

1 **«(p)ppGpp and its role in bacterial persistence: New challenges»**

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33 **Keywords:** persistence, (p)ppGpp, TA systems, slow growth, PRDP.

34 **Running title:** (p)ppGpp and bacterial persistence

35 **ABSTRACT**

36 Antibiotic failure is not only due to the development of resistance by pathogens, but it can also
37 often be explained by persistence and tolerance. Persistence and tolerance can be included in
38 the “persistent phenotype”, with high relevance for clinics. Two of the most important
39 molecular mechanisms involved in tolerance and persistence are toxin-antitoxin (TA) modules
40 and signaling via guanosine pentaphosphate/tetraphosphate (p)ppGpp, also known as “magic
41 spot”). (p)ppGpp is a very important stress alarmone which orchestrates the stringent
42 response in bacteria; hence, (p)ppGpp is produced during amino acid or fatty acid starvation
43 by proteins belonging to the RelA/SpoT homologs family (RSH). However, (p)ppGpp levels can
44 also accumulate in response to a wide range of signals, including oxygen variation, pH
45 downshift, osmotic shock, temperature shift or even exposure to darkness. Furthermore, the
46 stringent response is not only involved in responses to environmental stresses (starvation for
47 carbon sources, fatty acids, phosphate or heat shock), but it is also used in bacterial
48 pathogenesis, host invasion, antibiotic tolerance and persistence. Given the exhaustive and
49 contradictory literature surrounding the role of (p)ppGpp in bacterial persistence, and with the
50 aim of summarizing what is known so far about the “magic spot” in this bacterial stage, this
51 review provides new insights into the link between the stringent response and persistence.
52 Moreover, we review some of the innovative treatments that have (p)ppGpp as a target, which
53 are in the spotlight of the scientific community as candidates for effective anti-persistence
54 agents.

55 **1. Introduction**

56 Antimicrobial resistance crisis is a serious health problem worldwide. During the past fifty
57 years, very few new anti-infective molecules have been discovered (1). Hence, microbial
58 pathogens have been able to accumulate molecular mechanisms enabling them to counteract
59 antibiotics.

60 Nonetheless, there are more antibiotic evasion strategies other than resistance that are of
61 great interest, such as persistence and tolerance. Persisters are a subpopulation of cells that
62 are non-growing, non-replicative, dormant bacteria that exhibit transient high levels of
63 tolerance to antibiotics without affecting their MICs (2-4). Once the drug pressure is removed,
64 these persisters can rapidly regrow, thus returning to an antibiotic sensitive state. Moreover,
65 the persistent state can be maintained for hours up to days before persisters revert to an
66 antibiotic-sensitive cell type, resuming growth under drug-free conditions (5).

67 The term “triggered persistence” has been recently coined to indicate a form of persistence
68 that is induced by particular signals, such as starvation and nutrient transitions, acid- and
69 oxidant-stress, DNA damage, subinhibitory concentrations of antibiotics and intracellular
70 infections (6).

71 Similar to persisters, tolerant cells are populations of bacteria that can also overcome
72 antibiotic therapy. Tolerance allows cells to temporarily counteract the lethal consequences of
73 high doses of antibiotics, maintaining their vital processes slowed (4, 7, 8). Also, tolerant
74 bacteria arise when the whole population slows its growth (e.g., stationary-phase) whereas
75 persister bacteria are a small subpopulation of the population (4).

76 Both tolerant and persistent bacteria can be included in the “persistent phenotype”, which has
77 high relevance in clinics because: (i) there is evidence that persistent cells are responsible for
78 relapses of infections, which is common in tuberculosis, cystic fibrosis and Lyme disease (9,
79 10); (ii) antibiotic therapy does not effectively work against these types of infections; (iii)
80 persisters are responsible for the majority of biofilm-associated infections (11, 12) and (iv) they
81 are associated with better survival of bacteria inside macrophages (13). Furthermore, persister
82 cells can also survive in immune-compromised patients and in patients in whom antibiotics do
83 not effectively kill pathogenic bacteria, as they might deploy immune-evasion strategies (14).

84 Differences between resistance, persistence and tolerance have been established;
85 nonetheless, there are also relationships among these bacterial populations which are worthy
86 of consideration. Despite evidence showing that tolerance and persistence to antibiotics
87 promote the evolution of resistance in bacteria (8, 14, 15) both mechanisms are currently
88 underestimated by the scientific and medical communities.

89 There are several molecular mechanisms involved in bacterial persistence and tolerance to
90 antibiotics, reviewed by Trastoy and colleagues (2018), which include: (p)ppGpp network;
91 toxin-antitoxin (TA) system; the quorum sensing (QS) system; drug efflux pumps; reactive
92 oxygen species (ROS); the SOS response; and RpoS (sigma factor of stationary phase) (7).
93 (p)ppGpp orchestrates the stringent response (SR) in bacteria, thus it is produced during
94 nutrient stress (such as amino acid or fatty acid starvation) by proteins belonging to the
95 RelA/SpoT Homologs family (RSH) (16). In *E. coli*, RelA is the (p)ppGpp synthetase I or GTP-
96 pyrophosphokinase that synthesizes (p)ppGpp from GTP/GDP and ATP, whereas SpoT is a
97 bifunctional (p)ppGpp synthetase II or pyrophosphohydrolase (17). However, (p)ppGpp levels
98 in bacteria do not depend exclusively on nutrient availability (18), since it can also accumulate
99 in response to a wide range of signals, including oxygen variation (19), pH downshift (20),
100 osmotic shock, temperature shift (21) or even exposure to darkness (22). Furthermore, the SR
101 is not only involved in responses to environmental stresses (starvation for carbon sources,
102 fatty acids, phosphate or heat shock), but also in bacterial pathogenesis (23), host invasion
103 (24), antibiotic tolerance and persister cell formation (25).

