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# Aeromonas: the multifaceted middleman in the One Health world

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1 ***Aeromonas*: the multifaceted middleman in the *One Health* world**

2

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16

17 **Highlights**

18

19 - *Aeromonas* is an ubiquitous hydrotelluric bacterium

20 - *Aeromonas* is at the interface between humans, animals and the environment

21 - *Aeromonas* can be responsible for human infections following leech therapy

22 - *Aeromonas* has a high level of genome plasticity and capability of acquiring genes

23 - *Aeromonas* contributes to antimicrobial resistance gene dissemination

24

25

26 **Abstract**

27 *Aeromonas* is at the interface of all the *One Health* components and represents an amazingly  
28 sound test case in the *One Health* approach, from economic loss in aquaculture to challenges  
29 related to antibiotic-resistant bacteria selected from the environment. In human health,  
30 infections following leech therapy is an outstanding example of such *One Health* challenges.  
31 *Aeromonads* are not only ubiquitous environmental bacteria, able to rapidly colonize and  
32 cause opportunistic infections in humans and animals, they are also capable of promoting  
33 interactions and gene exchanges between the *One Health* components. This makes this genus  
34 a key amplifier of genetic transfer, especially of antibiotic resistance genes.

35

## 36 ***Aeromonas* in the *One Health* world: a ubiquitous “Jack of all trades”**

37 The genus *Aeromonas* belongs to the Aeromonadaceae family, which itself is part of the  
38 Aeromonadales order and Gammaproteobacteria class [1]. This genus, which currently  
39 comprises 36 species (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi>), is  
40 organized in a complex of species, *i.e.*, heterogeneous groups of closely-related species with  
41 unclear boundaries [2], as observed for other Gram-negative bacteria like *Vibrio*,  
42 *Acinetobacter*, *Pseudomonas*, *Burkholderia*, and several Enterobacterales [3]. From this  
43 complex of species, some more specialized clones may emerge [4]. Of these, the complex *A.*  
44 *salmonicida*, which is responsible for fish diseases, is to date the only species that has  
45 successfully become specialized to cause a specific disease [5]. While the primary reservoir of  
46 *Aeromonas* is aquatic environments and soils where it is almost always present, it is also  
47 capable of rapidly colonizing a wide range of niches and hosts [1]. *Aeromonas* has a notable  
48 ability to colonize the animal gut, including the guts of leeches, fish, cows and humans [6,7]  
49 as well as many other host organisms.

50 Data from Pubmed, using close to 10,000 descriptions since 1944,  
51 (<https://pubmed.ncbi.nlm.nih.gov/?term=aeromonas&sort=date&size=20>) provides a biased  
52 view of this epidemiology, with >50% of *Aeromonas* publications linked to humans or  
53 animals including livestock, companions and wildlife. The IMNGS 16S rRNA-based  
54 metagenomic website provides a more accurate and realistic picture of *Aeromonas*  
55 epidemiology [8]. *Aeromonas* is mostly detected from water and soil samples, and is present  
56 in 20% of rhizosphere and aquatic metagenomes (Figure 1). Detection from animal samples is  
57 infrequent, except from fish gut metagenomes and, to a lesser extent, from bovine gut  
58 metagenomes [9,10]. In humans, detection remains exceptionally rare. Relative abundance  
59 data from positive metagenomes also highlights the importance of *Aeromonas* in hydrotelluric  
60 environments with anthropic pollution. The highest relative abundance is found in wastewater

61 metagenomes (Figure 1), as a partial consequence of gut-related waste. Relative abundance of  
62 *Aeromonadaceae* in animals is very low, below 0.1% (Figure 1). One exception is leech gut  
63 where relative abundance of *Aeromonas* seems very important, estimated at 36% [11].  
64 The environmental reservoir of *Aeromonas* allows it to be at the interface of all the *One*  
65 *Health* components (Figure 2). With its ability to produce biofilm and its large metabolic  
66 capacity that facilitates its rapid adaptation to environmental changes [12,13], *Aeromonas* is  
67 viable in a large range of conditions. These extended capabilities that allow *Aeromonas* to  
68 persist and rapidly propagate in continuously changing environments [12-17] has earned this  
69 genus the nickname of a “Jack-of-all-trades” [12].

