] and hence optimal T3SS activity.

294 These studies illustrate how *E. coli* senses changes in physical force and alters the expression of
295 virulence factors in response (LEE operon genes). Despite the specific attachment factor responsible
296 for binding to the polylysine coated substrate not being reported by Sirisaengtaksin et al. [106], the

297 flagellum of pathogenic *E. coli* have been shown to play a role in adhesion [107] and more recently in
298 mechanosensing [108].

299 Laganenka et al. [108] show that the flagella of various pathogenic *E. coli* act as mechanosensors
300 during infection, aiding in the regulation of motility to improve survival within the host. Laganenka et
301 al. [108] compared motility of a variety of pathogenic and commensal *E. coli* strains by soft agar
302 motility assays and single-bacterium movement tracking. Increased motility was observed in
303 pathogenic strains when grown in low percentage agar plates compared to liquid media. This was not
304 the case in commensal strains, which showed similar motility in both media forms. To examine the
305 underlying regulatory mechanism, changes in flagellar gene expression were monitored using GFP
306 fluorescence reporters. This revealed that in pathogenic strains *fliA* (encoding the sigma factor
307 controlling flagellar genes) and *fliC* (encoding flagellin, the major flagellar structural protein) [109]
308 were highly downregulated in liquid culture [108].

309 Laganenka et al. [108] hypothesize that increased flagellar impedance due to the porous structure of
310 the low percentage agar compared to liquid media results in an increased physical load on the flagellar
311 motor. *E. coli* flagella have been shown to respond to flagellar motor load by the recruitment of
312 additional stators (the force generation units used to drive motor motion) [110]. Knockout mutants of
313 the *fliC* and *motA* genes, which encode key components of the flagellar filament and the motor-stator
314 complex respectively, were constructed. These mutants had either lower physical loads on the motor
315 ($\Delta fliC$) or non-functional motors ($\Delta motA$). Both modifications resulted in pathogenic strains that were
316 unable to activate motility in either liquid or agar media. As previously discussed in this review,
317 impedance of the flagella can also take place due to attachment or contact with a surface [46], [111].
318 Laganenka et al. [108] studied the effects of increasing flagellar load by forced surface contact during
319 centrifugation and by growth on semi-solid agar, with both conditions resulting in increased
320 expression of *fliC*.

321 These observations indicate that upregulation of flagellar genes and the associated motility phenotype
322 is important in certain pathogenic but not commensal *E. coli* strains and that this is mediated by
323 increased physical loads on the flagellar motor. During infection, flagella act as an antigen that the
324 immune system can quickly recognise and mount a response to [112]. Laganenka et al. [108] therefore
325 also hypothesize that flagellar mechanosensing aids in successful host colonisation by increasing
326 expression of flagella in the early stages of infection when motility is useful in promoting contact with
327 the epithelial cells. The authors expect decreasing flagella expression in later infection stages, possibly
328 via quorum sensing, to reduce the hosts immune response to the flagella [108]. Mechanosensors such
329 as flagella and their associated signalling systems allow for careful regulation of virulence,
330 incorporating information from both chemical and physical cues. This allows pathogenic *E. coli* such
331 as EHEC to produce the appropriate response to a highly dynamic and hostile host environment,
332 promoting their survival and persistence.

333

334 ***Vibrio cholerae***

335 The Vibrionaceae represent a diverse family of marine bacteria that can exist in a free-living planktonic
336 state in the water column and also in a surface-attached state in shellfish, copepods and
337 phytoplankton (natural hosts) or indeed within human hosts where they are opportunistic pathogens
338 [113]. As such, the sensing of surface attachment is of critical importance in determining appropriate
339 changes in gene expression. In planktonic *Vibrio* cells, swimmer cell morphology predominates, with
340 motility being driven by a single polar flagellum that is powered by the sodium motive force (SMF)
341 [114]–[116].

342 Inhibition of flagellar rotation through surface contact is thought to disrupt ion flux through the
343 flagellar motor, leading to a transient membrane hyperpolarisation [117]. In *Vibrio cholerae*, deletion
344 of the flagellar motor and chemical disruption of the SMF prevent this hyperpolarisation, thereby
345 blocking the ability of *V. cholerae* to form robust monolayers [117]. Importantly, it has been shown

346 that *V. cholerae* mutants with defective motility display enhanced expression of ToxT-regulated
347 virulence factors including cholera toxin, cell-associated haemolysin and the toxin co-regulated pilus
348 [118]. Chemical inhibition and deletion of the NADH ubiquinone oxidoreductase Nqr, which functions
349 as a sodium extruding pump, were shown to hyperactivate *V. cholerae* ToxT [119]. Surface-attached
350 *V. cholerae* produces biofilms encased in exopolysaccharide (EPS) matrix, the production of which is
351 facilitated by two *vps* (*Vibrio* polysaccharide) gene clusters [120]. *V. cholerae* mutants lacking the
352 major flagellin FlaA display constitutive production of EPS, through loss of the ability to sense surface
353 contact, a phenotype which is mediated through phosphorylation of the biofilm master regulator VpsR
354 [121]. Deletion of motor components MotB and MotY in the $\Delta flaA$ background restored wild type
355 levels of EPS production indicating that both a functional flagellum and the motor-produced SMF are
356 required for fine control of EPS production. The authors observed that the non-flagellated, EPS
357 overproducing $\Delta flaA$ mutant produced reduced amounts of cholera toxin and toxin co-regulated pilus
358 and was defective for colonisation in a mouse model, highlighting the importance of surface sensing
359 for optimal virulence [121]. Regulation of the switch from swim to stick, with the aforementioned
360 activation of virulence, is also subject to control via the nucleotide second messengers c-di-GMP and
361 guanosine pentaphosphate ((p)ppGpp). C-di-GMP functions by synergistically activating VpsT an
362 upstream activator of VpsR [122] and also manipulating the conformation of the VpsR/ σ 70-RNAP
363 complex at bound promoters [123]. All three (p)ppGpp synthases possessed by *V. cholerae*, RelA, SpoT
364 and RelV were required for *vpsR* transcription, while only RelV was required for transcription of *vpsT*
365 demonstrating that control of biofilm/attachment and virulence genes is also responsive to nutritional
366 status through stringent response control [124].