104 Given the exhaustive and contradictory literature surrounding the role of (p)ppGpp in bacterial
105 persistence, and with the aim of summarizing what is known so far about the “magic spot” in
106 this bacterial stage, this review provides new insights into the link between the SR and
107 persisters. Finally, we have reviewed and discussed some of the innovative treatments that
108 have (p)ppGpp as a target, which are in the spotlight of the scientific community as candidates
109 of effective anti-persistence agents.

110 **2. (p)ppGpp as a key regulator**

111 It was in 1969 that Cashel and Gallant described for the first time guanosine
112 penta/tetraphosphate (26). During these fifty years, many functions have been attributed to
113 this alarmone as it plays a key role in the physiology of bacteria, mainly controlling energetic
114 metabolism (26, 27) but also their virulence and immune evasion (26). Despite being widely
115 studied in the model organism *E. coli*, (p)ppGpp behaves differently in other species and its
116 regulation changes among phylogenetically-related bacterial groups (27). In *E. coli*, the
117 accumulation of (p)ppGpp causes the differential expression of approximately 500 genes, as it
118 activates RpoS and RpoE (the stress response sigma factor for misfolded proteins in the
119 periplasm) (28). Also in *E. coli*, (p)ppGpp directly inhibits DNA primase (29), and is thought to
120 inhibit the synthesis of rRNA, which also affects translation globally, by regulating the
121 transcription of the ribosomal modulation factor (Rmf) (30). More specifically, in response to
122 stresses such as amino acid starvation, in Gram negative bacteria (p)ppGpp binds to the RNA
123 polymerase inducing an allosteric signal to the catalytic Mg²⁺ site, which severally decreases

124 transcription causing a global re-wiring of the gene expression profile. Taken together, all
125 these changes lead to dormancy or slow growth for most cells (Figure 1) (31, 32).

126 Most Gram-positive bacteria possess ~~only~~ one long RSH, named Rel, which has both (p)ppGpp
127 synthetase and hydrolase activities (33, 34) together with a short RSH, named SAS (Small
128 Alarmone Synthetase) or SAH (Small Alarmone Hydrolase) (35). Nonetheless, the existence of a
129 diverse population of (p)ppGpp synthetases and hydrolases in bacteria has been demonstrated
130 (35-38).

131 There is evidence that (p)ppGpp is related to antibiotic tolerance and persister cell formation
132 (25, 39-42). For example, increased levels of (p)ppGpp inhibit negative supercoiling of DNA in
133 *E. coli*, thus preventing DNA replication and transcription, resulting in tolerance towards
134 ofloxacin and quinolones (Figure 1) (43, 44). Persister cells tend to form in biofilms, in which
135 the bacterial cells are embedded in a three-dimensional matrix that provides protection during
136 pathogenesis and other conditions. Thus, it is logical that bacteria in biofilms encounter limited
137 access to nutrients and therefore display the SR (45). Consistently, different groups have
138 shown that multidrug tolerance of *P. aeruginosa* and *E. coli* grown in biofilms depends on
139 (p)ppGpp (45-47). Also, in 2014, Helaine and colleagues performed an experiment where they
140 studied the invasion of mouse macrophages by *Salmonella enterica*, and they observed that
141 (p)ppGpp production by bacteria residing in acidified vacuoles of macrophages was required
142 for persistence (13).

143 **3. (p)ppGpp as a mediator in bacterial growth.**

144 Accumulation of (p)ppGpp promotes transcriptional alterations in the bacterial cell, such as
145 general repression of rapid growth genes and activation of genes involved in amino acid
146 biosynthesis and survival to stress (29). Therefore, loss of (p)ppGpp in some conditions (for
147 example minimal medium) leads to amino acid auxotrophy of the whole population and an
148 increased survival due to high tolerance. Similarly, many other conditions or mutations that
149 decrease bacterial growth rate have been shown to induce the same tolerant phenotype (48).
150 Several authors suggested that, at least in *Salmonella*, there was no specific molecular
151 pathway underlying bacterial persistence, but that slow growth was the main factor to induce
152 persistence (49, 50). Regarding the involvement of (p)ppGpp in bacterial growth, it has been
153 shown that *relA spoT* double null mutants of *E. coli*, completely depleted of (p)ppGpp, are
154 more elongated than wild-type cells (51). LpxC, a key enzyme that catalyzes one of the first
155 steps in the synthesis of lipopolysaccharide (LPS) in *E. coli*, is degraded during slow growth but
156 stabilized when cells grow faster (Figure 1) (52). Hence, in 2013 it was reported that in *relA*
157 *spot* double null mutants, there was a deregulation of LpxC degradation, resulting in rapid
158 proteolysis in fast-growing cells and stabilization during slow growth, in opposition to the

159 normal state where (p)ppGpp is present (52). In 2015, Yamaguchi and colleagues found that
160 elevated levels of (p)ppGpp led to inhibition of bacterial growth by interfering with the FtsZ
161 protein assembly in *Salmonella paratyphi* A (53). FtsZ is a protein essential for the prokaryotic
162 cell division that needs to form linear structures and has a GTP binding site; however,
163 increased levels of (p)ppGpp (20-fold higher than the required GTP levels) causes FtsZ to form
164 helical structures unable to form the Z-ring at the division site (53), which impairs the division
165 of the bacterial cell and, therefore, the population growth. In short, high levels of (p)ppGpp
166 can promote persistence by halting growth in a subpopulation (even in a rich-nutrient
167 medium), while absence of this alarmone can contribute to tolerance (by preventing the whole
168 population to appropriately handle a nutritional stress).