70

71

## 72 ***Aeromonas* in close contact with human activities**

73 *Aeromonas* is primarily able to develop long-term symbiotic relationships (e.g. with leeches),  
74 or to transiently colonize other animals and humans, where it can trigger cutaneous or  
75 digestive infections [16,18]. *Aeromonas* spp. are responsible for economic burdens of dozens  
76 of millions of dollars in aquaculture due to mortality, lost feeding days and costs associated  
77 with chemical and antibiotic therapy [19-22]. Among fish pathogens, *A. salmonicida* subsp.  
78 *salmonicida* (referred to as “typical”) is responsible for furunculosis disease in salmonids  
79 [23], while some hypervirulent clones have emerged (e.g., *A. hydrophila* ST251) in the catfish  
80 farming and shrimp industry [24,25].

81 Another *Aeromonas*-impacted area concerns ornamental fish that are traded worldwide (2  
82 billion/year). These exchanges occur mainly between Asian countries (the primary producer)  
83 and USA/Europe. In this industry, as observed for several years in fish farms [26,27], the  
84 misuse or overuse of antibiotics to fight bacterial diseases has selected for drug-resistant  
85 pathogens [28-30]. Recent studies underline the potential role of ornamental fish in the

86 dissemination of antibiotic-resistant bacteria, with possible consequences for private  
87 aquariums and human public health in importing countries [28].  
88 *Aeromonas* spp. have also been isolated from a wide range of foods of both plant and animal  
89 origin [31], including minimally processed and ready-to-eat seafood products that are gaining  
90 popularity [32]. The prevalence of *Aeromonas* in ready-to-eat products has been estimated to  
91 be between 8 and 52%, with resistance to clinically-relevant antibiotics also emerging [33-  
92 35]. This raises concerns of the potential for food spoilage and foodborne infections.  
93 *Aeromonas* is associated with human activities such as animal husbandry, animal slaughter  
94 [36-38], wastewater treatment [39], reclaiming irrigation water [40,41], recreational or  
95 occupational activities that are related to water exposure and those that exploit  
96 microbiological metabolic capabilities in biotechnological applications (Figure 2). These  
97 include the treatment of sewage and industrial wastewater with activated sludge that contains  
98 aeromonads at up to 2% of the total biomass [14,42]. Here, aeromonads are organized in  
99 aggregates and can resist the extreme conditions of pH, salinity, heavy metal toxicity, and  
100 temperature [14]. These aggregates are inserted in mixed species biofilms that are able to  
101 remove organic pollutants and improve both denitrification and phosphorus removal [43-45].

102

103

#### 104 **Human infections: by accident or by Trojan horse**

105 In humans, *Aeromonas* infections are primarily associated with contact with soil and/or water  
106 e.g., during recreational or occupational activities, or following road accidents [16,46].

107 Cutaneous, eye or digestive infections are the most frequent, although almost any type of  
108 infection is possible. Aeromonads are weak opportunistic pathogens in humans, and most  
109 infections are associated with a barrier disruption. Aeromonads can also spread from a  
110 colonized niche, typically the gut, and cause biliary or bloodstream infections notably in

111 immunocompromised patients [16,47]. While human infections are widely reported through  
112 hundreds of published case reports [48], they are poorly documented compared to other  
113 bacteria, with the notable exception of natural disaster situations, when thousands of wounded  
114 individuals are exposed to contaminated waters with poor access to healthcare facilities [16].  
115 No global study exists that compares prevalence among countries. The prevalence of  
116 bloodstream infections seems higher in Asia compared with European countries [46,49], and  
117 some species are more prevalent in tropical countries (e.g., *A. dhakensis*) [1]. One can expect  
118 that use of gastrointestinal syndromic tests targeting aeromonads will increase documentation  
119 and will provide a more exhaustive picture, as it was observed in this recent German study  
120 with a prevalence of 2.9% of *Aeromonas* sp. from 5032 stool samples [50].