367

368 ***Vibrio parahaemolyticus***

369 In the closely related pathogen *Vibrio parahaemolyticus*, swimmer cells behave similarly to those of *V.*
370 *cholerae* with a single SMF driven polar flagellum propelling the bacterium through liquid media [115].

371 Growth on solid surfaces however induces a marked change in cellular physiology with the formation
372 of filamentous, peritrichously flagellated cells [114]. Physical, chemical and genetic disruptions in polar
373 flagellum driven motility lead to activation of the peritrichous lateral flagella, encoded by the *laf* genes
374 [125]. In contrast to the polar flagellum, *laf* flagella are driven by the proton motive force [115].

375 Second messenger driven signalling has also been implicated in regulating the switch from planktonic
376 to attached lifestyles in *V. parahaemolyticus*. For example, ScrC possesses both diguanylate cyclase
377 and phosphodiesterase activity, with phosphodiesterase activity predominating in surface attached
378 cells [126]. Two proximally encoded genes (*scrAB*) were found to be capable of modulating the
379 function of ScrC, enabling reduction in the intracellular pool of c-di-GMP and facilitating the switch
380 between swarming motility (*laf* expression) and biofilm associated EPS production via the *cpsA-J* gene
381 cluster [126]. A screen for ScrABC regulated genes identified that in addition to the *laf* and previously
382 identified *cps* genes, a regulator encoding gene *cpsQ* was affected [127]. It was found that *cpsQ*
383 activated *cpsA-J* in a c-di-GMP-dependent manner. Lateral flagella and virulence factors including
384 T3SS1 and the *N*-acetyl glucosamine binding protein GbpA were found to be oppositely regulated to
385 *cpsA-J* indicating activation by ScrABC [127].

386 **Concluding remarks**

387 The investigation of mechanosensing is an exciting and developing field of inquiry that has great
388 potential to improve our understanding of pathogenic bacterial behaviour within the host. In this
389 review, we have discussed the main mechanisms bacteria use to sense mechanical stimuli. These
390 include flagellar impedance, resistance to type IV pili retraction and specific surface-bound adhesins.
391 These sensory mechanisms are known to feed into a variety of signal transduction pathways, often
392 acting by varying the levels of intracellular second messengers such as cAMP in *P. aeruginosa* and c-
393 di-GMP in *P. aeruginosa* and *Vibrio* species. Signals carried through these and other mechanosensing
394 linked pathways act on a wide range of different virulence-associated genes. These include genes
395 encoding additional attachment factors, toxins, secretory systems and motility organelles. These allow

396 the bacteria to spread rapidly across surfaces, invade host cells, and inject effector molecules and
397 release toxins which improve the success of pathogenic bacteria.

398 The prospect of future study in this field is exciting and there are many areas we look forward to seeing
399 developed further. These include a more detailed understanding of the conformational changes in
400 flagellar components as they are exposed to physical loads and how these allow for signal generation,
401 a more complete understanding of how mechanosensing is incorporated with other sensory
402 information such as sensing of host molecules and nutrients to fit into the wider picture of bacterial
403 virulence modulation, further exploration of other adhesins which may play similar roles to PilY1 as
404 mechanosensors and an expansion of the range of organisms whose mechanosensory systems are
405 studied to learn more about how well-conserved mechanisms are across different bacterial strains
406 and species.

407 Accurate sensing of environmental conditions is vital to allowing both pathogenic and non-pathogenic
408 bacteria to produce an appropriate behavioural response to their surroundings. Not only is this
409 important to bacterial survival but improved scientific understanding of this area could lead to new
410 treatments and therapies. A more complete picture of how mechanosensory systems in pathogens
411 activate virulence gene expression could allow for the development of new anti-virulence
412 interventions which target these systems, disrupting pathogenesis at the outset and improving patient
413 outcomes.

414 **Acknowledgements.** JM was supported by an Engineering and Physical Sciences Research Council
415 (EPSRC) Doctoral Training Programme ref: EP/N509668/1.

416

417 **Figure 1: Contact dependent sensing in *Pseudomonas aeruginosa*.** 1a) Contact with, and binding to,
418 a surface triggers the halting of flagellar rotation via interaction between components of the flagellar
419 machinery and FimV. 1b) Contact with a surface allows type IV pili to attach, causing resistance to
420 rhythmic pili retraction. This activates the Chp chemosensory system, triggering an interaction with
421 FimV. 2) FimV causes an increase in production of cAMP, increasing its intracellular concentration. 3)
422 cAMP binds to the Vfr virulence regulator which regulates the activity of over 200 virulence genes. 4a)
423 Genes positively regulated by Vfr include several proteases, toxins and surface localised virulence
424 factors such as the type II and III secretion systems. 4b) The type IV pilus itself is also positively
425 regulated by Vfr and so gives rise to a positive feedback loop of increased surface detection signal and
426 virulence expression. 5) Vfr promotes expression of FimS-AlgR system. 6) AlgR upregulates expression
427 of PilY1, which in turn feeds back into FimS-AlgR, PilJ and Vfr to autoregulate its expression. 7a) PilY1
428 signals through SadC to increase c-di-GMP production. 7b) Surface growth signals are recognised by
429 WspA and transmitted via the other components of the Wsp system (WspBCDEF) resulting in
430 phosphorylation of WspR. Phosphorylated WspR then synthesises c-di-GMP. 8) C-di-GMP activates
431 biofilm formation, suppresses cell motility and triggers virulence activation.

432 **Figure 2: Contact dependent sensing in *Proteus mirabilis*.** 1) Impedance of flagellar rotation signals
433 surface contact. 2) This signal triggers the expression of 50 genes, resulting in the differentiation of
434 small swimmer cells into elongated swarmer cells. These swarmer cells have increased virulence and
435 numbers of flagella, improving their survival on a host surface. 3) ZapA is upregulated, producing a
436 metalloprotease that is able to degrade antibacterial peptides utilised by the immune system of the
437 host organism. 4) HpmB, the first gene in the HpmBA operon, is upregulated. This triggers the
438 production of haemolysin, a major virulence factor responsible for aiding cell invasion and tissue
439 damage of host cells.

440 **Figure 3: Contact dependent sensing in *Escherichia coli*.** 1) Shear forces result in GrlA transitioning
441 from the inner cell membrane to the cytoplasm. 2) GrlA activates expression of Ler, which in turn
442 activates expression of the rest of the LEE operon. 3) Expression of the LEE genes results in the
443 assembly of the type III secretion system. This virulence factor allows the injection of specific effector
444 molecules into a host cell, altering the host cytoskeleton and mediating disease. Remodelling of the
445 host allows for close attachment of EHEC, improving survival.

