

1 Manuscript No: WR63860R2

2 **Making waves: How does the emergence of antimicrobial resistance affect**
3 **policymaking?**

4 Ana Carolina Maganha de Almeida Kumlien^{1,2}, Edgar González-Villalobos^{1,2}, José L.
5 Balcázar^{1,2*}

6 ¹Catalan Institute for Water Research (ICRA), 17003 Girona, Spain

7 ²University of Girona, 17004 Girona, Spain

8 *Correspondence: jlbacazar@icra.cat (José L. Balcázar)

9

10 **Abstract**

11 This article considers current trends in antimicrobial resistance (AMR) research and
12 knowledge gaps relevant to policymaking in the water sector. Specifically, biological
13 indicators of AMR (antibiotic-resistant bacteria and their resistance genes) and detection
14 methods that have been used so far are identified and discussed, as well as the problems
15 with and solutions to the collection of AMR data, sewage surveillance lessons from the
16 COVID-19 pandemic, and the financial burden caused by AMR, which could be
17 synergically used to improve advocacy on AMR issues in the water sector. Finally, this
18 article proposes solutions to overcoming existing hurdles and shortening the time it will
19 take to have an impact on policymaking and regulation in the sector.

20

21 **Keywords**

22 AMR surveillance, microbial indicators, precautionary approach, regulation, water sector

23

24 **1. Introduction**

25 Antimicrobials and, specifically, antibiotics have become one of the main pillars of
26 modern medicine, saving millions of lives since they were first introduced in the 1940s.
27 Antibiotics are essential in treating bacterial infections in both humans and animals, but
28 the emergence of antimicrobial resistance (AMR) has limited their effectiveness (Nathan,
29 2020). As a result, governments, industry, and scientists are adamant the AMR crisis is
30 one of the most pressing global threats. Several initiatives are in place to deal with this,
31 mainly in clinical and environmental settings. In clinical settings, the focus has been on
32 surveillance, reducing the use of existing drugs, establishing incentives for the discovery
33 and production of new antibiotics, implementing global guidelines, and, when possible,
34 local regulations. In environmental settings, the focus has predominantly been on research
35 initiatives to monitor the presence and impact of antibiotics, decreasing antimicrobial
36 therapy in agriculture and livestock, determining minimal acceptable thresholds for
37 antibiotics in treated effluents, and exploring the potential role of wastewater treatment
38 to reduce antibiotics and AMR determinants in treated water (Hong et al., 2018; Stanton
39 et al., 2020; Murray et al., 2021). However, the ability to monitor how AMR spreads from
40 the environment to clinical settings is limited (Hofer, 2019) due to the lack of a single or
41 set of universal biological indicators that can establish the rate of AMR spread in
42 environmental settings and their potential risk to human health. The only short-term
43 solution repeatedly recommended is the precautionary approach (Manaia, 2017).

44 In this article the precautionary principle has been expanded with the following
45 objectives: (i) exploring how AMR surveillance has been implemented and data has been
46 generated in both clinical and water/environmental settings; (ii) discussing how biological
47 indicators related to AMR have been used in pilot surveillance efforts and how data has
48 been generated and shared; (iii) reflecting on sewage surveillance lessons from the

49 COVID-19 pandemic and how this could help better manage AMR in water; and (iv)
50 commenting on the financial burden of AMR and how this could be used to drive change
51 in policymaking. The aim of this article is therefore to highlight current knowledge gaps,
52 anticipate future trends, and suggest actionable insights to advance AMR regulation in
53 the water sector.

54

55 **2. AMR in the water sector**

56 Antimicrobial resistance is complex to define and quantify. Broadly speaking, AMR is
57 an intrinsic or acquired ability of microorganisms to resist an antimicrobial. In the latter
58 case, they can acquire resistance to antimicrobials by either genetic mutation or by
59 accepting AMR genes from other bacteria. In fact, AMR genes are considered as
60 environmental pollutants if anthropogenic disturbances increase their prevalence above
61 the usually occurring background levels (Martinez, 2009). Moreover, bacteria associated
62 with hospital acquired infections and their ability to resist antibiotic treatment are under
63 the spotlight in the AMR crisis (Chandler, 2019). AMR extends not only to antibiotics
64 but to a number of chemical classes, including heavy metals and disinfectants/biocides
65 (Singer et al., 2016).

66 The accepted framework for dealing with AMR is the “One Health” approach.
67 Fundamental to this is interdisciplinary collaboration and communication on health in the
68 human, animal, and environmental sectors. Areas of action include monitoring targets
69 known to decrease infectious risk, such as improving sanitation, providing access to clean
70 water, improving medical care, tackling environmental pollution, and managing the
71 overuse of antimicrobials in both human healthcare and animal husbandry (Essack, 2018;
72 Jovanovic et al., 2021).

73 As water bodies frequently receive treated and untreated wastewater effluents and
74 anthropogenic pollution, water is an ideal environment for the acquisition and spread of
75 AMR. In fact, this impact can be exacerbated in developing countries where the presence
76 of wastewater treatment is limited or even absent (Pandit and Kumar, 2015; Pandey et al.,
77 2021). Consequently, the “One Water” approach has been suggested to complement the
78 One Health framework in order to monitor and manage AMR in the water sector. The
79 One Water approach proposes that drinking and wastewater are interconnected and need
80 to be managed holistically. Both the One Health and the One Water frameworks guide us
81 to holistically manage wicked problems – such as global water supply, climate change,
82 and the AMR crisis – while considering the environment, and human and animal health
83 (Shafer and Fox, 2016; Hong et al., 2018). Moreover, considering that the United Nations
84 Sustainable Development Goals (SDGs) will be the point of reference for any strategy or
85 policy towards a more sustainable future, those goals relating to water and sanitation
86 should be taken into account in formulating effective policies. The SDGs include eight
87 targets that address drinking water, sanitation and hygiene services, wastewater treatment,
88 water quality, water use, water management, transboundary cooperation, water-related
89 ecosystems, official development assistance and participation of local communities
90 (WHO-UNICEF, 2021).