169 **4. Association between other molecular mechanisms and (p)ppGpp in persistence**

170 According to Trastoy and colleagues (7), some of the molecular mechanisms that have been
171 related to bacterial persistence are TA systems, QS and secretion systems, efflux pumps, SOS
172 system and ROS response (Figure 2A). We focus only on those where a link between (p)ppGpp
173 or SR and persistence has been reported: TA systems, efflux pumps and ROS systems (Figure
174 2B):

175 4.1 TA systems

176 The persistent state actually describes many different growth-arrested physiologies and it has
177 been associated, during years, with the activity of TA systems, at least partially (54, 55). TA
178 systems are a module of two genes encoding a stable toxin and a usually unstable antitoxin
179 which is degraded under stress conditions; however, bound antitoxin to toxin is not likely the
180 source of free toxin since the two proteins are bound tightly (56) (Figure 2A and B). Once
181 unbound toxin is produced, the harmful toxin slows growth, maintains plasmids (57), inhibits
182 phage (58) and induces biofilm formation (59, 60). TA systems are widely distributed in
183 pathogenic bacteria and found in the bacterial chromosome, plasmids and bacteriophages (61,
184 62).

185 In 1983, Moyed and Bertrand identified the first persistence gene related to increased survival
186 in presence of ampicillin in *E. coli* (63). They discovered a high persistence, gain of function
187 mutation, named *hipA7*; *hipA* encodes the toxin of the HipA/HipB TA system. Similarly, the
188 second link between TA systems and persistence was reported by Aizenman and colleagues in
189 1996, when they observed that (p)ppGpp was required to activate MazF toxicity, the toxin of
190 the MazF/MazE TA system (64). In 2003, Korch and colleagues studied the role of HipAB TA
191 system in persistence, showing that the ability of *E. coli* to survive to a prolonged exposure to
192 penicillin was due to two mutations in the non-toxic *hipA7* allele (65). Both mutations, G22S
193 and D291A, were required for the full range of phenotypes associated with high persistence,

194 increasing 1,000- to 10,000-fold the frequency of persisters. Moreover, in this study they also
195 demonstrated that *relA* knockouts diminished the high persistent phenotype in *hipA7* mutants,
196 and that *relA spoT* knockouts completely eliminated this high persistence, suggesting that
197 *hipA7* facilitates the establishment of the persistent state by inducing (p)ppGpp synthesis (65).
198 This result was confirmed in 2011 by Nguyen and colleagues in *P. aeruginosa*, where a *relA*
199 *spot* double mutant led to a decrease of 68-fold in persistence (45). Interestingly, Correia and
200 colleagues demonstrated that HipA exhibits a eukaryotic serine-threonine kinase activity,
201 required for both the inhibition of cell growth and the stimulation of persister cells (66). In
202 2009, Schumacher and colleagues suggested that HipA inhibited cell growth by the
203 phosphorylation of the essential Elongation Factor Tu (EF-Tu), involved in translation (67).
204 Notwithstanding, in 2013, Germain and colleagues challenged the previous model in which
205 HipA inactivated translation by the phosphorylation of the EF-Tu, and proposed a novel
206 paradigm in which HipA inactivates the glutamyl-tRNA-synthetase (GltX) by phosphorylation of
207 the conserved Ser²³⁹ near the active center (68). In addition, the authors claimed that this
208 phosphorylation inhibited aminoacylation, which halts translation and induces the SR by the
209 generation of “hungry” codons at the ribosomal A site. Thus, RelA binds to the ribosome, is
210 activated, and increases (p)ppGpp levels that inhibit translation, transcription, replication and
211 cell-wall synthesis, thereby leading to slow growth, multidrug tolerance, and persistence
212 (Figure 1) (47, 68-70).

213 In this context, further studies have been conducted to unravel the association of TA systems
214 and (p)ppGpp in persistence. In 2012, Gerdes and Maisonneuve reported that the removal of
215 10 mRNAse-encoding TA loci of *E. coli* led to a dramatic decrease of persistence in the
216 presence of the antibiotic (71). A similar phenomenon was observed with a mutant lacking Lon
217 protease, which indicated that TA systems and Lon protease were somehow correlated and
218 both implicated in the persistence of *E. coli* (72). Since many antitoxins of *E. coli* were
219 degraded by Lon protease, Gerdes and Maisonneuve hypothesized that HipB was one of the
220 targets. In *E. coli*, Lon can be activated by polyphosphate (PolyP), synthesized by
221 polyphosphate kinase (PPK) and degraded by an exopolyphosphatase (PPX). PPX is inhibited by
222 (p)ppGpp, which leads to an increase in PolyP. Hence, these authors claimed that high levels of
223 (p)ppGpp associated with persistence inhibited PPX, thus allowing PolyP to activate Lon
224 protease, which would degrade the HipB antitoxin. Furthermore, they suggested that PolyP
225 functions as an intracellular signaling molecule controlled by the SR, and (p)ppGpp reprograms
226 the cells to survive starvation. (71). In 2014, these authors completed this model by adding one
227 additional step, which is a speculative positive-feedback loop that ensures even more synthesis
228 of (p)ppGpp (42). Thus, the model predicts that the degradation of HipB enables free HipA to