446 **Figure 4: Contact dependent sensing in *Vibrio cholerae*.** 1a) Surface contact inhibits the rotation of
447 the flagella, causing disruption to the flow of ions through the flagellar motor. This results in transient
448 hyperpolarisation of the membrane. 1b) C-di-GMP also acts to control virulence gene regulation. C-di-
449 GMP activates VpsT which in turn activates VpsR which binds with RNA polymerase to transcribe
450 target genes. 1c) ((p)ppGpp) acts to control virulence regulation by regulating the expression of the
451 aforementioned VpsT and VpsR proteins. 2) Genes are upregulated in response to these multiple
452 sensory inputs. These include virulence genes encoding factors such as cholera toxin, haemolysin and
453 attachment factors such as the toxin co-regulated pilus. 3) Motility associated genes such as those
454 that encode flagellar components are downregulated by this signalling.

455 **References**

456

- 457 [1] J. W. Costerton, Z. Lewandowski, D. E. Caldwell, D. R. Korber, and H. M. Lappin-Scott,
458 'Microbial Biofilms - Annual Review of Microbiology, 49(1):711', *Annu. Rev. Microbiol.*, vol.
459 49, pp. 711–45, Jan. 1995.
- 460 [2] G. G. Geesey, W. T. Richardson, H. G. Yeomans, R. T. Irvin, and J. W. Costerton, 'Microscopic
461 examination of natural sessile bacterial populations from an alpine stream', *Can. J. Microbiol.*,
462 vol. 23, no. 12, pp. 1733–1736, Dec. 1977.
- 463 [3] C. E. Zobell, 'The Effect of Solid Surfaces upon Bacterial Activity¹', *J. Bacteriol.*, vol. 46, no. 1,
464 pp. 39–56, Jul. 1943.
- 465 [4] H. Heukelekian and A. Heller, 'Relation between Food Concentration and Surface for Bacterial
466 Growth.', *J. Bacteriol.*, vol. 40, no. 4, pp. 547–58, Oct. 1940.
- 467 [5] B. Winnen *et al.*, 'Hierarchical Effector Protein Transport by the Salmonella Typhimurium SPI-
468 1 Type III Secretion System', *PLoS One*, vol. 3, no. 5, p. e2178, May 2008.
- 469 [6] M. C. Schlumberger *et al.*, 'Real-time imaging of type III secretion: Salmonella SipA injection
470 into host cells', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 102, no. 35, pp. 12548–12553, Aug. 2005.
- 471 [7] A. M. Krachler and K. Orth, 'Targeting the bacteria-host interface strategies in anti-adhesion
472 therapy', *Virulence*, vol. 4, no. 4. Taylor and Francis Inc., pp. 284–294, 2013.
- 473 [8] C. J. Van Oss, 'Hydrophobic, hydrophilic and other interactions in epitope-paratope binding',
474 *Mol. Immunol.*, vol. 32, no. 3, pp. 199–211, Feb. 1995.
- 475 [9] A. K. John, M. Schmalzer, N. Khanna, and R. Landmann, 'Reversible daptomycin tolerance of
476 adherent staphylococci in an implant infection model', *Antimicrob. Agents Chemother.*, vol.
477 55, no. 7, pp. 3510–3516, Jul. 2011.

- 478 [10] S. S. Branda, J. E. González-Pastor, S. Ben-Yehuda, R. Losick, and R. Kolter, 'Fruiting body
479 formation by *Bacillus subtilis*', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 98, no. 20, pp. 11621–11626,
480 Sep. 2001.
- 481 [11] H.-C. Flemming, J. Wingender, U. Szewzyk, P. Steinberg, S. A. Rice, and S. Kjelleberg, 'Biofilms:
482 an emergent form of bacterial life', *Nat. Rev. Microbiol.* 2016 149, vol. 14, no. 9, p.
483 nrmicro.2016.94, Aug. 2016.
- 484 [12] P. L. Bishop, 'The role of biofilms in water reclamation and reuse', *Water Sci. Technol.*, vol. 55,
485 no. 1–2, pp. 19–26, Jan. 2007.
- 486 [13] S. E. Coetser and T. E. Cloete, 'Biofouling and Biocorrosion in Industrial Water Systems', *Crit.*
487 *Rev. Microbiol.*, vol. 31, no. 4, pp. 213–232, Jan. 2005.
- 488 [14] G. H. Wadhams and J. P. Armitage, 'Making sense of it all: Bacterial chemotaxis', *Nature*
489 *Reviews Molecular Cell Biology*, vol. 5, no. 12. Nature Publishing Group, pp. 1024–1037, Dec-
490 2004.
- 491 [15] M. Boer, A. Anishkin, and S. Sukharev, 'Adaptive MscS gating in the osmotic permeability
492 response in *E. coli*: The question of time', *Biochemistry*, vol. 50, no. 19, pp. 4087–4096, May
493 2011.
- 494 [16] J. M. Wood, 'Bacterial responses to osmotic challenges', *Journal of General Physiology*, vol.
495 145, no. 5. Rockefeller University Press, pp. 381–388, 01-May-2015.
- 496 [17] J. P. R. Connolly *et al.*, 'The host metabolite D-serine contributes to bacterial niche specificity
497 through gene selection', *ISME J.*, vol. 9, no. 4, pp. 1039–1051, Mar. 2015.
- 498 [18] N. O'Boyle, N. C. A. Turner, A. J. Roe, and J. P. R. Connolly, 'Plastic Circuits: Regulatory
499 Flexibility in Fine Tuning Pathogen Success', *Trends in Microbiology*, vol. 28, no. 5. Elsevier
500 Ltd, pp. 360–371, 01-May-2020.