121 The particular case of healthcare-associated infections caused by ciprofloxacin-resistant  
122 aeromonads following leech therapy is an example of the *One Health* challenges posed by  
123 these bacteria, with resistant strains selected from the environment and spread to patients  
124 (Figure 3). Medicinal leeches may be administered to patients after orthopedic surgery or  
125 reconstructive surgery to treat venous congestion that threatens flap outcome through  
126 necrosis. This salvage treatment actively removes blood and improves outcomes, at the  
127 expense of a risk of serious wound infection leading to flap loss, amputation and sepsis.  
128 Indeed, the leech regurgitates its symbiont during bloodlettings. While the most abundant  
129 species among leech symbionts is by far *A. veronii*, *A. hydrophila* is the most frequently  
130 reported species associated with infection following leech therapy (88%) [51]. This underlines  
131 that the bacterial load during leech regurgitation is not the only factor to contribute to  
132 infection and that some yet unknown virulence factors in *A. hydrophila* are likely involved  
133 [52]. This risk of infection is controlled with ciprofloxacin-based prophylactic treatment  
134 [51,53]. However, since the early 2010s, several cases of infections following leech therapy  
135 were suddenly reported worldwide by aeromonads resistant to ciprofloxacin [54,55]. As



136 detailed in Figure 3, investigations showed that these events resulted from complex  
137 relationships between the antibiotic that disseminates in the environment, the leech microbiota  
138 where there is competition between fluoroquinolone (FQ)-resistant and FQ-susceptible  
139 bacteria, a leech trade based on a limited number of suppliers that disseminate leech with  
140 closely related FQ-resistant strains, and immunocompromised patients [52].  
141 The use of antimicrobials in a natural setting facilitates the spread of resistance markers in  
142 *Aeromonas*, even when used at very low-levels [56,57], and this spread may occur between  
143 distant locations through a vector and Trojan horse such as the leech. This example highlights  
144 the consequences of the selective pressure in the leech environment with subsidiary  
145 consequences to human health. Such resistance spread is not limited to FQ, with some reports  
146 recently identifying *Aeromonas* that harboured resistance to 3<sup>rd</sup> generation cephalosporins or  
147 cotrimoxazole, which exemplifies the capability of aeromonads to acquire diverse antibiotic  
148 resistance genes (ARGs) [55,58].

149

150

### 151 **How to uptake DNA: the Swiss Army knife**

152 Bacteria of the *Aeromonas* genus have a 4-5 Mbp genome, which is smaller than other Gram-  
153 negative bacteria like Enterobacterales or *Pseudomonas*. *Aeromonas* compensates for this  
154 relatively small genome size by its tremendous capacity to acquire several mobile genetic  
155 elements (MGE), including plasmids, transposons, genomic islands or integron gene cassettes.  
156 The core genome of these bacteria is represented by only 16% of the genes in the whole  
157 genome, with the remaining (84%) consisting of variably represented genes. This highlights  
158 the exceptional level of genome plasticity in *Aeromonas* due to horizontal gene transfers  
159 (HGT) both from close relatives in the genus and from several other families [13,59]. An  
160 exciting yet unanswered question is to know whether the environment shapes aeromonad

161 plasticity and whether their accessory genome correlates with their origin. This mobilome  
162 [60] allows for the acquisition of hundreds of antibiotic or heavy metal resistance genes,  
163 genes involved in molecular function or biological process, as well as genes encoding  
164 metabolic enzymes, transporters and bacterial defense mechanisms [59,61]. These genes  
165 enable the survival of *Aeromonas* in hostile environments. All known mechanisms of HGT  
166 have been described within the *Aeromonas* genus [62]: transformation (as most *Aeromonas*  
167 species are naturally competent [63,64]), transduction and conjugation. A wide variety of  
168 lysogenic phages has been described especially amongst the species *A. salmonicida* and *A.*  
169 *hydrophila* [65,66]. Conjugation remains the most efficient mechanism of HGT, with  
170 hundreds of conjugative plasmids identified in aeromonads. This plasmidome remains poorly  
171 characterised, with the exception of that of *A. salmonicida* [67].