91

92 **3. Surveillance as a tool for AMR containment**

93 AMR cannot be eradicated either in clinical or environmental settings. The containment
94 of AMR, however, is possible (Jovanovic et al., 2021), and to achieve this the World
95 Health Organization (WHO) has highlighted that surveillance of AMR is essential. Data
96 acquired through surveillance can be used to monitor the development and spread of
97 AMR, and also to measure the impact of strategies and interventions to mitigate it (Smith

98 and Coast, 2002). Although the consensus that resistance development, rather than just
99 transmission, exists in environmental settings and is vital to AMR containment, this
100 precautionary topic has been extremely difficult to advocate and gain the attention of
101 policymakers (Wellcome Trust, 2020). In order to address this, several AMR databases
102 and data collection initiatives have been revisited to better connect the resulting data,
103 thereby generating new insights and influencing policymaking.

104

105 **4. Databases generated on AMR surveillance**

106 The major surveillance programs targeting AMR at global scale have placed emphasis on
107 monitoring of clinically relevant pathogens (such initiatives are listed below).
108 Surveillance of AMR emergence and spread in water/environmental settings has been
109 more consistently done in research at local level (Rodriguez-Mozaz et al., 2015; Majeed
110 et al., 2021), regional/continental monitoring campaigns (Cacace et al., 2019; Pärnänen
111 et al., 2019) or selected countries at global scale (Hendriksen et al., 2019), targeting
112 particular antimicrobial resistance ‘hotspots’, such as wastewater treatment plants
113 (Lekunberri et al., 2017), contaminated watersheds (Koczura et al., 2016),
114 soil/agricultural land (Singer et al., 2016), and seawater ecosystems (Blanco-Picazo et al.,
115 2020). Moreover, there is insufficient or no information from other countries or regions,
116 especially from low-income and middle-income countries where the AMR surveillance
117 in water is limited.

118 The global open-access triple antimicrobial resistance database led by the WHO, the Food
119 and Agriculture Administration (FAO) and the World Organisation for Animal Health
120 (OIE) provides access to information on the status of countries’ implementation of the
121 global action plan and actions to address antimicrobial resistance across all sectors. Data
122 collection here is based on a country self-assessment questionnaire, the *Global Database*

123 *for the Tripartite Antimicrobial Resistance AMR Country Self-assessment Survey*
124 (TrACSS) (<https://amrcountryprogress.org/>). A second database of interest is the Global
125 Antimicrobial Resistance Surveillance System (GLASS)
126 (<https://www.who.int/glass/en/>), which focuses on eight target pathogens detected in four
127 human specimen types (blood, urine, stool, and genital swabs)
128 (<https://www.who.int/glass/en/>). A third initiative, led by the US based Centre for Disease
129 Dynamics, Economics & Policy (CDDEP), put together a resistance map using data
130 collected from North America, more than 30 European countries, and several low and
131 medium-income countries (<https://resistancemap.cddep.org/>). This database monitors
132 resistance of principal pathogens versus various classes of antibiotics. Others include the
133 US Centers for Disease Control (CDC), which has its own database
134 (<https://arpsp.cdc.gov/profile/geography>) that maps various statistics on pathogens per
135 US state; and the European Centre for Disease Prevention and Control (ECDC), which
136 has a “surveillance atlas” on a country-by-country basis
137 (<https://www.ecdc.europa.eu/en/antimicrobial-resistance/surveillance-and-disease->
138 [data/data-ecdc](https://www.ecdc.europa.eu/en/antimicrobial-resistance/surveillance-and-disease-data/data-ecdc)). The most recent input date in the atlas is 2019. The ECDC is also focused
139 on producing surveillance reports for the continent. The Sweden based Joint
140 Programming Initiative on Antimicrobial Resistance (JPIAMR) – an international
141 collaborative platform engaging 28 nations and the European Commission to curb
142 antimicrobial resistance (AMR) – has various funding and project consortium initiatives
143 to fund AMR research globally and has gathered a collection of multipurpose databases
144 (<https://www.jpiamr.eu/>).

145 The recently formed Global AMR R&D Hub is a knowledge center focused on
146 monitoring R&D and investment initiatives to address challenges and improve
147 coordination and collaboration in global AMR research development using the One

148 Health approach. It is a partnership of countries, non-governmental, and
149 intergovernmental organizations (<https://globalamrhub.org/>). Other organizations include
150 PAR, The Foundation to Prevent Antibiotic Resistance (<https://parfoundation.org/>); the
151 industry consultancy-led AMR Insights (<https://www.amr-insights.eu/>); and the STAR-
152 IDAZ International Consortium on Animal Health (<https://www.star-idaz.net/>).

153 These various initiatives are encouraging; however, in order to fully extract and utilize
154 the value and meaning of their data, these databases need to be harmonized so that trends
155 can be truly observed, actions be taken, and overarching environmental AMR regulations
156 implemented (Aarestrup and Koopmans, 2016; WHO, 2015). Recently, it has been
157 suggested that data technologies, such as blockchain, IoT (Internet of Things) and others,
158 may help to achieve better management and use of AMR data globally ([https://www.amr-
160 insights.eu/](https://www.amr-
159 insights.eu/)). For that to occur, however, legal barriers impeding data sharing between
160 countries and organizations will need to be tackled at governmental levels.

161

162 **5. How far advanced are biological indicators for AMR in water?**

163 For implementing impactful surveillance of AMR in environmental settings, a standard
164 methodology should be selected, as well as a set of relevant biological indicators, to be
165 able to establish an economically feasible and long-term sustainable monitoring regime.
166 Although standard culture-based methods used to evaluate microbial safety of drinking
167 water and wastewater have provided valuable information (Marano et al., 2020), these
168 methods have limited applicability in AMR surveillance and are biased towards cultivable
169 organisms. AMR is mostly related to microorganisms harboring antibiotic resistance
170 genes (ARGs), for which the detection depends almost exclusively on molecular methods
171 (Gao and Sui, 2020).