229 phosphorylate GltX and inhibits charging of tRNA-glu. When uncharged tRNAs enter the
230 ribosomal A site, RelA-dependent synthesis of (p)ppGpp is triggered (Table 1 and Figure 1)
231 (42). Even though this model became very influential, the authors retracted the key articles in
232 2018, claiming that the apparent inhibition of persistence in the multiple-deletion strain was
233 due to an inadvertent lysogenisation with the bacteriophage Φ 80, a contaminant that caused
234 artefacts in their experiments (73). In addition, there were conflicting reports for the
235 (p)ppGpp/PolyP/Lon persistence model, such as that Lon protease is not activated but
236 deactivated by PolP (74), or not required for persistence (Table 1 and Figure 2B) (75).
237 In 2019, Pontes and Groisman studied the implication of TA modules and (p)ppGpp in the
238 persistence of *Salmonella* and they revealed that low cytoplasmic Mg^{2+} induced tolerance to
239 antibiotics independently of (p)ppGpp and TA modules (Table 1) (49). In fact, a *relA spoT*
240 double mutant of *Salmonella*, unable to produce (p)ppGpp, exhibited similar tolerance to
241 antibiotics after growing in low Mg^{2+} than the wild-type strain. The same phenomenon
242 occurred with the mutant strain lacking 12 TA systems (Δ 12TA). However, when the antibiotic
243 treatment was added at neutral pH, they saw five- to eightfold fewer persisters compared to
244 WT both in the Δ 12TA strain and in double mutant *relA spoT* (49). Nonetheless, when they
245 deleted one single TA module found that this mutation had no effect in persistence (49)
246 (Figure 2B).
247 Recently, Song and Wood (2020), claimed that TA systems were not involved in the formation
248 of persistent bacteria (76). The many contradictory observations in diverse experimental
249 setups lead to no clear conclusive understanding of the implications of TA systems in
250 persistence and further work is needed.

251 4.2 Efflux Pumps

252 Efflux pumps are proteic complexes that allow bacteria to draw out intracellular toxins or
253 antibiotic molecules. Some genes encoding efflux pumps are upregulated in cells that
254 constitute biofilms, which are composed mainly by non-growing, persistent cells (77). This
255 upregulation in persister cells can be triggered by different signals, such as ROS response, QS
256 and (p)ppGpp (78).

257 The first data that linked SR with efflux pumps were reported by Wang and colleagues, who
258 observed that a *ppx2* (encoding the exopolyphosphatase that degrades poly(P)) knockout
259 mutant of *M. tuberculosis* (where poly(P) and (p)ppGpp accumulate) exhibited increased levels
260 of several efflux genes, including *iniA*, *iniB*, *mmpL10* and *Rv2459* (Figure 2B). Notwithstanding,
261 the authors concluded that the element which contributed the most to isoniazid tolerance in
262 this mutant was the changes in the cell wall thickness, as they limited the diffusion of polar
263 molecules such as isoniazid (79).

264 Some years later, in 2018, Ge and colleagues described that a glucose/galactose transporter of
265 *H. pylori*, Hp1174, functions as an efflux pump and is highly expressed in biofilm-forming and
266 MDR *H. pylori* strains. This transporter, encoded by the *gluP* gene, is upregulated by SpoT (78).
267 A *H. pylori* mutant lacking *gluP* gene and its product Hp1174 constituted an unstructured
268 biofilm whose matrix was damaged. As this study revealed that SpoT enzyme upregulates
269 Hp1174 in persistent biofilm-forming cells, and provided that the transcription of this gene is
270 controlled by an alternative sigma factor (σ^{54}), they hypothesized that SpoT may upregulate
271 the expression of *gluP* by a σ^{54} -dependent transcription.

272 Finally, Pu and colleagues demonstrated that β -lactam-induced *E. coli* persisters exhibited less
273 cytoplasmic drug accumulation because of an enhanced efflux activity compared to non-
274 persister cells. Combining time-lapse imaging and mutagenesis techniques, scientists
275 determined a positive correlation between *tolC* expression and arising of *E. coli* persisters (80).

276 4.3 ROS response

277 The reactive oxygen species (ROS) are produced as a natural response to the normal
278 metabolism of the oxygen and perform important functions in cell signaling and homeostasis.
279 However, when cells are exposed to environmental pressure, such as antibiotics, UV, or heat
280 pressure, ROS levels can increase; this increase can cause damages in the DNA, lipids and
281 proteins, which subsequently leads to cell death. Like all molecular mechanisms, ROS are
282 subject to regulation (Figure 2B). Among the molecules capable of eliminating ROS, we find
283 enzymes, such as superoxide dismutase (SOD) and catalase, as well as antioxidant agents, such
284 as glutathione and vitamin C. However, when an increase in ROS levels occurs due to an
285 imbalance between the production and elimination mechanisms, cells are said to be subject to
286 oxidative stress (7).

287 The relationship between ROS response and persistent bacteria are widely described in the
288 literature. Nguyen and colleagues, in 2011, showed that the survival of multidrug-tolerant
289 persisters in biofilms of *P. aeruginosa* was largely dependent on catalase or SOD enzymes,
290 which are under the control of the (p)ppGpp signaling (45). Along the same lines, the study of
291 Khakimova and colleagues (2013) demonstrated that the SR regulates catalases, likely through
292 a complex interplay of regulators (81) (Figure 2A and B). Furthermore, they also demonstrated
293 that H₂O₂ and antibiotic tolerance were the result of a balance between prooxidant stress and
294 antioxidant stress (81). Similarly, the work of Molina-Quiroz and colleagues (2018), gave more
295 evidence of the relationship between oxidative stress and bacterial survival to antibiotics. In
296 this study, the authors demonstrated the impact of ROS on the generation of persister cells,
297 exposing the cultures of a WT strain and its corresponding mutant lacking the cAMP synthase
298 adenylate cyclase (Δ *cyaA*) under the antibiotic pressure of ampicillin in the presence and

299 absence of oxygen. For both strains, they observed a 100-fold increase of ampicillin survival in
300 absence of oxygen compared to the strain under aerobic conditions. This study concludes that
301 the damage that ROS cause in the DNA was regulated by cAMP, a negative regulator of
302 persistence in uropathogenic *E. coli* (82).