- 501 [19] E. Pérez-Rueda and J. Collado-Vides, 'The repertoire of DNA-binding transcriptional regulators
502 in Escherichia coli K-12', 2000.
- 503 [20] A. M. Stock, V. L. Robinson, and P. N. Goudreau, 'Two-Component Signal Transduction', *Annu.
504 Rev. Biochem.*, vol. 69, no. 1, pp. 183–215, Jun. 2000.
- 505 [21] B. B. Finlay and S. Falkow, 'Common themes in microbial pathogenicity revisited.', *Microbiol.
506 Mol. Biol. Rev.*, vol. 61, no. 2, pp. 136–169, Jun. 1997.
- 507 [22] D. J. Lee, S. D. Minchin, and S. J. W. Busby, 'Activating Transcription in Bacteria', *Annu. Rev.
508 Microbiol.*, vol. 66, no. 1, pp. 125–152, Oct. 2012.
- 509 [23] S. E. Maddocks and P. C. F. Oyston, 'Structure and function of the LysR-type transcriptional
510 regulator (LTTR) family proteins', *Microbiology*, vol. 154, no. 12, pp. 3609–3623, Dec. 2008.
- 511 [24] C. Berne, C. K. Ellison, A. Ducret, and Y. V. Brun, 'Bacterial adhesion at the single-cell level',
512 *Nature Reviews Microbiology*, vol. 16, no. 10. Nature Publishing Group, pp. 616–627, 01-Oct-
513 2018.
- 514 [25] M. K. Hospenthal, T. R. D. Costa, and G. Waksman, 'A comprehensive guide to pilus
515 biogenesis in Gram-negative bacteria', *Nature Reviews Microbiology*, vol. 15, no. 6. Nature
516 Publishing Group, pp. 365–379, 01-Jun-2017.
- 517 [26] C. N. Spaulding *et al.*, 'Functional role of the type 1 pilus rod structure in mediating host-
518 pathogen interactions', *Elife*, vol. 7, Jan. 2018.
- 519 [27] C. K. Ellison *et al.*, 'Obstruction of pilus retraction stimulates bacterial surface sensing',
520 *Science (80-.)*, vol. 358, no. 6362, pp. 535–538, Oct. 2017.
- 521 [28] V. D. Gordon and L. Wang, 'Bacterial mechanosensing: The force will be with you, always', *J.
522 Cell Sci.*, vol. 132, no. 7, Apr. 2019.
- 523 [29] C. A. Rodesney *et al.*, 'Mechanosensing of shear by *Pseudomonas aeruginosa* leads to

- 524 increased levels of the cyclic-di-GMP signal initiating biofilm development', *Proc. Natl. Acad.*
525 *Sci. U. S. A.*, vol. 114, no. 23, pp. 5906–5911, Jun. 2017.
- 526 [30] G. Alsharif, S. Ahmad, M. S. Islam, R. Shah, S. J. Busby, and A. M. Krachler, 'Host attachment
527 and fluid shear are integrated into a mechanical signal regulating virulence in *Escherichia coli*
528 O157:H7', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 112, no. 17, pp. 5503–5508, Apr. 2015.
- 529 [31] T. Najrana and J. Sanchez-Esteban, 'Mechanotransduction as an adaptation to gravity',
530 *Frontiers in Pediatrics*, vol. 4, no. DEC. Frontiers Media S.A., p. 140, 01-Dec-2016.
- 531 [32] T. E. P. Kimkes and M. Heinemann, 'How bacteria recognise and respond to surface contact',
532 *FEMS Microbiol. Rev.*, vol. 029, pp. 106–122.
- 533 [33] L. Turner, A. S. Stern, and H. C. Berg, 'Growth of Flagellar Filaments of *Escherichia coli* Is
534 Independent of Filament Length', 2012.
- 535 [34] S. B. Guttenplan and D. B. Kearns, 'Regulation of flagellar motility during biofilm formation',
536 *FEMS Microbiology Reviews*, vol. 37, no. 6. Oxford Academic, pp. 849–871, 01-Nov-2013.
- 537 [35] L. McCarter, M. Hilmen, and M. Silverman, 'Flagellar dynamometer controls swarmer cell
538 differentiation of *V. parahaemolyticus*', *Cell*, vol. 54, no. 3, pp. 345–351, Jul. 1988.
- 539 [36] Q. Wang, A. Suzuki, S. Mariconda, S. Porwollik, and R. M. Harshey, 'Sensing wetness: a new
540 role for the bacterial flagellum', *EMBO J.*, vol. 24, no. 11, pp. 2034–2042, Jun. 2005.
- 541 [37] P. P. Lele, B. G. Hosu, and H. C. Berg, 'Dynamics of mechanosensing in the bacterial flagellar
542 motor', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 110, no. 29, pp. 11839–11844, Jul. 2013.
- 543 [38] C. J. Gode-Potratz, R. J. Kustusch, P. J. Breheny, D. S. Weiss, and L. L. McCarter, 'Surface
544 sensing in *Vibrio parahaemolyticus* triggers a programme of gene expression that promotes
545 colonization and virulence', *Mol. Microbiol.*, vol. 79, no. 1, pp. 240–263, Jan. 2011.
- 546 [39] M. Schniederberend *et al.*, 'Modulation of flagellar rotation in surface-attached bacteria: A

- 547 pathway for rapid surface-sensing after flagellar attachment', *PLoS Pathog.*, vol. 15, no. 11, p.
548 e1008149, Nov. 2019.
- 549 [40] L. S. Cairns, V. L. Marlow, E. Bissett, A. Ostrowski, and N. R. Stanley-Wall, 'A mechanical signal
550 transmitted by the flagellum controls signalling in *Bacillus subtilis*', *Mol. Microbiol.*, vol. 90,
551 no. 1, pp. 6–21, Oct. 2013.
- 552 [41] L. Craig *et al.*, 'Type IV pilin structure and assembly: X-ray and EM analyses of *Vibrio cholerae*
553 toxin-coregulated pilus and *Pseudomonas aeruginosa* PAK pilin', *Mol. Cell*, vol. 11, no. 5, pp.
554 1139–1150, May 2003.
- 555 [42] B. Averhoff and A. Friedrich, 'Type IV pili-related natural transformation systems: DNA
556 transport in mesophilic and thermophilic bacteria', *Archives of Microbiology*, vol. 180, no. 6.
557 Springer, pp. 385–393, 31-Dec-2003.
- 558 [43] G. Reguera, K. D. McCarthy, T. Mehta, J. S. Nicoll, M. T. Tuominen, and D. R. Lovley,
559 'Extracellular electron transfer via microbial nanowires', *Nature*, vol. 435, no. 7045, pp. 1098–
560 1101, Jun. 2005.
- 561 [44] V. Pelicic, 'Type IV pili: e pluribus unum?', *Mol. Microbiol.*, vol. 68, no. 4, pp. 827–837, May
562 2008.
- 563 [45] L. Craig, K. T. Forest, and B. Maier, 'Type IV pili: dynamics, biophysics and functional
564 consequences', *Nature Reviews Microbiology*, vol. 17, no. 7. Nature Publishing Group, pp.
565 429–440, 01-Jul-2019.
- 566 [46] J. S. Mattick, 'Type IV Pili and Twitching Motility', *Annu. Rev. Microbiol.*, vol. 56, no. 1, pp.
567 289–314, Oct. 2002.
- 568 [47] D. E. Bradley, 'Evidence for the retraction of *Pseudomonas aeruginosa* RNA phage pili',
569 *Biochem. Biophys. Res. Commun.*, vol. 47, no. 1, pp. 142–149, Apr. 1972.