172 Cutting-edge genomics (e.g., microarray technology) and metagenomics have been
173 proposed as a possible next step to achieve global monitoring of AMR in
174 water/environmental settings (Duarte et al., 2020; Hendriksen et al., 2019; Hong et al.,
175 2018). They have been successfully used in sewage surveillance and have proven to be
176 flexible, scalable, relatively easy to implement and standardize – features that could
177 potentially benefit also their application in low and medium-income countries (MacLean
178 and San Millan, 2019). However, these methods are not exempt from disadvantages and
179 limitations, such as how the complexity in sequence assembly and/or functional genes of
180 one microorganism cannot be fully linked to its phylogeny (Forbes et al., 2017; Cheng et
181 al., 2019). The joint use of standard culture-based methods and cutting-edge genomics
182 can therefore overcome these limitations. Trends observed using these methods need to
183 be correlated with observations in clinical settings so that insightful correlations can be
184 established between the emergence of antibiotic-resistant pathogens and ARGs
185 encountered in the environment.

186 Such evidence is essential to persuade both the public and policymakers of the urgent
187 need to act on AMR (Jovanovic et al., 2021). Specific examples that establish how the
188 spread of ARGs occurred from water/environmental sources to impact on clinical settings
189 are starting to emerge. These include the mobility of *bla*_{CTX-M} (gene encoding resistance
190 for β -lactamases responsible for inactivating third generation cephalosporins) (Cantón,
191 2009; Jovanovic et al., 2021), *mcr-1* (resistance to colistin or polymyxins), *bla*_{NDM-1}
192 (resistance to a large range of β -lactamases, including carbapenems) (Jovanovic et al.,
193 2021). The risk of the spread of ARGs from antibiotic-resistant bacteria to final
194 consumers has recently been established in animal farming settings (Van Gompel et al.,
195 2020).

196 Recommended approaches to determine biological indicators for AMR surveillance in
197 water include monitoring resistance in: (i) microorganisms watched by official lists
198 (WHO, UNESP, USCDC, ECDC, etc.) (Jovanovic et al., 2021); (ii) faecal and other
199 benchmark microbial indicators (such as bacteriophages) routinely monitored in drinking
200 and wastewater facilities (Larsson et al., 2018); (iii) clinical relevant antibiotic-resistant
201 bacteria; and (iv) the general presence of ARGs in the target water setting, also known as
202 evaluation of the environmental ‘resistome’.

203 While the correlations between the presence of these AMR ‘precautionary microbial
204 indicators’ and the risk they may pose of migrating from water to a clinical setting are
205 established, the precautionary approach can further inform improving water safety. In
206 established high risk environments for AMR spread, such as effluents of hospital and
207 antibiotic production facilities, wastewater treatment facilities need to be upgraded to
208 reduce pollution and to more effectively remove not only antibiotics and antimicrobials
209 but also AMR indicators such as resistant bacteria and ARGs (Hong et al., 2018). These
210 changes, however, are only likely to occur with enforcement of stronger water
211 regulations. Compliance here will depend upon the development and availability of fit-
212 for-purpose and economically viable water treatment technologies (de Almeida Kumlien
213 et al., 2021). An important case-study to help advance AMR regulations in water can be
214 drawn from the latest pandemic, our views on which are discussed below.

215

216 **6. Lessons from the COVID-19 pandemic**

217 The COVID-19 pandemic has quickly advanced our knowledge and practice of sewage
218 surveillance and epidemiology of SARS-CoV-2 studies in water, which has extensively
219 benefited from wastewater-based epidemiology. This latter is a relatively new approach
220 that has the potential to provide comprehensive health information using community-

221 derived wastewater (Sims and Kasprzyk-Hordern, 2020). In fact, the European
222 Commission has recently proposed recommendations for a common approach to establish
223 a systematic surveillance of SARS-CoV-2 and its variants in wastewaters in the EU
224 (European Commission, 2021), which would undoubtedly help to identify health-related
225 relevant parameters to be regularly monitored in wastewaters. These initiatives represent
226 an opportunity to implement their recommendations and advance AMR surveillance
227 (Wilson et al., 2020).

228 Even though a conclusive quantitative microbial risk assessment (QMRA) to influence
229 policymaking on AMR in water is needed given the threat AMR poses to public health,
230 the case for using the precautionary approach should be considered, particularly when
231 data is still not conclusive. Risks that cannot be calculated can be predicted, or at least
232 estimated, by deploying data analytics, scientific leadership, and knowledge and, within
233 local financial and technical limits, be corroborated on a pilot scale through multinational
234 projects. This, however, needs to happen through parallel taskforces that also focus on
235 driving changes in current water legislation.

236 Established networks and projects rapidly pivoted during the years 2020 and 2021, such
237 as the Dutch led ‘Sewers for COVID’ (<https://devpost.com/software/sewers4covid>) and
238 the Spanish ‘SARSAIGUA’ (<https://sarsaigua.icra.cat/>), and can be aligned with existing
239 AMR surveillance initiatives to speed up AMR surveillance and containment in the
240 environment (Singer et al., 2016). Using the precautionary approach, existing strategies
241 to determine AMR precautionary indicators, even though not definitive, could be used to
242 pilot more significant AMR surveillance schemes in water. One concrete way to drive
243 that change is to add such indicators to watchlists and, with more aggressive advocacy by
244 the right actors, to water regulations. Here, the ideal target monitoring sites would be

245 hospital and antibiotic facilities wastewaters, potentially regulated through changes in
246 overarching and enforcing law, such as the Water Framework Directive in Europe.
247 The question that should be asked at this point is: how can actionable insights be created
248 to influence policymaking with the data available now? For a vital issue such as AMR,
249 advocacy on the theme is both relevant and recommended. The important action is to
250 determine who are the actors at community, research, policymaking, and water utility
251 levels that need to be involved, both in arguing for the AMR cause and in driving change.
252 A way to bring these actor together is through smart specialization clusters, a
253 collaboration strategy mediated by governmental funding schemes, well known to speed
254 up innovation in the water sector (de Almeida Kumlien et al., 2019, 2018). Figure 1
255 illustrates a systematic process to develop policies that can address public health problems
256 such as AMR.