303 **5. PRDP: (p)ppGpp ribosome dimerization persister model**

304 Song and Wood, proposed a novel model in which the alarmone (p)ppGpp would generate
305 persister cells by inactivating ribosomes via the Rmf and the hibernation promoting factor
306 (Hpf) (Figure 1 and 2B, Table 1) (83). Among their findings, the following should be highlighted:
307 (i) *E. coli* persisters contain a large fraction of inactivated 100S ribosomes; (ii) Rmf and Hpf
308 induced persistence, and the inactivation of these proteins increased the single cell persister
309 resuscitation, and (iii) (p)ppGpp did not affect the single-cell persister resuscitation. In another
310 work it was reported that (p)ppGpp induced the Hpf, converting the 90S ribosomes into 100S
311 ribosomes, and that overproduction of Rmf and Hpf increased persistence as well as reduced
312 single cell resuscitation (84). Furthermore, authors based their theory on the fact that
313 (p)ppGpp inhibits the ribosome-associated GTPase Era, essential in the assembling of
314 ribosomal 30S subunits in *Staphylococcus aureus* (85). Hence, a connection between (p)ppGpp
315 and persistence via ribosome dimerization was demonstrated.

316 In 2019, Libby and colleagues showed that there was an enormous variability in *sasA*
317 expression (the gene encoding SasA in *B. subtilis*) among bacterial cells, linking a higher
318 expression of *sasA* with an increase in antibiotic survival (86). (p)ppGpp synthetases in *B.*
319 *subtilis*, such as SasA, are important in ribosome dimerization, as YwaC induces the
320 transcription of *yvyD* gene, whose product, YvyD protein, is essential for the dimerization of
321 70S ribosomes (87). 70S dimers are similar to the above-mentioned 100S ribosomes in *E. coli*,
322 therefore translationally inactive. These results agree with the PRDP model, where (p)ppGpp
323 would induce bacterial persistence by promoting ribosome dimerization and compromising the
324 translation inside the cells (83).

325 **6. Anti-persisters treatments with (p)ppGpp as a target**

326 Most antibiotics used in clinics target active metabolic processes. Therefore, bacteria that
327 exhibit a reduction in metabolism and growth rate, such as tolerant or persistent cells, are not
328 a target for the classic antibiotics. In the literature, a few reviews summarizing some of the
329 most useful strategies to combat persistent infectious diseases can be found (2, 88, 89).

330 As the activation of the SR leads to the shutdown of nearly all metabolic processes and the
331 entrance into a state of dormancy, an interesting therapeutic approach to combat persistent
332 infections is the inhibition of the SR network. Hobbs and Boranson (2019) reviewed the recent
333 attempts that have been made to design and discover inhibitors of the SR, and they concluded

334 that there are currently two approaches: (i) inhibition of (p)ppGpp synthetases by using
335 (p)ppGpp analogs and (ii) inhibition of (p)ppGpp accumulation by using protein inhibitors (90).

336 i. Inhibition of (p)ppGpp synthetases by using (p)ppGpp analogs

337 Several *in vitro* studies using double *relA spoT* null mutants in *E. coli* have shown that this
338 bacterium lacks the (p)ppGpp and therefore has significantly reduced persistence to
339 antibiotics. In this context, some compounds that inhibit the (p)ppGpp production (thus SR),
340 had been developed to abolish persistence. Relacin, one of these compounds, was first
341 designed in 2012 by Wexselblatt and colleagues, and was shown to inhibit Rel-mediated
342 (p)ppGpp synthesis, leading to the death of *B. subtilis* with an estimated IC₅₀ of 200 μM (Table
343 2) (91). Importantly, relacin also prevented the formation of spores and biofilm in this species.
344 Before bacterial death, relacin also induced a prolonged exponential phase. In 2017, Syal and
345 colleagues performed a slight modification of relacin and found that cells of *Mycobacterium*
346 *smegmatis* treated with this molecule were not able to establish any biofilm and were
347 elongated, showing exactly the same phenotype as a *relF* mutant (92). Interestingly, this
348 relacin-derived compound lacked toxicity with human red blood cells and has good
349 permeability into the human lung epithelial cells. One of the most persistent pathogens, *M.*
350 *tuberculosis*, could be potentially targeted with this (p)ppGpp inhibitor if its evaluation in
351 humans turns to be effective and safe (Table 2).

352 In order to find other inhibitors of Rel protein, Dutta and colleagues (2019) performed a high-
353 throughput screening approach, using Rel from *M. tuberculosis* and a novel (p)ppGpp
354 synthetase assay, based on detection of AMP released after Rel catalyzes the transfer of
355 pyrophosphate groups from ATP to GTP/GDP (93). This screening led to the identification of
356 the most potent Rel inhibitor to date, the compound X9, which exhibited an IC₅₀ of ~15 μM
357 against purified Rel. At 4 μM, when *M. tuberculosis* was nutrient-starved, it enhanced its
358 susceptibility against isoniazid (Table 2). Even if the molecular mechanism by which X9 inhibits
359 Rel is not fully understood yet, this compound displays the most potent activity of any Rel
360 inhibitor to date.