- 570 [48] D. E. Bradley, 'A function of *Pseudomonas aeruginosa* PAO polar pili: twitching motility', *Can.*
571 *J. Microbiol.*, vol. 26, no. 2, pp. 146–154, Feb. 1980.
- 572 [49] L. L. Burrows, '*Pseudomonas aeruginosa* Twitching Motility: Type IV Pili in Action', *Annu. Rev.*
573 *Microbiol.*, vol. 66, no. 1, pp. 493–520, Oct. 2012.
- 574 [50] J. S. Mattick, 'Type IV Pili and Twitching Motility', *Annu. Rev. Microbiol.*, vol. 56, no. 1, pp.
575 289–314, Oct. 2002.
- 576 [51] R. T. Sadikot, T. S. Blackwell, J. W. Christman, and A. S. Prince, 'Pathogen-host interactions in
577 *pseudomonas aeruginosa* pneumonia', *American Journal of Respiratory and Critical Care*
578 *Medicine*, vol. 171, no. 11. American Thoracic Society, pp. 1209–1223, 01-Jun-2005.
- 579 [52] K. A. Coggan and M. C. Wolfgang, '*P. aeruginosa* Environmental Lifestyle and Virulence 47
580 Global Regulatory Pathways and Cross-talk Control *Pseudomonas aeruginosa* Environmental
581 Lifestyle and Virulence Phenotype'.
- 582 [53] K. Streeter and M. Katouli, '*Pseudomonas aeruginosa*: A review of their Pathogenesis and
583 Prevalence in Clinical Settings and the Environment', *Infect Epidemiol Med. 2016 Winter*, vol.
584 2, no. 1, pp. 25–32, 2016.
- 585 [54] S. Stefani *et al.*, 'Relevance of multidrug-resistant *Pseudomonas aeruginosa* infections in
586 cystic fibrosis', *International Journal of Medical Microbiology*, vol. 307, no. 6. Elsevier GmbH,
587 pp. 353–362, 01-Sep-2017.
- 588 [55] S. J. Cole and V. T. Lee, 'Cyclic Di-GMP Signaling Contributes to *Pseudomonas aeruginosa*-
589 Mediated Catheter-Associated Urinary Tract Infection', 2015.
- 590 [56] T. L. Yahr and E. P. Greenberg, 'The genetic basis for the commitment to chronic versus acute
591 infection in *Pseudomonas aeruginosa*', *Molecular Cell*, vol. 16, no. 4. Cell Press, pp. 497–498,
592 19-Nov-2004.

- 593 [57] N. C. Caiazza and G. A. O'Toole, 'SadB is required for the transition from reversible to
594 irreversible attachment during biofilm formation by *Pseudomonas aeruginosa* PA14', *J.*
595 *Bacteriol.*, vol. 186, no. 14, pp. 4476–4485, Jul. 2004.
- 596 [58] J. C. Conrad *et al.*, 'Flagella and pili-mediated near-surface single-cell motility mechanisms in
597 *P. aeruginosa*', *Biophys. J.*, vol. 100, no. 7, pp. 1608–1616, Apr. 2011.
- 598 [59] B. I. Kazmierczak and D. R. Hendrixson, 'Spatial and numerical regulation of flagellar
599 biosynthesis in polarly flagellated bacteria', *Molecular Microbiology*, vol. 88, no. 4. pp. 655–
600 663, May-2013.
- 601 [60] T. S. Murray and B. I. Kazmierczak, 'FlhF Is required for swimming and swarming in
602 *Pseudomonas aeruginosa*', *J. Bacteriol.*, vol. 188, no. 19, pp. 6995–7004, Oct. 2006.
- 603 [61] M. C. Wolfgang, V. T. Lee, M. E. Gilmore, and S. Lory, 'Coordinate regulation of bacterial
604 virulence genes by a novel adenylate cyclase-dependent signaling pathway', *Dev. Cell*, vol. 4,
605 no. 2, pp. 253–263, Feb. 2003.
- 606 [62] S. J. Suh *et al.*, 'Effect of *vfr* mutation on global gene expression and catabolite repression
607 control of *Pseudomonas aeruginosa*', *Microbiology*, vol. 148, no. 5, pp. 1561–1569, May
608 2002.
- 609 [63] S. E. H. West, A. K. Sample, and L. J. Runyen-Janecky, 'The *vfr* gene product, required for
610 *Pseudomonas aeruginosa* exotoxin A and protease production, belongs to the cyclic AMP
611 receptor protein family', *J. Bacteriol.*, vol. 176, no. 24, pp. 7532–7542, Dec. 1994.
- 612 [64] S. A. Beatson, C. B. Whitchurch, J. L. Sargent, R. C. Levesque, and J. S. Mattick, 'Differential
613 regulation of twitching motility and elastase production by *Vfr* in *Pseudomonas aeruginosa*',
614 *J. Bacteriol.*, vol. 184, no. 13, pp. 3605–3613, Jul. 2002.
- 615 [65] E. Ferrell, N. L. Carty, J. A. Colmer-Hamood, A. N. Hamood, and S. E. H. West, 'Regulation of
616 *Pseudomonas aeruginosa* *ptxR* by *Vfr*', *Microbiology*, vol. 154, no. 2, pp. 431–439, Feb. 2008.