257

258 **7. Driving change in policymaking of AMR in water**

259 Similarly to the dispersion of data collected in various AMR surveillance efforts, the
260 current and future costs of the AMR crisis to countries are still only estimates. Apart from
261 realizing robust QMRA data, a fundamental factor to drive change in AMR policymaking
262 in water is by clearly demonstrating the financial losses caused by this crisis (Roope et
263 al., 2019). Although data here is still approximate, estimates show a difficult scenario on
264 the horizon for global economies. Recent estimates put the AMR cost globally at US\$100
265 trillion through loss of productivity. In the USA, (data from 2019) more than 2.8 million
266 multidrug-resistant bacterial infections occur annually, with an estimated 35,000 deaths
267 and a US\$20 billion health-care burden (Strathdee et al., 2020). In Europe, the annual
268 economic cost associated with the treatment of antibiotic-resistant infections has been
269 estimated to be around €1500 million. This figure includes the economic impact

270 associated with the number of days of lost productivity, estimated to be approximately
271 €450 million each year (Roca et al., 2015). AMR affects national budgets, mortality, and
272 related disability-adjusted life-years (DALYs). In the EU and European Economic Area
273 (EEA) its impact has been comparable to the combined effects of tuberculosis, influenza,
274 and HIV (Cassini et al., 2019).

275 Progress has been made in establishing methodologies to determine AMR costs. A
276 comprehensive framework for categorization of AMR costs, which evaluates human,
277 animal, and environmental factors, and its effects up through societal levels is “The
278 Global Antimicrobial Resistance Platform for ONE-Burden Estimates (GAP-ONE)”. This
279 initiative, funded under the JPIAMR, considers local direct and indirect epidemiological
280 costs and data, and is adaptable for a broad range of etiological pathogens and geographic
281 locations (Morel et al., 2020).

282 Recommendations by the WHO, or, in the absence of a central government that regulates
283 AMR stewardship, by other organizations which act locally, have shown slow progress.
284 Currently, only 5% of countries have a multisectoral AMR action plan that has been
285 implemented with identified funding sources and monitoring processes in place (O’Neill,
286 2016). Compliance, even when it is attained in some countries, might not be possible to
287 achieve due to lack of financial and human resources (Chandler, 2019; Roope et al.,
288 2019). The cost of implementing AMR governance is considerable, and most likely
289 unaffordable for developing nations. The cost of remediating the AMR crisis, however,
290 will be much higher.

291 The WHO has recently highlighted the need to develop new AMR regulations with global
292 reach (Hoffman et al., 2015). This could be achieved by revising the International Health
293 Regulations (IHR), developing a new treaty on pandemics, or a separate agreement on

294 AMR. Regardless of the path of action chosen, we need to seize chances to achieve new
295 regulations for AMR now.

296 Given this, scientific leadership is essential to advise policymakers on which are the best
297 control points and methodologies for implementing regulation of AMR in the water
298 sector. Among them, the following should be taken into consideration: (i) precautionary
299 indicators to achieve more effective surveillance of AMR in water/environmental
300 settings; (ii) harmonization and better accessibility of methodologies to detect AMR and
301 data generated; (iii) reflecting on lessons learnt from the pandemics, especially regarding
302 sewage surveillance schemes; and (iv) making the case on the financial impact of the
303 AMR crisis.

304 These points need to be advocated, aligned, and incorporated in a centralized enforcing
305 AMR regulation, pivoted by the right leadership (being at WHO or UN level), and only
306 achievable with stronger collaboration between AMR stakeholders, at
307 community/country, research, industry, water utility and policymaking levels.

308

309 **8. Conclusions**

- 310 • Polluted aquatic environments (e.g., wastewaters) present a potentially high risk
311 of the spread of AMR affecting public health and thus should be carefully
312 monitored.
- 313 • Scientific leadership needs to work with policymakers to advocate for immediate
314 water regulation based on precautionary microbial indicators and methodologies
315 to detect and evaluate the potential impact of AMR on human health.
- 316 • Harmonization of detection methodologies and indicators through the combined
317 participation of research institutions worldwide is crucial to reach these goals.

- 318 • The generation of new data, improvements in existing data communication,
319 accessibility, and harmonization between global AMR databases will help
320 generate insights into the impact of AMR from the water environment on human
321 health.
- 322 • Lessons on sewage surveillance learnt from the COVID-19 pandemic and the
323 estimated financial impact of the AMR crisis can help drive better advocacy for
324 new regulations in water.

325

326 **Acknowledgements**

327 “This project has received funding from the European Union’s Horizon 2020 research
328 and innovation programme under the Marie Skłodowska-Curie grant agreement No
329 792686”. This work was also supported by the Generalitat de Catalunya (ICRA-ENV
330 2017 SGR 1124) and by a New Lecturer Research Grant from the Society for Applied
331 Microbiology. EGV thanks the National Council for Science and Technology
332 (CONACYT, Mexico) for the postdoctoral fellowship (CVU no. 441304). The authors
333 are grateful for valuable contributions shared by Resistomap and AMR Insights, and
334 funding from the CERCA Program of the Catalan Government.

335

336 **References**

- 337 Aarestrup, F.M., Koopmans, M.G., 2016. Sharing data for global infectious disease
338 surveillance and outbreak detection. *Trends Microbiol.* 24, 241–245.
339 <https://doi.org/10.1016/j.tim.2016.01.009>
- 340 Almeida Kumlien, A.C.M. de, Coughlan, P., Dreyer-Gibney, K., Mc Nabola, A., 2019.
341 Learning to innovate through action learning, collaborative prototyping and
342 demonstration. In: *26th Innovation and Product Development Management
343 Conference, Leicester, UK, June 9-11th 2019*, pp. 1–14.
- 344 Almeida Kumlien, A.C.M. de, Coughlan, P., Mc Nabola, A., Novara, D., Fernandes, I.,
345 2018. Demonstrating learning in action in an energy and water smart specialisation
346 cluster. In: *19th International CINet Conference “Continuous Innovation: Spinning*