172 Aeromonads are diversely equipped with the type II, III, IV and VI secretion systems (TSS)  
173 [13]. Whilst the study of these nanomachines in *Aeromonas* has mostly focused on their  
174 virulence properties, the T4SS and T6SS are also likely to be implicated in gene transfer, as  
175 they are typically involved in Gram-negative bacterial conjugation and transformation  
176 respectively [68,69]. For instance, competence-induced T6SS-mediated bacterial killing has  
177 been demonstrated in *V. cholerae*, and occurs through a complex system that involves chitin-  
178 composed exoskeleton-associated-biofilms (e.g. in copepods), quorum sensing and the  
179 metabolic activity of chitinase [68,70]. Because *Aeromonas* shares aforementioned features  
180 with the closely-related *Vibrio* spp., it is conceivable that the T6SS plays a role, albeit still  
181 unravelled, in *Aeromonas* DNA uptake. Whatever the mechanisms involved, the lifestyle of  
182 aeromonads is associated with biofilm in sheltering organisms (e.g., copepods) that are  
183 hotspots for genetic exchanges [71].

184 Given its importance in human and animal health, the acquisition of ARGs is the most  
185 described event of this genetic exchange capability of *Aeromonas*. The genus can be

186 considered as a “sponge” because it can easily absorb and redistribute genes [67]. A recent *in*  
187 *silico* analysis on plasmids retrieved from *Aeromonas* species revealed that more than one  
188 third of plasmids carry ARGs [72]. These ARGs can affect all antibiotic families, including  $\beta$ -  
189 lactams, with extended-spectrum  $\beta$ -lactamases (CTX-M, GES, VEB) and carbapenemases  
190 (VIM, KPC, NDM-like), but also aminoglycosides, cyclins, trimethoprim, sulfonamides, FQ  
191 (with notably the *qnr* and *qepA* genes [73]) and even colistin, with the recent description of  
192 the *mcr* genes carried on *Aeromonas* plasmids [55,58,74-78].

193

#### 194 **Integrins in *Aeromonas*: witnesses of horizontal gene transfers?**

195 Due to the environmental location of *Aeromonas* and its capability to acquire multiple MGE  
196 under selective pressure, it can be expected that detection of virulence or ARGs in  
197 aeromonads could constitute potential biomarkers of anthropic pollution. Unfortunately, these  
198 genes are too diverse for this approach to be feasible. One alternative attractive possibility in  
199 the search for a unique biomarker of anthropic pollution would be to detect integrins from  
200 *Aeromonas* isolates. Combining a relevant microorganism capable of acquiring hundreds of  
201 genes under selective pressure (*Aeromonas*) and a marker of antimicrobial resistance  
202 frequently hosted by *Aeromonas* isolates and easy to detect (integrins) could constitute a  
203 potential interesting tool. In fact, class 1 integrins can be easily detected [79] and are now  
204 considered as a good proxy for anthropic pollution [80,81]. Integrins are non-mobile genetic  
205 elements carried by plasmids or transposons [82,83] that can carry hundreds of mobile gene  
206 cassettes, most of them involved in antimicrobial resistance. The prevalence of class 1  
207 integrins within the *Aeromonas* genus is difficult to determine and can greatly vary (from 7 to  
208 72%) depending on the origins of the samples [84-86]. Irrespective, their description among  
209 the *Aeromonas* species is frequent, as is their association with multidrug resistance, as

210 previously demonstrated for Enterobacterales [87,88]. Whilst gene cassettes are relatively  
211 diverse in *Aeromonas* [89] (Table S1), the presence of these integrons demonstrates that  
212 aeromonads readily acquire MGEs following selective pressure.

213

214

## 215 **Conclusions**

216 Although aeromonads are often described as possessing a significant pathogenic potential,  
217 these opportunistic pathogens seldom cause infections, and when they do, it is usually in the  
218 context of a disrupted barrier or a compromised immune system.