- 617 [66] N. Dasgupta, E. P. Ferrell, K. J. Kanack, S. E. H. West, and R. Ramphal, 'fleQ, the gene encoding
618 the major flagellar regulator of *Pseudomonas aeruginosa*, is σ 70 dependent and is
619 downregulated by Vfr, a homolog of *Escherichia coli* cyclic AMP receptor protein', *J.*
620 *Bacteriol.*, vol. 184, no. 19, pp. 5240–5250, Oct. 2002.
- 621 [67] J. A. Driscoll, S. L. Brody, and M. H. Kollef, 'The epidemiology, pathogenesis and treatment of
622 *Pseudomonas aeruginosa* infections', *Drugs*, vol. 67, no. 3. Springer, pp. 351–368, 18-Sep-
623 2007.
- 624 [68] Y. Luo *et al.*, 'A hierarchical cascade of second messengers regulates *Pseudomonas*
625 *aeruginosa* Surface Behaviors', *MBio*, vol. 6, no. 1, Jan. 2015.
- 626 [69] A. Persat, Y. F. Inclan, J. N. Engel, H. A. Stone, and Z. Gitai, 'Type IV pili mechanochemically
627 regulate virulence factors in *Pseudomonas aeruginosa*', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 112,
628 no. 24, pp. 7563–7568, Jun. 2015.
- 629 [70] Y. F. Inclan *et al.*, 'A scaffold protein connects type IV pili with the Chp chemosensory system
630 to mediate activation of virulence signaling in *Pseudomonas aeruginosa*', *Mol. Microbiol.*, vol.
631 101, no. 4, pp. 590–605, Aug. 2016.
- 632 [71] Y. F. Inclan, M. J. Huseby, and J. N. Engel, 'FimL Regulates cAMP Synthesis in *Pseudomonas*
633 *aeruginosa*', *PLoS One*, vol. 6, no. 1, p. e15867, Jan. 2011.
- 634 [72] N. B. Fulcher, P. M. Holliday, E. Klem, M. J. Cann, and M. C. Wolfgang, 'The *Pseudomonas*
635 *aeruginosa* Chp chemosensory system regulates intracellular cAMP levels by modulating
636 adenylate cyclase activity', *Mol. Microbiol.*, vol. 76, no. 4, pp. 889–904, 2010.
- 637 [73] R. W. Heiniger, H. C. Winther-Larsen, R. J. Pickles, M. Koomey, and M. C. Wolfgang, 'Infection
638 of human mucosal tissue by *Pseudomonas aeruginosa* requires sequential and mutually
639 dependent virulence factors and a novel pilus-associated adhesin', *Cell. Microbiol.*, vol. 12,
640 no. 8, pp. 1158–1173, Aug. 2010.

- 641 [74] A. Siryaporn, S. L. Kuchma, G. A. O'Toole, Z. Gitai, and F. M. Ausubel, 'Surface attachment
642 induces *Pseudomonas aeruginosa* virulence', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 111, no. 47,
643 pp. 16860–16865, Nov. 2014.
- 644 [75] W. Kong *et al.*, 'ChIP-seq reveals the global regulator AlgR mediating cyclic di-GMP synthesis
645 in *Pseudomonas aeruginosa*', *Nucleic Acids Res.*, vol. 43, no. 17, pp. 8268–8282, Sep. 2015.
- 646 [76] J. L. Moake, N. A. Turner, N. A. Stathopoulos, L. H. Nolasco, and J. D. Hellums, 'Involvement of
647 large plasma von Willebrand Factor (vWF) multimers and unusually large vWF forms derived
648 from endothelial cells in shear stress-induced platelet aggregation', *J. Clin. Invest.*, vol. 78, no.
649 6, pp. 1456–1461, Dec. 1986.
- 650 [77] J. Kim, C. Z. Zhang, X. Zhang, and T. A. Springer, 'A mechanically stabilized receptor-ligand
651 flex-bond important in the vasculature', *Nature*, vol. 466, no. 7309, pp. 992–995, Aug. 2010.
- 652 [78] S. Tammam *et al.*, 'PilMNOPQ from the *Pseudomonas aeruginosa* type IV pilus system form a
653 transenvelope protein interaction network that interacts with Pila', *J. Bacteriol.*, vol. 195, no.
654 10, pp. 2126–2135, May 2013.
- 655 [79] J. H. Merritt, K. M. Brothers, S. L. Kuchma, and G. A. O'Toole, 'SadC reciprocally influences
656 biofilm formation and swarming motility via modulation of exopolysaccharide production and
657 flagellar function', in *Journal of Bacteriology*, 2007, vol. 189, no. 22, pp. 8154–8164.
- 658 [80] L. Alibaud *et al.*, '*Pseudomonas aeruginosa* virulence genes identified in a *Dictyostelium* host
659 model', *Cell. Microbiol.*, vol. 10, no. 3, pp. 729–740, Mar. 2008.
- 660 [81] S. Pukatzki, R. H. Kessin, and J. J. Mekalanos, 'The human pathogen *Pseudomonas aeruginosa*
661 utilizes conserved virulence pathways to infect the social amoeba *Dictyostelium discoideum*',
662 *Proc. Natl. Acad. Sci. U. S. A.*, vol. 99, no. 5, pp. 3159–3164, Mar. 2002.
- 663 [82] J. R. O'Connor, N. J. Kuwada, V. Huangyutitham, P. A. Wiggins, and C. S. Harwood, 'Surface
664 sensing and lateral subcellular localization of WspA, the receptor in a chemosensory-like