- 347 *out and Spinning in”, Dublin, Ireland, September 9-11th 2018*, pp. 225–238.
- 348 Almeida Kumlien, A.C.M. de, Borrego, C.M., Balcázar, J.L., 2021. Antimicrobial
349 resistance and bacteriophages: An overlooked intersection in water disinfection.
350 *Trends Microbiol.* 29, 517–527. <https://doi.org/10.1016/j.tim.2020.12.011>
- 351 Blanco-Picazo, P., Roscales, G., Toribio-Avedillo, D., Gómez-Gómez, C., Avila, C.,
352 Ballesté, E., Muniesa, M., Rodríguez-Rubio, L., 2020. Antibiotic resistance genes in
353 phage particles from Antarctic and Mediterranean seawater ecosystems.
354 *Microorganisms* 8, 1293. <https://doi.org/10.3390/microorganisms8091293>
- 355 Cacace, D., Fatta-Kassinos, D., Manaia, C.M., Cytryn, E., Kreuzinger, N., Rizzo, L.,
356 Karaolia, P., Schwartz, T., Alexander, J., Merlin, C., Garelick, H., Schmitt, H., de
357 Vries, D., Schwermer, C.U., Meric, S., Ozkal, C.B., Pons, M.N., Kneis, D.,
358 Berendonk, T.U., 2019. Antibiotic resistance genes in treated wastewater and in the
359 receiving water bodies: A pan-European survey of urban settings. *Water Res.* 162,
360 320–330. <https://doi.org/10.1016/j.watres.2019.06.039>
- 361 Cantón, R., 2009. Antibiotic resistance genes from the environment: A perspective
362 through newly identified antibiotic resistance mechanisms in the clinical setting.
363 *Clin. Microbiol. Infect.* 15, 20–25. [https://doi.org/10.1111/j.1469-](https://doi.org/10.1111/j.1469-0691.2008.02679.x)
364 [0691.2008.02679.x](https://doi.org/10.1111/j.1469-0691.2008.02679.x)
- 365 Cassini, A., Högberg, L.D., Plachouras, D., Quattrocchi, A., Hoxha, A., Simonsen, G.S.,
366 Colomb-Cotinat, M., Kretzschmar, M.E., Devleeschauwer, B., Cecchini, M.,
367 Ouakrim, D.A., Oliveira, T.C., Struelens, M.J., Suetens, C., Monnet, and the Burden
368 of AMR Collaborative Group, 2019. Attributable deaths and disability-adjusted life-
369 years caused by infections with antibiotic-resistant bacteria in the EU and the
370 European Economic Area in 2015: a population-level modelling analysis. *Lancet*
371 *Infect. Dis.* 19, 56–66. [https://doi.org/10.1016/S1473-3099\(18\)30605-4](https://doi.org/10.1016/S1473-3099(18)30605-4)
- 372 Chandler, C.I.R., 2019. Current accounts of antimicrobial resistance: stabilisation,
373 individualisation and antibiotics as infrastructure. *Palgrave Commun.* 5, 53.
374 <https://doi.org/10.1057/s41599-019-0263-4>
- 375 Cheng, M., Cao, L., Ning, K., 2019. Microbiome big-data mining and applications using
376 single-cell technologies and metagenomics approaches toward precision medicine.
377 *Front. Genet.* 10, 972. <https://doi.org/10.3389/fgene.2019.00972>
- 378 Duarte, A.S.R., Stärk, K.D.C., Munk, P., Leekitcharoenphon, P., Bossers, A., Luiken, R.,
379 Sarrazin, S., Lukjancenko, O., Pamp, S.J., Bortolaia, V., Nissen, J.N., Kirstahler, P.,
380 Van Gompel, L., Poulsen, C.S., Kaas, R.S., Hellmér, M., Hansen, R.B., Gomez,
381 V.M., Hald, T., 2020. Addressing learning needs on the use of metagenomics in
382 antimicrobial resistance surveillance. *Front. Public Health.* 8, 38.
383 <https://doi.org/10.3389/fpubh.2020.00038>
- 384 Essack, S.Y., 2018. Environment: the neglected component of the One Health triad.
385 *Lancet Planet. Health.* 2, e238–e239. [https://doi.org/10.1016/S2542-](https://doi.org/10.1016/S2542-5196(18)30124-4)
386 [5196\(18\)30124-4](https://doi.org/10.1016/S2542-5196(18)30124-4)
- 387 European Commission, 2021. Commission recommendation of 17.3.2021 on a common
388 approach to establish a systematic surveillance of SARS-CoV-2 and its variants in
389 wastewaters in the EU. Brussels. Retrieved from
390 https://ec.europa.eu/environment/pdf/water/recommendation_covid19_monitoring