219 One intriguing question is why a microorganism that bears many so-called virulence factors  
220 rarely causes infection. Understanding pathogenicity in *Aeromonas* remains elusive [15], with  
221 virtually all studies failing to successfully predict pathogenicity in aeromonads from the  
222 expression of so-called virulence factors. One assumption to reconcile this paradox is that the  
223 genes that we, from a very anthropocentric analysis, consider to encode virulence factors may  
224 indeed have other primary functions. Several arguments suggest that exaptation, the process  
225 by which features acquire functions for which they were not originally adapted or selected  
226 [90], may have occurred in *Aeromonas*. For example, aeromonad hydrolytic enzymes are now  
227 thought to be primarily involved in essential functions of general cell metabolism [15].

228 Exaptation may have then changed the function of these genes during the course of  
229 evolutionary succession. Other examples of possible exaptation are *mcr-3* or *qnr* genes, which  
230 evolved long before the synthesis and clinical use of colistin and quinolones, respectively  
231 [91,92]. A complementary hypothesis is that the multiple varied environments and organisms  
232 that aeromonads colonize act as a nursery to pre-adapt to pathogenicity, because such  
233 relationships need to overcome the innate defense of their hosts [71].

234 Finally, some questions also arise regarding the role of integron gene cassettes in *Aeromonas*.  
235 While mostly associated with ARGs, they existed even prior to the antibiotic era, and they  
236 operate as a general gene capture system. As such, they are likely to be an important factor in  
237 the more general process of HGT during the evolution of bacterial genomes and in bacterial  
238 adaptation [93], and they may contribute to shaping the plasticity, versatility and flexibility of  
239 the *Aeromonas* genus [67].  
240 Irrespective of the original functions in the genus and its evolutionary changes, *Aeromonas* to  
241 date carries all the characteristics of a potential pathogen with resistance to multiple  
242 antibiotics. Taking into account its weaponry and its lifestyles that encompass all the *One*  
243 *Health* components, aeromonads have the potential to one day emerge as more prevalent  
244 pathogens than they are currently, and to wreak havoc in the future. Therefore, it is essential  
245 that we maintain a close watch on these fascinating bacteria.

246 **Competing interest**

247 The authors declare that they have no known competing financial interests or personal  
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249