361 ii. Inhibition of (p)ppGpp accumulation

362 A second approach to design anti-persistence strategies that target (p)ppGpp would be the
363 inhibition of the accumulation of this alarmone. Biofilms are very important in the
364 establishment and maintenance of many infections caused by pathogenic bacteria, therefore
365 some cationic peptides with anti-biofilm abilities have been tested and proposed to act via
366 disruption of the SR (11, 90).

367 The 1018 peptide (VRLIVAVRIWRR-NH₂) is a small, synthetic, L-amino acid peptide derived
368 from a bovine host defense peptide. De la Fuente and colleagues (2014) first described that

369 1018 marks (p)ppGpp for degradation, exhibiting potent activity against biofilms produced by
370 Gram-positive (*S. aureus*) and Gram-negative bacteria (*E. coli*, *P. aeruginosa*, *K. pneumoniae* or
371 *A. baumannii*), but not in planktonic cultures (94). They also observed that the 1018 peptide
372 prevented the biofilm formation and degraded the pre-formed biofilm (as old as 2 days). As an
373 overproduction of (p)ppGpp leads to resistance to the 1018 peptide, the authors suggested
374 that this peptide specifically targeted SR (Table 2). The same research group generated
375 another small peptide, called 1037, and observed its effects on biofilm formation and
376 swarming motility in *P. aeruginosa*, *Burkholderia cenocepacia* and Gram-positive *Listeria*
377 *monocytogenes* (Table 2) (95). They observed that 1037 reduced flagella-dependent swimming
378 in *P. aeruginosa* PA14, *P. aeruginosa* PAO1, and *B. cenocepacia*; consistently, transcriptomic
379 analysis revealed that, in the presence of 1037, several genes related to flagella were
380 downregulated by 2- to 3-fold. This is interesting because flagella are involved in biofilm
381 formation and swarming motility, both significantly inhibited by the action of 1037 in the
382 tested species (95).

383 Notwithstanding, the study of Andresen and colleagues in 2016 rejected the idea that 1018
384 peptide specifically targets the SR alarmone (p)ppGpp (96). Furthermore, they observed that in
385 *P. aeruginosa* this peptide showed anti-bacterial activity both in planktonic and in biofilm-
386 derived cells.

387 Interestingly, Allison and colleagues published an innovative article in 2011 where they killed *E.*
388 *coli* and *S. aureus* persisters combining different metabolites with aminoglycosides (97). They
389 reported that glucose, pyruvate, mannitol or fructose significantly increased the PMF; this
390 leads to a higher uptake of the aminoglycoside and the consequent killing of the persisters,
391 either in vitro and in a mouse model carrying a catheter colonized by uropathogenic *E. coli*. In
392 conclusion, these findings mean that some of these PMF-stimulating metabolites might be a
393 good adjuvant to aminoglycoside to treat persistent, chronic infections (97).

394 **7. Discussion**

395 We have summarized the functions of (p)ppGpp regarding its role as a global transcription and
396 translation regulator of metabolism, slow growth and dormancy, nutrient starvation, different
397 kinds of stress, virulence, tolerance to antibiotics, persister cell formation and even persistence
398 inside macrophages. However, an accurate role of this alarmone in persistence has not been
399 determined yet. Clearly, evidence relates this molecule to the persistent phenotype, based on
400 its dominant role in the stress response of bacteria.

401 The diversity among the conclusions obtained by laboratories around the globe raised the
402 question of whether persisters in phylogenetically close organisms are produced through
403 different pathways (49, 98). Nevertheless, this seems unlikely as the SR is a universal, highly

404 conserved network in many phyla, and all microbes use it to protect themselves against
405 different types of stress.

406 The relevance of the role of the ATP in the antibiotic persistence is revealed as tolerant cells
407 slow down their metabolism and persistent cells are quiescent. Pontes and Groisman (2019)
408 showed that *Salmonella* pre-exposed to chloramphenicol resisted the killing by bactericidal
409 antibiotics (49). However, contradictory results have been obtained from different groups
410 indicating that ATP does not control persistence (49, 99, 100), or even that persister cell
411 formation is based on reducing ATP (101-104).

412 The results of Pontes and Groisman (2019) (49), agree with the findings of both Hobby (105)
413 and Bigger (106) and with many other researchers who have shown that deliberate induction
414 of bacteriostasis promotes antibiotic tolerance (15). Whereas deliberate induction of
415 bacteriostasis overrides bacterial control of growth, it remains to be explored what
416 mechanisms promote growth arrest in individual cells. They showed that *Salmonella* persists
417 emerged as a result of slow growth alone and transitory disturbances to core activities,
418 regardless of the underlying physiological process. They also performed studies with
419 *Salmonella* mutants lacking 12 TA modules and observed their implication in persistence in
420 some conditions (49). Kaldalu and colleagues (2019) claimed that there was no specific
421 molecular mechanism involved in persistence but this latter was simply produced by slow
422 growth of bacteria (50).

423 It remains unclear if efflux pumps and the SOS-system have a real link with (p)ppGpp. Despite
424 being important molecular mechanisms widely studied in pathogenic bacteria, there is still few
425 literature linking (p)ppGpp metabolism with these mechanisms, and it is even trickier the
426 association of these to persistence; a proof of that is the article of Ge and colleagues, where
427 they claim that bifunctional SpoT enzyme up-regulates the Hp1174 efflux pump of *H. pylori*,
428 contributing to biofilm formation (78). Regarding the role of ROS-system in persistence,
429 different research groups have demonstrated that (p)ppGpp and the SR regulate the
430 expression of antioxidant enzymes, e.g SOD or catalases, in order to avoid the intracellular
431 accumulation of ROS (82). Even if the intermediate regulators involved in this pathway need
432 further research, this opens the door to anti-persister therapies targeting SR (45, 81).