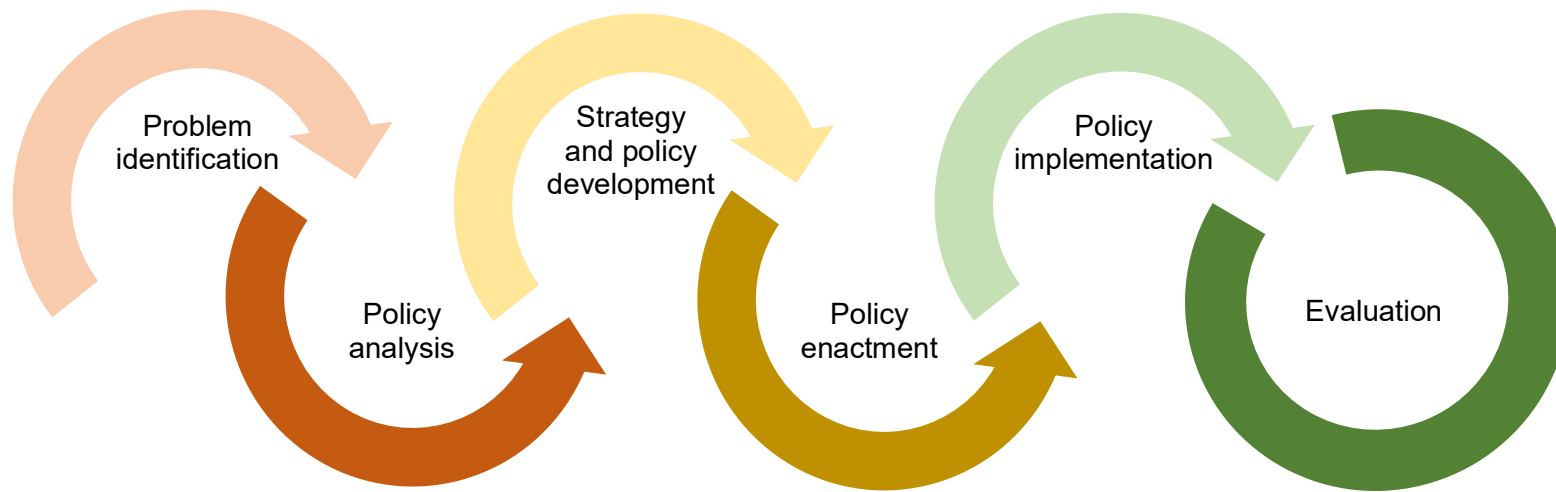
391 _wastewaters.pdf

- 392 Forbes, J.D., Knox, N.C., Ronholm, J., Pagotto, F., Reimer, A., 2017. Metagenomics: the
393 next culture-independent game changer. *Front. Microbiol.* 8, 1069.
394 <https://doi.org/10.3389/fmicb.2017.01069>
- 395 Gao, R., Sui, M., 2020. Antibiotic resistance fate in the full-scale drinking water and
396 municipal wastewater treatment procedures: A review. *Environ. Eng. Res.* 26,
397 200324. <https://doi.org/10.4491/eer.2020.324>
- 398 Hendriksen, R.S., Bortolaia, V., Tate, H., Tyson, G.H., Aarestrup, F.M., McDermott,
399 P.F., 2019. Using genomics to track global antimicrobial resistance. *Front. Public*
400 *Health.* 7, 242. <https://doi.org/10.3389/fpubh.2019.00242>
- 401 Hendriksen, R.S., Munk, P., Njage, P., van Bunnik, B., McNally, L., Lukjancenko, O.,
402 Röder, T., Nieuwenhuijse, D., Pedersen, S.K., Kjeldgaard, J., Kaas, R.S., Clausen,
403 P., Vogt, J.K., Leekitcharoenphon, P., van de Schans, M., Zuidema, T., de Roda
404 Husman, A.M., Rasmussen, S., Petersen, B., Global Sewage Surveillance project
405 consortium, Amid, C., Cochrane, G., Sicheritz-Ponten, T., Schmitt, H., Alvarez,
406 J.R.M., Aidara-Kane, A., Pamp, S.J., Lund, O., Hald, T., Woolhouse, M.,
407 Koopmans, M.P., Vigre, H., Petersen, T.N., Aarestrup, F.M., 2019. Global
408 monitoring of antimicrobial resistance based on metagenomics analyses of urban
409 sewage. *Nat. Commun.* 10, 1124. <https://doi.org/10.1038/s41467-019-08853-3>
- 410 Hofer, U., 2019. The cost of antimicrobial resistance. *Nat. Rev. Microbiol.* 17, 3.
- 411 Hoffman, S.J., Outtersen, K., Røttingen, J.A., Cars, O., Clift, C., Rizvi, Z., Rotberg, F.,
412 Tomson, G., Zorzet, A., 2015. An international legal framework to address
413 antimicrobial resistance. *Bull. World Health Organ.* 93, 66.
414 <https://doi.org/10.2471/BLT.15.152710>
- 415 Hong, P.Y., Julian, T.R., Pype, M.L., Jiang, S.C., Nelson, K.L., Graham, D., Pruden, A.,
416 Manaia, C.M., 2018. Reusing treated wastewater: Consideration of the safety aspects
417 associated with antibiotic-resistant bacteria and antibiotic resistance genes. *Water*
418 10, 244. <https://doi.org/10.3390/w10030244>
- 419 Jovanovic, O., Amábile-Cuevas, C.F., Shang, C., Wang, C., Ngai, K.W., 2021. What
420 water professionals should know about antibiotics and antibiotic resistance: An
421 Overview. *ACS EST Water* 1, 1334–1351.
422 <https://doi.org/10.1021/acsestwater.0c00308>
- 423 Koczura, R., Mokracka, J., Taraszewska, A., Łopacinska, N., 2016. Abundance of class
424 1 integron-integrase and sulfonamide resistance genes in river water and sediment is
425 affected by anthropogenic pressure and environmental factors. *Microb. Ecol.* 72,
426 909–916. <https://doi.org/10.1007/s00248-016-0843-4>
- 427 Larsson, D.G.J., Andremont, A., Bengtsson-Palme, J., Brandt, K.K., de Roda Husman,
428 A.M., Fagerstedt, P., Fick, J., Flach, C.F., Gaze, W.H., Kuroda, M., Kvint, K.,
429 Laxminarayan, R., Manaia, C.M., Nielsen, K.M., Plant, L., Ploy, M.C., Segovia, C.,
430 Simonet, P., Smalla, K., Snape, J., Topp, E., van Hengel, A.J., Verner-Jeffreys,
431 D.W., Virta, M.P.J., Wellington, E.M., Wernersson, A.S., 2018. Critical knowledge
432 gaps and research needs related to the environmental dimensions of antibiotic
433 resistance. *Environ. Int.* 117, 132–138. <https://doi.org/10.1016/j.envint.2018.04.041>
- 434 Lekunberri, I., Villagrana, M., Balcázar, J.L., Borrego, C.M., 2017. Contribution of