250

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255

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301 genome was variable with hundreds of gene expansions and contractions, horizontally transferred  
302 genes, and mobile genetic elements, which emphasized the heterogeneity of the genus. This is one of  
303 the first study that deeply compared genome contents; this bioinformatics analysis highlighted  
304 differences between acquired genes and abundance of some genes that may reflect environmental  
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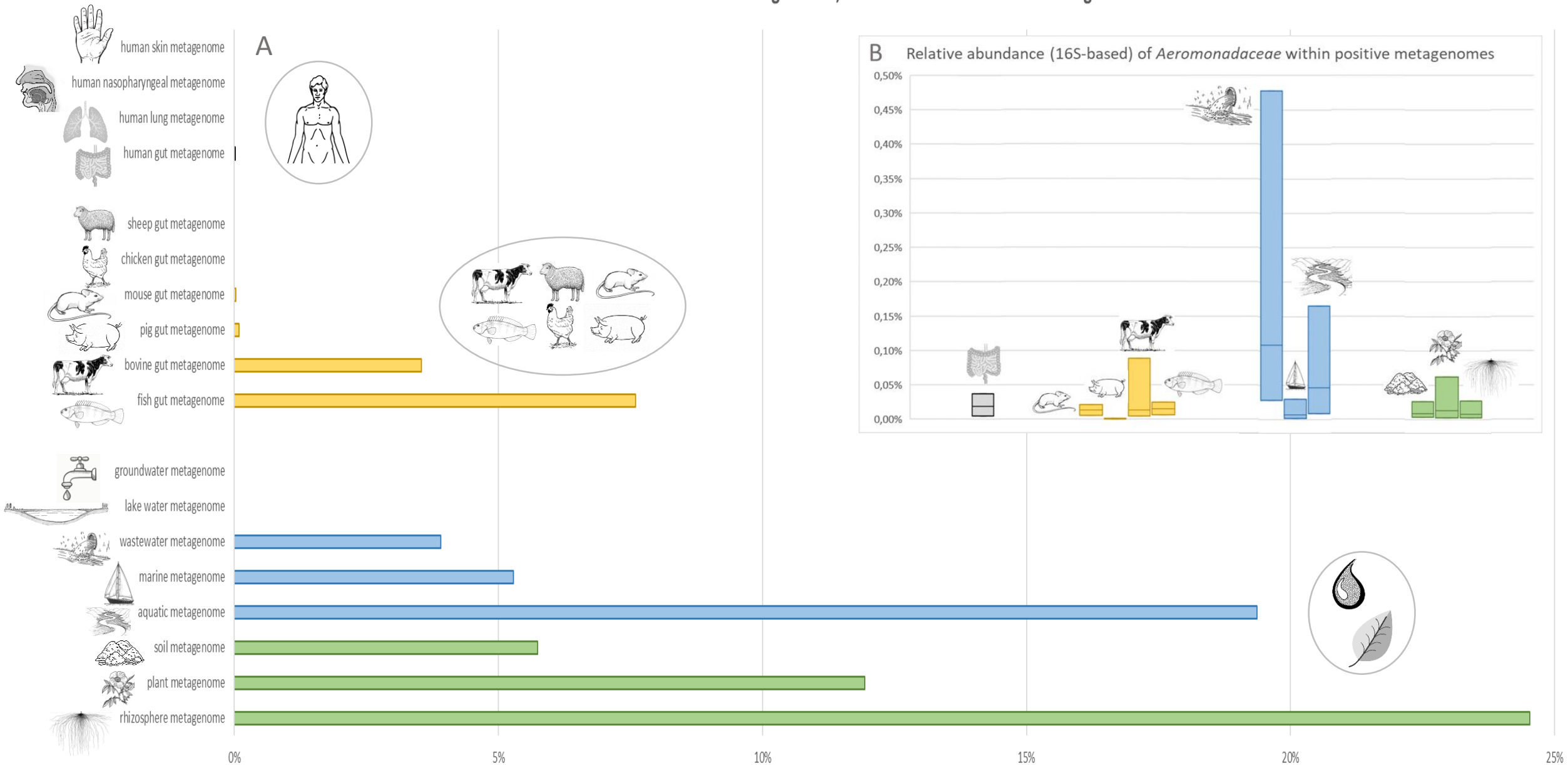
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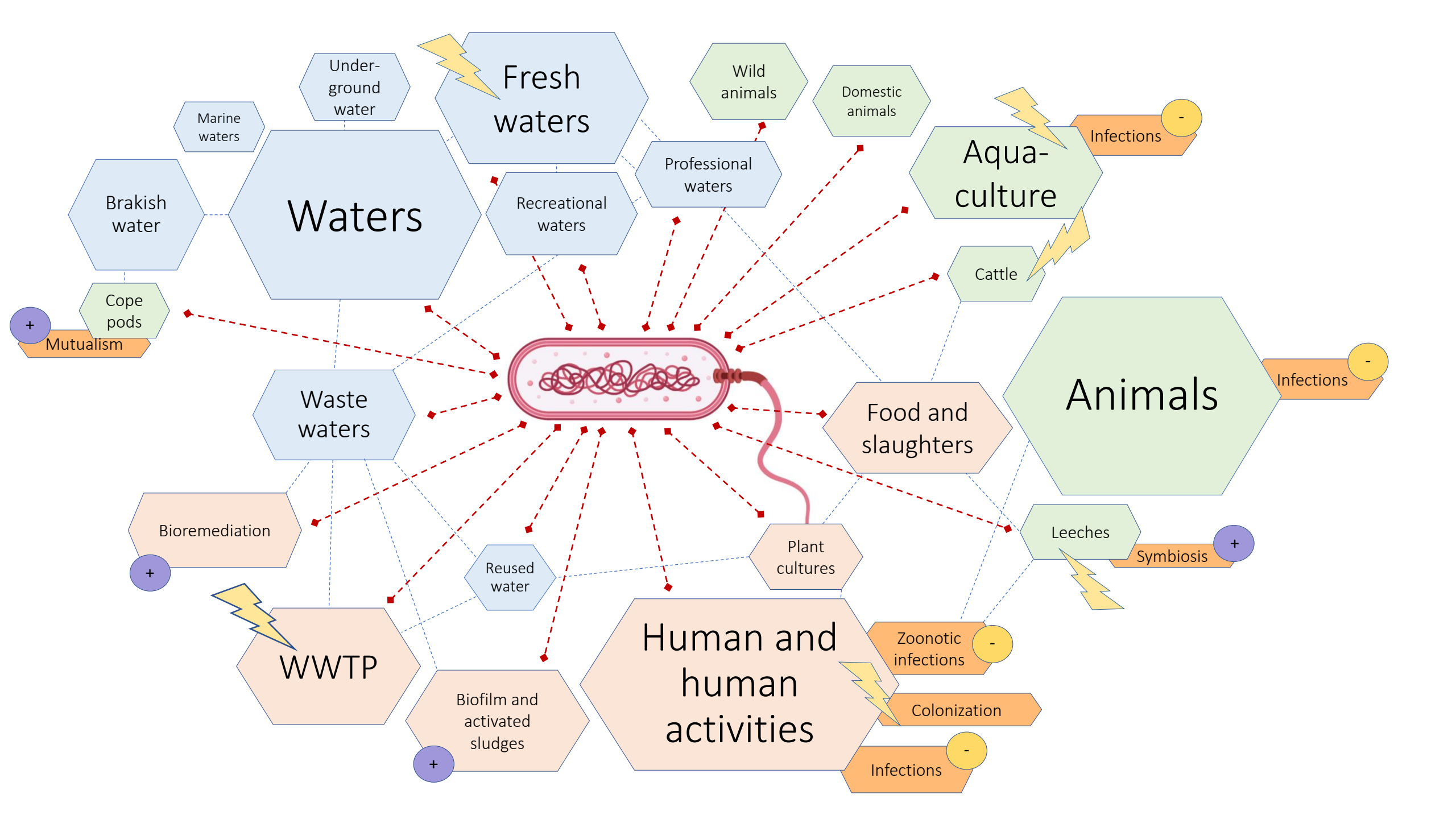
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# Prevalence of *Aeromonadaceae* among human, animal and environmental metagenomes