433 Traditionally, the persistence of the bacteria has been widely attributed to TA systems, as
434 Chowdhury and colleagues published in 2016, where they claimed that persister cells can form
435 in the absence of (p)ppGpp (although at much-reduced levels), mainly due to the effect of
436 production of any toxic protein (75). Nevertheless, Dr T. K. Wood, reported some years later an
437 essential role of (p)ppGpp in the establishment of persistence via induction of dimerization of

438 ribosomes. In this new model, called PRDP and proposed by Song and colleagues in 2020,
439 there is evidence of a direct role of the magic spot in the persistent phenotype (83).

440 An interesting issue is the individual variability within a population of cells regarding their
441 tolerance to antibiotics. Whether this heterogeneity is regulated or, on the contrary, is an
442 unavoidable consequence of stochastic fluctuations, remains unknown. In 2004, Balaban and
443 colleagues showed that spontaneous persisters are rare, suggesting that they were not
444 stochastically produced (3). Similarly, the PRDP model also suggests that both persistence and
445 resuscitation are sophisticatedly-regulated by ribosome content and their activation status
446 (83). Finally, another hint of the regulation of SR was proposed by Libby and colleagues (2019),
447 based on the fact that SasA in *B. subtilis* has multiple sites of phosphorylation, which can
448 explain the cell-to-cell variability in *sasA* expression (86, 87). These differences may be the
449 reason for the physiologically relevant variability in (p)ppGpp levels and shed some light into
450 the heterogeneity within a bacterial population and their phenotypic variability.

451 There are some arguments in favor of the PRDP model: one is that Hpf, which converts 90S
452 ribosomes into inactivated 100S ribosomes in *E. coli*, is highly conserved in most bacteria (84);
453 secondly, other (p)ppGpp synthetases found in *B. subtilis* are essential for ribosome
454 dimerization in Gram-positive bacteria, generating translationally inactive ribosomes
455 associated with persistence (87).

456 In this review we have contrasted different models that have been proposed over many years
457 all of them aiming at answering the same question: what is the precise role of (p)ppGpp and SR
458 in bacterial persistence? Definitely, after comparing all those models we can conclude that
459 uncontrolled variables such as contaminants
460 (as $\Phi 80$ phage), particular setups that differ from lab to lab, artifacts that mislead to
461 conclusions, changes in the tested strains and, in short, different experimental conditions can
462 be some of the underlying reasons to explain the controversy around this question.

463 The current lack of effective antibiotics against multi-drug resistant, persister and tolerant
464 pathogens leads the urgency to develop new antibacterial treatments, as the anti-persistent
465 treatments targeting the (p)ppGpp network. The inhibitors of (p)ppGpp synthetases are good
466 candidates as antimicrobial agents, because of their high efficacy in avoiding biofilm formation
467 (91), in the loss of the persistent phenotype and even in the prolongation of exponential
468 phase, when bacteria replicate more actively, being more susceptible to antibiotics. This also
469 opens the door to the possibility of a combination of therapies (inhibitors of (p)ppGpp
470 synthetase with antibiotics) and to the establishment of potential synergies. Even if no effect
471 of the Rel inhibitor relacin was observed in *E. coli*, the authors suggested that this could be due
472 to the inability of relacin to penetrate Gram negative cells and reach its target. However,

473 agents as polymyxins can destabilize the outer membrane in Gram negatives facilitating the
474 entrance of therapeutic molecules, e. g., relacin, or endolysins (108). The absence of known
475 (p)ppGpp synthetases in mammalian cells and the specificity of these inhibitors for the Rel
476 protein, make this protein a good candidate as an antibacterial agent.

477 The second strategy of inhibition of (p)ppGpp accumulation, supported by the 1018 and 1037
478 peptides, exhibited promising anti-persistent activities as they specifically targeted biofilm-
479 forming cells and had no effect on planktonic cells (94, 95). According to the few studies that
480 focus on inhibiting the SR as an anti-persistent therapeutic approach, we can consider this as
481 an emerging field; therefore, further research and financial investment are needed to
482 efficiently prevent persistent, chronic and life-threatening infections.

483 **8. Conclusion**

484 The emergence of contradictory models about the involvement of the “magic spot” in bacterial
485 persistence highlights the need to deepen the studies in this field. In summary, one potential
486 strategy to fight persistent infectious disease resides in specifically targeting SR or (p)ppGpp of
487 pathogenic bacteria, but further knowledge is necessary to provide a better understanding of
488 the complexity of bacterial persistence, as well as its implications in clinics.

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508 **Legends**509 **Figure 1.** Physiological pathways regulated by (p)ppGpp and the stringent response in *E. coli*.