- 435 bacteriophage and plasmid DNA to the mobilization of antibiotic resistance genes in
 436 a river receiving treated wastewater discharges. *Sci. Total Environ.* 601-602, 206–
 437 209. <https://doi.org/10.1016/j.scitotenv.2017.05.174>
- 438 MacLean, R.C., San Millan, A., 2019. The evolution of antibiotic resistance. *Science* 365,
 439 1082–1083. <https://doi.org/10.1126/science.aax3879>
- 440 Majeed, H.J., Riquelme, M.V., Davis, B.C., Gupta, S., Angeles, L., Aga, D.S., Garner,
 441 E., Pruden, A., Vikesland, P.J., 2021. Evaluation of metagenomic-enabled antibiotic
 442 resistance surveillance at a conventional wastewater treatment plant. *Front.*
 443 *Microbiol.* 12, 657954. <https://doi.org/10.3389/fmicb.2021.657954>
- 444 Manaia, C.M., 2017. Assessing the risk of antibiotic resistance transmission from the
 445 environment to humans: Non-direct proportionality between abundance and risk.
 446 *Trends Microbiol.* 25, 173–181. <https://doi.org/10.1016/j.tim.2016.11.014>
- 447 Marano, R.B.M., Fernandes, T., Manaia, C.M., Nunes, O., Morrison, D., Berendonk,
 448 T.U., Kreuzinger, N., Tenson, T., Corno, G., Fatta-Kassinos, D., Merlin, C., Topp,
 449 E., Jurkevitch, E., Henn, L., Scott, A., Heß, S., Slipko, K., Laht, M., Kisand, V., Di
 450 Cesare, A., Karaolia, P., Michael, S.G., Petre, A.L., Rosal, R., Pruden, A., Riquelme,
 451 V., Agüera, A., Esteban, B., Luczkiewicz, A., Kalinowska, A., Leonard, A., Gaze,
 452 W.H., Adegoke, A.A., Stenstrom, T.A., Pollice, A., Salerno, C., Schwermer, C.U.,
 453 Krzeminski, P., Guilloteau, H., Donner, E., Drigo, B., Libralato, G., Guida, M.,
 454 Bürgmann, H., Beck, K., Garelick, H., Tacão, M., Henriques, I., Martínez-Alcalá, I.,
 455 Guillén-Navarro, J.M., Popowska, M., Piotrowska, M., Quintela-Baluja, M., Bunce,
 456 J.T., Polo-López, M.I., Nahim-Granados, S., Pons, M.N., Milakovic, M., Udikovic-
 457 Kolic, N., Ory, J., Ousmane, T., Caballero, P., Oliver, A., Rodriguez-Mozaz, S.,
 458 Balcazar, J.L., Jäger, T., Schwartz, T., Yang, Y., Zou, S., Lee, Y., Yoon, Y., Herzog,
 459 B., Mayrhofer, H., Prakash, O., Nimonkar, Y., Heath, E., Baraniak, A., Abreu-Silva,
 460 J., Choudhury, M., Munoz, L.P., Krizanovic, S., Brunetti, G., Maile-Moskowitz, A.,
 461 Brown, C., Cytryn, E., 2020. A global multinational survey of cefotaxime-resistant
 462 coliforms in urban wastewater treatment plants. *Environ. Int.* 144, 106035.
 463 <https://doi.org/10.1016/j.envint.2020.106035>
- 464 Martinez, J.L., 2009. Environmental pollution by antibiotics and by antibiotic resistance
 465 determinants. *Environ. Pollut.* 157, 2893–2902.
 466 <https://doi.org/10.1016/j.envpol.2009.05.051>
- 467 Morel, C., Alm, R., Ardal, C., Bandera, A., Bruno, G., Carrara, E., Colombo, G., Kraker,
 468 M. de, Essack, S., Frost, I., Gonzalez-Zorn, H.B., Goossens, H., Guardabassi, L.,
 469 Harbarth, S., Jørgensen, P., Kanj, S., Kostyanov, T., Laxminarayan, R., Leonard, F.,
 470 Hara, G.L., Mendelson, M., Mikulska, M., Mutter, N., Outtersson, K., Baño, J.R.,
 471 Tacconelli, E., Scudeller, L., and the GAP-ONE network, 2020. A one health
 472 framework to estimate costs of antimicrobial resistance. *Antimicrob. Resist. Infect.*
 473 *Control* 9, 187. <https://doi.org/10.1186/s13756-020-00822-6>
- 474 Murray, A.K., Stanton, I., Gaze, W.H., Snape, J., 2021. Dawning of a new ERA:
 475 Environmental Risk Assessment of antibiotics and their potential to select for
 476 antimicrobial resistance. *Water Res.* 200, 117233.
 477 <https://doi.org/10.1016/j.watres.2021.117233>
- 478 Nathan, C., 2020. Resisting antimicrobial resistance. *Nat. Rev. Microbiol.* 18, 259–260.
 479 <https://doi.org/10.1038/s41579-020-0348-5>