- 665 system leading to c-di-GMP production', *Mol. Microbiol.*, vol. 86, no. 3, pp. 720–729, Nov.
666 2012.
- 667 [83] P. Kiratisin, K. D. Tucker, and L. Passador, 'LasR, a Transcriptional Activator of *Pseudomonas*
668 *aeruginosa* Virulence Genes, Functions as a Multimer', *J. Bacteriol.*, vol. 184, no. 17, pp.
669 4912–4919, 2002.
- 670 [84] C. Allison and C. Hughes, 'Bacterial swarming: an example of prokaryotic differentiation and
671 multicellular behaviour', *Science Progress (1933-)*, vol. 75. Sage Publications, Ltd., pp. 403–
672 422, 1991.
- 673 [85] H. L. T. Mobley and R. Belas, 'Swarming and pathogenicity of *Proteus mirabilis* in the urinary
674 tract', *Trends Microbiol.*, vol. 3, no. 7, pp. 280–284, Jul. 1995.
- 675 [86] K. A. Coggan and M. C. Wolfgang, 'Global regulatory pathways and cross-talk control
676 *pseudomonas aeruginosa* environmental lifestyle and virulence phenotype', *Curr. Issues Mol.*
677 *Biol.*, vol. 14, no. 2, pp. 47–70, 2012.
- 678 [87] R. Belas, J. Manos, and R. Suvanasuthi, 'Proteus mirabilis ZapA metalloprotease degrades a
679 broad spectrum of substrates, including antimicrobial peptides', *Infect. Immun.*, vol. 72, no. 9,
680 pp. 5159–5167, Sep. 2004.
- 681 [88] M. Alavi and R. Belas, 'Surface sensing, swarmer cell differentiation, and biofilm
682 development', *Methods Enzymol.*, vol. 336, pp. 29–40, Jan. 2001.
- 683 [89] R. Belas and R. Suvanasuthi, 'The ability of *Proteus mirabilis* to sense surfaces and regulate
684 virulence gene expression involves fliL, a flagellar basal body protein', *J. Bacteriol.*, vol. 187,
685 no. 19, pp. 6789–6803, Oct. 2005.
- 686 [90] Y. Y. Lee, J. Patellis, and R. Belas, 'Activity of *Proteus mirabilis* FliL is viscosity dependent and
687 requires extragenic DNA', *J. Bacteriol.*, vol. 195, no. 4, pp. 823–832, Feb. 2013.

- 688 [91] C. Ariison, H. -C Lai, and C. Hughes, 'Co-ordinate expression of virulence genes during swarm-
689 cell differentiation and population migration of *Proteus mirabilis*', *Mol. Microbiol.*, vol. 6, no.
690 12, pp. 1583–1591, 1992.
- 691 [92] O. Tenaillon, D. Skurnik, B. Picard, and E. Denamur, 'The population genetics of commensal
692 *Escherichia coli*', *Nature Reviews Microbiology*, vol. 8, no. 3. Nature Publishing Group, pp.
693 207–217, Mar-2010.
- 694 [93] T. K. Davis, N. C. A. J. Van De Kar, and P. I. Tarr, 'Shiga Toxin/Verocytotoxin-Producing
695 *Escherichia coli* Infections: Practical Clinical Perspectives', *Microbiol. Spectr.*, vol. 2, no. 4,
696 Aug. 2014.
- 697 [94] J. J. LeBlanc, 'Implication of Virulence Factors in *Escherichia coli* O157:H7 Pathogenesis',
698 *Critical Reviews in Microbiology*, vol. 29, no. 4. CRC Press LLC, pp. 277–296, 2003.
- 699 [95] A. J. Roe, D. E. E. Hoey, and D. L. Gally, 'Regulation, secretion and activity of type III-secreted
700 proteins of enterohaemorrhagic *Escherichia coli* O157', in *Biochemical Society Transactions*,
701 2003, vol. 31, no. 1, pp. 98–103.
- 702 [96] S. J. Lloyd, J. M. Ritchie, and A. G. Torres, 'Fimbriation and curliation in *Escherichia coli*
703 O157:H7 a paradigm of intestinal and environmental colonization', *Gut Microbes*, vol. 3, no.
704 3, pp. 272–276, 2012.
- 705 [97] S. J. Elliott *et al.*, 'The locus of enterocyte effacement (LEE)-encoded regulator controls
706 expression of both LEE- and non-LEE-encoded virulence factors in enteropathogenic and
707 enterohemorrhagic *Escherichia coli*', *Infect. Immun.*, vol. 68, no. 11, pp. 6115–6126, Nov.
708 2000.
- 709 [98] T. K. Mcdaniel, K. G. Jarvis, M. S. Donnenberg, and J. B. Kaper, 'A genetic locus of enterocyte
710 effacement conserved among diverse enterobacterial pathogens', *Proc. Natl. Acad. Sci. U. S.*
711 *A.*, vol. 92, no. 5, pp. 1664–1668, Feb. 1995.

- 712 [99] A. E. Jerse, J. Yu, B. D. Tall, and J. B. Kaper, 'A genetic locus of enteropathogenic Escherichia
713 coli necessary for the production of attaching and effacing lesions on tissue culture cells',
714 *Proc. Natl. Acad. Sci. U. S. A.*, vol. 87, no. 20, pp. 7839–7843, 1990.
- 715 [100] V. Sperandio, A. G. Torres, J. A. Girón, and J. B. Kaper, 'Quorum sensing is a global regulatory
716 mechanism in enterohemorrhagic Escherichia coli O157:H7', *J. Bacteriol.*, vol. 183, no. 17, pp.
717 5187–5197, Sep. 2001.
- 718 [101] B. W. James and C. W. Keevil, 'Influence of oxygen availability on physiology, verocytotoxin
719 expression and adherence of Escherichia coli O157', *J. Appl. Microbiol.*, vol. 86, no. 1, pp.
720 117–124, Jan. 1999.
- 721 [102] B. Kenny, A. Abe, M. Stein, and B. B. Finlay, 'Enteropathogenic Escherichia coli protein
722 secretion is induced in response to conditions similar to those in the gastrointestinal tract',
723 *Infect. Immun.*, vol. 65, no. 7, pp. 2606–2612, Jul. 1997.
- 724 [103] F. Ebel, C. Deibel, A. U. Kresse, C. A. Guzmán, and T. Chakraborty, 'Temperature- and
725 medium-dependent secretion of proteins by Shiga toxin-producing Escherichia coli.', *Infect.*
726 *Immun.*, vol. 64, no. 11, pp. 4472–4479, Nov. 1996.
- 727 [104] V. Sperandio, A. G. Torres, B. Jarvis, J. P. Nataro, and J. B. Kaper, 'Bacteria-host
728 communication: The language of hormones', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 100, no. 15,
729 pp. 8951–8956, Jul. 2003.
- 730 [105] M. S. Islam, L. E. H. Bingle, M. J. Pallen, and S. J. W. Busby, 'Organization of the LEE1 operon
731 regulatory region of enterohaemorrhagic Escherichia coli O157:H7 and activation by GrlA',
732 *Mol. Microbiol.*, vol. 79, no. 2, pp. 468–483, Jan. 2011.
- 733 [106] N. Sirisaengtaksin, M. A. Odem, R. E. Bosserman, E. M. Flores, and A. M. Krachler, 'The E. Coli
734 transcription factor GrlA is regulated by subcellular compartmentalization and activated in
735 response to mechanical stimuli', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 117, no. 17, pp. 9519–