510 Some of the most common human opportunistic pathogens are represented, such as
511 biofilm-forming *P. aeruginosa*, intestinal *E. coli* and skin-borne opportunistic pathogen
512 *S. aureus*. Focusing on *E. coli*: 1) increased levels of (p)ppGpp induce transcription of
513 RpoS, sigma factor for the stationary phase, and RpoE, the sigma factor that regulates
514 the expression of genes related to misfolded proteins; 2) (p)ppGpp inhibits DNA
515 primase thus the replication of the chromosome; 3) (p)ppGpp also inhibits
516 transcription of rRNA, affecting the general translation; 4) (p)ppGpp also deregulates
517 LpxC, an enzyme catalyzing the first step of LPS formation; 5) (p)ppGpp binds to RNAP
518 (RNA polymerase) regulating the transcription of many genes; 6) according to certain
519 models, HipA toxin would phosphorylate glutamyl-tRNA-synthetase (GltX), inactivating
520 it and therefore impairing aminoacylation. Empty tRNAs then trigger the stringent
521 response: RelA associates to ribosome and synthesizes (p)ppGpp from GTP/GDP + ATP;
522 7) (p)ppGpp can directly inhibit negative supercoiling of DNA in *E. coli*, associated with
523 resistance to quinolones; 8) (p)ppGpp induces the transcription of the ribosome
524 modulating factor (Rmf) and hibernation promoting factor (Hpf), which play a role in
525 ribosome dimerization, typical from persister cells. (p)ppGpp is also involved in
526 immune evasion, virulence and human pathogenesis.

527 **Figure 2. A.** Molecular mechanisms underlying bacterial persistence. **B.** Different models
528 explaining the involvement of (p)ppGpp in persistence and representative
529 publications.

530 **Table 1.** Summary of the main ppGpp models.531 **Table 2.** Summary of the main treatments having ppGpp as a target.

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541 **Acknowledgements**

542 This study was funded by grant PI16/01163 and PI19/00878 awarded to M. Tomás within the
543 State Plan for R+D+I 2013-2016 (National Plan for Scientific Research, Technological
544 Development and Innovation 2008-2011) and co-financed by the ISCIII-Deputy General
545 Directorate for Evaluation and Promotion of Research - European Regional Development Fund
546 "A way of Making Europe" and Instituto de Salud Carlos III FEDER, Spanish Network for the
547 Research in Infectious Diseases (REIPI, RD16/0016/0006 and RD16/0016/0011) and by the
548 Study Group on Mechanisms of Action and Resistance to Antimicrobials, GEMARA (SEIMC,
549 <http://www.seimc.org/>). M.Tomás was financially supported by the Miguel Servet Research
550 Programme (SERGAS and ISCIII). Fernández-García postdoctoral fellowship from the
551 Diputation A Coruña (Xunta Galicia). TJK is supported by a National Health and Medical
552 Research Council Early Career Fellowship (GNT1088448).

553 **AUTHOR CONTRIBUTIONS**

554 O.P., L.B., I.B., L.F-G., A.A., M.L., wrote the manuscript; G.B., R.C., R.G-C., T.K.W., M.T.,
555 supervised and revised the manuscript.

556 **TRANSPARENCY DECLARATIONS**

557 All authors declare no conflict of interest

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Year	Journal	Author	Model	References
2014	Cell	Maisonneuve E. and Gerdes K.	(p)ppGpp induces persistence by activating TA loci via PolyP and Lon protease in <i>E. coli</i> K-12 strain MG1655.	(42, 71-73)* (3, 65, 109)
2016	Scientific Reports	Chowdhury N., Kwan B.W, and Wood T.K.	The formation of persister cells in <i>E. coli</i> K-12 strain MG1655 is attributed to production of any toxic protein (e.g., MazF, RelB and YafO) and (p)ppGpp is not essential but increases persistence by 1000X.	(75)
2019	Science Signalling	Pontes M.H. and Groisemann E.A.	Low cytoplasmic Mg ²⁺ induces <i>S. typhimurium</i> tolerance to antibiotic independently of (p)ppGpp and TA modules. However, (p)ppGpp reduces antibiotic tolerance under certain conditions.	(49)
2020	Biochemical and Biophysical Research Communication	Song S. and Wood T.K.	(p)ppGpp generates persister cells directly by inactivation of ribosomes via Rmf and Hpf.	(83)

Table 1.

Rmf: ribosome modulation factor, Hpf: hibernation promoting factor. *Some of these publications have been retracted due to the contamination with the Φ 80 bacteriophage causing artefacts in the results

Year	Author	Strategy	Mechanism of action	References
2012	Wexselblatt and colleagues	(p)ppGpp analogs inhibit Rel protein: relacin	Relacin produced death of <i>B. subtilis</i> with an IC_{50} =200 μ M, prevention of sporulation and biofilm formation and induction of a prolonged exponential phase.	(91)
2012	De la Fuente-Núñez and colleagues	Inhibition of (p)ppGpp accumulation: 1037 peptide	1037 reduced expression of flagella-associated genes that favorize biofilm establishment in <i>P. aeruginosa</i> and <i>B. cenocepacia</i> . It also reduced the swarming motility.	(95)
2014	De la Fuente-Núñez and colleagues	Inhibition of (p)ppGpp accumulation: 1018 peptide	1018 marked (p)ppGpp for degradation*: broad anti-biofilm activity against Gram positive and negative bacteria and lack of effect for planktonic cultures.	(94)
2017	Syal and colleagues	(p)ppGpp analog to inhibit Rel protein: modification of relacin	Impairing of biofilm formation by <i>M. smegmatis</i> and arising of elongated cells. Lack of toxicity, good permeability to human lung epithelial cells.	(92)
2019	Dutta and colleagues	(p)ppGpp analog to inhibit Rel protein: compound X9	Highest inhibitory activity against Rel protein: IC_{50} of \sim 15 μ M against purified Rel of <i>M. tuberculosis</i> . Enhancement of susceptibility against isoniazid.	(93)

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Table 2.

864 *Andresen and colleagues rejected this hypothesis two years later, questioning its specificity for (p)ppGpp and for biofilm-forming cells (96).

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