- 480 O'Neill, J., 2016. Tackling drug-resistant infections globally: Final report and
 481 recommendations. The Review on Antimicrobial Resistance, London, UK.
 482 Retrieved from [https://amr-](https://amr-review.org/sites/default/files/160518_Final%20paper_with%20cover.pdf)
 483 [review.org/sites/default/files/160518_Final%20paper_with%20cover.pdf](https://amr-review.org/sites/default/files/160518_Final%20paper_with%20cover.pdf)
- 484 Pandey, D., Verma, S., Verma, P., Mahanty, B., Dutta, K., Daverey, A., Arunachalam,
 485 K., 2021. SARS-CoV-2 in wastewater: Challenges for developing countries. *Int. J.*
 486 *Hyg. Environ. Health.* 231, 113634. <https://doi.org/10.1016/j.ijheh.2020.113634>.
- 487 Pandit, A.B., Kumar, J.K., 2015. Clean water for developing countries. *Annu. Rev. Chem.*
 488 *Biomol. Eng.* 6, 217–246. [https://doi.org/10.1146/annurev-chembioeng-061114-](https://doi.org/10.1146/annurev-chembioeng-061114-123432)
 489 [123432](https://doi.org/10.1146/annurev-chembioeng-061114-123432)
- 490 Pärnänen, K.M.M., Narciso-da-Rocha, C., Kneis, D., Berendonk, T.U., Cacace, D., Thuy
 491 Do, T., Elpers, C., Fatta-Kassinos, D., Henriques, I., Jaeger, T., Karkman, A., Luis
 492 Martinez, J., Michael, S.G., Michael-Kordatou, I., Rodriguez-Mozaz, S., Schwartz,
 493 T., Sheng, H., Sørum, H., Stedtfeld, R.D., Tiedje, J.M., Varela Della Giustina, S.,
 494 Walsh, F., Vaz-Moreira, I., Virta, M., Manaia, C.M., 2019. Antibiotic resistance in
 495 European wastewater treatment plants mirrors the pattern of clinical antibiotic
 496 resistance prevalence. *Sci. Adv.* 5, eaau9124.
 497 <https://doi.org/10.1126/sciadv.aau9124>
- 498 Roca, I., Akova, M., Baquero, F., Carlet, J., Cavaleri, M., Coenen, S., Cohen, J., Findlay,
 499 D., Gyssens, I., Heure, O.E., Kahlmeter, G., Kruse, H., Laxminarayan, R., Liébana,
 500 E., López-Cerero, L., MacGowan, A., Martins, M., Rodríguez-Baño, J., Rolain,
 501 J.M., Segovia, C., Sigauque, B., Taconelli, E., Wellington, E., Vila, J., 2015. The
 502 global threat of antimicrobial resistance: Science for intervention. *New Microbes*
 503 *New Infect.* 6, 22–29. <https://doi.org/10.1016/j.nmni.2015.02.007>
- 504 Rodríguez-Mozaz, S., Chamorro, S., Marti, E., Huerta, B., Gros, M., Sánchez-Melsió, A.,
 505 Borrego, C.M., Barceló, D., Balcázar, J.L., 2015. Occurrence of antibiotics and
 506 antibiotic resistance genes in hospital and urban wastewaters and their impact on the
 507 receiving river. *Water Res.* 69, 234–242.
 508 <https://doi.org/10.1016/j.watres.2014.11.021>
- 509 Roope, L.S.J., Smith, R.D., Pouwels, K.B., Buchanan, J., Abel, L., Eibich, P., Butler,
 510 C.C., Tan, P.S., Sarah Walker, A., Robotham, J. V., Wordsworth, S., 2019. The
 511 challenge of antimicrobial resistance: What economics can contribute. *Science* 364,
 512 eaau4679. <https://doi.org/10.1126/science.aau4679>
- 513 Shafer, K., Fox, R., 2016. One Water Roadmap: The sustainable management of life's
 514 most essential resource. US Water Alliance, Oakland, USA. Retrieved from
 515 [http://uswateralliance.org/sites/uswateralliance.org/files/publications/Roadmap%2](http://uswateralliance.org/sites/uswateralliance.org/files/publications/Roadmap%20FINAL.pdf)
 516 [0FINAL.pdf](http://uswateralliance.org/sites/uswateralliance.org/files/publications/Roadmap%20FINAL.pdf)
- 517 Sims, N., Kasprzyk-Hordern, B., 2020. Future perspectives of wastewater-based
 518 epidemiology: Monitoring infectious disease spread and resistance to the community
 519 level. *Environ. Int.* 139, 105689. <https://doi.org/10.1016/j.envint.2020.105689>
- 520 Singer, A.C., Shaw, H., Rhodes, V., Hart, A., 2016. Review of antimicrobial resistance
 521 in the environment and its relevance to environmental regulators. *Front. Microbiol.*
 522 7, 1728. <https://doi.org/10.3389/fmicb.2016.01728>
- 523 Smith, R.D., Coast, J., 2002. Antimicrobial resistance: a global response. *Bull. World*

- 524 Health Organ. 80, 126–133.
- 525 Stanton, I.C., Murray, A.K., Zhang, L., Snape, J., Gaze, W.H., 2020. Evolution of
526 antibiotic resistance at low antibiotic concentrations including selection below the
527 minimal selective concentration. *Commun. Biol.* 3, 467.
528 <https://doi.org/10.1038/s42003-020-01176-w>
- 529 Strathdee, S.A., Davies, S.C., Marcelin, J.R., 2020. Confronting antimicrobial resistance
530 beyond the COVID-19 pandemic and the 2020 US election. *Lancet* 396, 1050–1053.
531 [https://doi.org/10.1016/S0140-6736\(20\)32063-8](https://doi.org/10.1016/S0140-6736(20)32063-8)
- 532 Van Gompel, L., Luiken, R.E.C., Hansen, R.B., Munk, P., Bouwknegt, M., Heres, L.,
533 Greve, G.D., Scherpenisse, P., Jongerius-Gortemaker, B.G.M., Tersteeg-Zijderveld,
534 M.H.G., García-Cobos, S., Dohmen, W., Dorado-García, A., Wagenaar, J.A.,
535 Urlings, B.A.P., Aarestrup, F.M., Mevius, D.J., Heederik, D.J.J., Schmitt, H.,
536 Bossers, A., Smit, L.A.M., 2020. Description and determinants of the faecal
537 resistome and microbiome of farmers and slaughterhouse workers: A metagenome-
538 wide cross-sectional study. *Environ. Int.* 143, 105939.
539 <https://doi.org/10.1016/j.envint.2020.105939>
- 540 Wellcome Trust, 2020. The Global Response to AMR: Momentum, success, and critical
541 gaps. Wellcome Trust, London, UK. Retrieved from
542 <https://cms.wellcome.org/sites/default/files/2020-11/wellcome-global-response->
543 [amr-report.pdf](https://cms.wellcome.org/sites/default/files/2020-11/wellcome-global-response-amr-report.pdf)
- 544 Wilson, L.A., Rogers Van Katwyk, S., Fafard, P., Viens, A.M., Hoffman, S.J., 2020.
545 Lessons learned from COVID-19 for the post-antibiotic future. *Global Health* 16,
546 94. <https://doi.org/10.1186/s12992-020-00623-x>
- 547 WHO, 2015. Global Antimicrobial Resistance Surveillance System: Manual for early
548 implementation. World Health Organization, Geneva, Switzerland. Retrieved from
549 https://apps.who.int/iris/bitstream/handle/10665/188783/9789241549400_eng.pdf
- 550 WHO-UNICEF, 2021. Progress on household drinking water, sanitation and hygiene,
551 2000–2020: Five years into the SDGs. World Health Organization (WHO) and the
552 United Nations Children’s Fund (UNICEF), Geneva, Switzerland. Retrieved from
553 <https://apps.who.int/iris/rest/bitstreams/1369501/retrieve>
- 554
- 555



556 **Figure 1.** A proposed framework to identify the different actions and steps in the policy process. This figure has been adapted from the CDC's Policy Analytical Framework (<https://www.cdc.gov/>).