- 736 9528, Apr. 2020.
- 737 [107] J. A. Girón, A. G. Torres, E. Freer, and J. B. Kaper, 'The flagella of enteropathogenic Escherichia
738 coli mediate adherence to epithelial cells', *Mol. Microbiol.*, vol. 44, no. 2, pp. 361–379, Apr.
739 2002.
- 740 [108] L. Laganenka, M. E. López, R. Colin, and V. Sourjik, 'Flagellum-mediated mechanosensing and
741 rflp control motility state of pathogenic escherichia coli', *MBio*, vol. 11, no. 2, Mar. 2020.
- 742 [109] T. Iino *et al.*, 'New Unified Nomenclature for the Flagellar Genes of Escherichia coli and
743 Salmonella typhimurium', 1988.
- 744 [110] P. P. Lele, B. G. Hosu, and H. C. Berg, 'Dynamics of mechanosensing in the bacterial flagellar
745 motor', *Proc. Natl. Acad. Sci. U. S. A.*, vol. 110, no. 29, pp. 11839–11844, Jul. 2013.
- 746 [111] R. Belas, 'Biofilms, flagella, and mechanosensing of surfaces by bacteria', *Trends in
747 Microbiology*, vol. 22, no. 9. Elsevier Ltd, pp. 517–527, 01-Sep-2014.
- 748 [112] S. Il Yoon *et al.*, 'Structural basis of TLR5-flagellin recognition and signaling', *Science (80-.)*,
749 vol. 335, no. 6070, pp. 859–864, Feb. 2012.
- 750 [113] F. L. Thompson, T. Iida, and J. Swings, 'Biodiversity of Vibrios', *Microbiol. Mol. Biol. Rev.*, vol.
751 68, no. 3, pp. 403–431, Sep. 2004.
- 752 [114] R. D. Allen and P. Baumann, 'Structure and arrangement of flagella in species of the genus
753 *Beneckea* and *Photobacterium fischeri*', *J. Bacteriol.*, vol. 107, no. 1, pp. 295 LP – 302, Jul.
754 1971.
- 755 [115] T. Atsumi, L. McCarter, and Y. Imae, 'Polar and lateral flagellar motors of marine Vibrio are
756 driven by different ion-motive forces', *Nature*, vol. 355, no. 6356, pp. 182–184, 1992.
- 757 [116] S. Kojima, K. Yamamoto, I. Kawagishi, and M. Homma, 'The polar flagellar motor of *Vibrio
758 cholerae* is driven by an Na⁺ motive force', *J. Bacteriol.*, vol. 181, no. 6, pp. 1927 LP – 1930,

759 Mar. 1999.

760 [117] K. L. Van Dellen, L. Houot, and P. I. Watnick, 'Genetic analysis of *Vibrio cholerae* monolayer
761 formation reveals a key role for $\Delta\Psi$ in the transition to permanent attachment', *J. Bacteriol.*,
762 vol. 190, no. 24, pp. 8185–8196, Dec. 2008.

763 [118] C. L. Gardel and J. J. Mekalanos, 'Alterations in *Vibrio cholerae* motility phenotypes correlate
764 with changes in virulence factor expression.', *Infect. Immun.*, vol. 64, no. 6, pp. 2246 LP –
765 2255, Jun. 1996.

766 [119] C. C. Häse and J. J. Mekalanos, 'Effects of changes in membrane sodium flux on virulence
767 gene expression in *Vibrio cholerae*', *Proc. Natl. Acad. Sci.*, vol. 96, no. 6, pp. 3183 LP – 3187,
768 Mar. 1999.

769 [120] J. C. N. Fong, K. A. Syed, K. E. Klose, and F. H. Yildiz, 'Role of *Vibrio* polysaccharide (*vps*) genes
770 in VPS production, biofilm formation and *Vibrio cholerae* pathogenesis', *Microbiology*, vol.
771 156, no. Pt 9, pp. 2757–2769, Sep. 2010.

772 [121] C. M. Lauriano, C. Ghosh, N. E. Correa, and K. E. Klose, 'The sodium-driven flagellar motor
773 controls exopolysaccharide expression in *Vibrio cholerae*', *J. Bacteriol.*, vol. 186, no. 15, pp.
774 4864 LP – 4874, Aug. 2004.

775 [122] P. V Krasteva *et al.*, '*Vibrio cholerae* VpsT regulates matrix production and motility by directly
776 sensing cyclic di-GMP', *Science (80-.)*, vol. 327, no. 5967, pp. 866 LP – 868, Feb. 2010.

777 [123] M.-L. Hsieh, D. M. Hinton, and C. M. Waters, 'VpsR and cyclic di-GMP together drive
778 transcription initiation to activate biofilm formation in *Vibrio cholerae*', *Nucleic Acids Res.*,
779 vol. 46, no. 17, pp. 8876–8887, Jul. 2018.

780 [124] H. He, J. N. Cooper, A. Mishra, and D. M. Raskin, 'Stringent response regulation of biofilm
781 formation in *Vibrio cholerae*', *J. Bacteriol.*, vol. 194, no. 11, pp. 2962 LP – 2972, Jun. 2012.

- 782 [125] I. Kawagishi, M. Imagawa, Y. Imae, L. McCarter, and M. Homma, 'The sodium-driven polar
783 flagellar motor of marine *Vibrio* as the mechanosensor that regulates lateral flagellar
784 expression', *Mol. Microbiol.*, vol. 20, no. 4, pp. 693–699, May 1996.
- 785 [126] R. B. R. Ferreira, L. C. M. Antunes, E. P. Greenberg, and L. L. McCarter, 'Vibrio
786 parahaemolyticus ScrC modulates cyclic dimeric GMP regulation of gene expression relevant
787 to growth on surfaces', *J. Bacteriol.*, vol. 190, no. 3, pp. 851–860, Feb. 2008.
- 788 [127] R. B. R. Ferreira, D. M. Chodur, L. C. M. Antunes, M. J. Trimble, and L. L. McCarter, 'Output
789 targets and transcriptional regulation by a cyclic dimeric GMP-responsive circuit in the *Vibrio*
790 parahaemolyticus scr network', *J. Bacteriol.*, vol. 194, no. 5, pp. 914–924, Mar. 2012.
- 791