**Figure 1: Prevalence of *Aeromonadaceae* among human, animal and environmental metagenomes.**

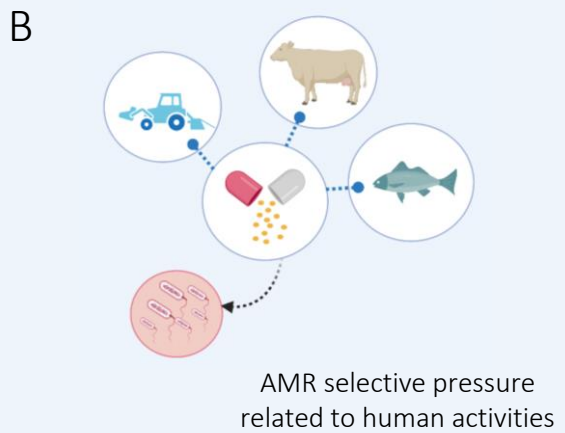
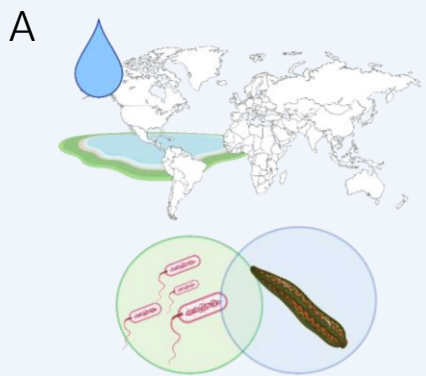
Figure 1A presents for the 3 compartments of the *One Health* world the percentage of metagenomes in which *Aeromonadaceae* are detected. This ecological distribution is based on 16S rRNA studies: grey, human metagenomes; yellow, fish and other animal metagenomes; blue, water metagenomes; green, soil and plant metagenomes. These data were obtained using the IMNGS database (<http://imngs.org>) [8] queried in May 2021 using reads matching the *Aeromonadaceae* taxonomy. Figure 1B indicates the relative abundance of *Aeromonadaceae* retrieved for each type of positive metagenome, presented with box plots.



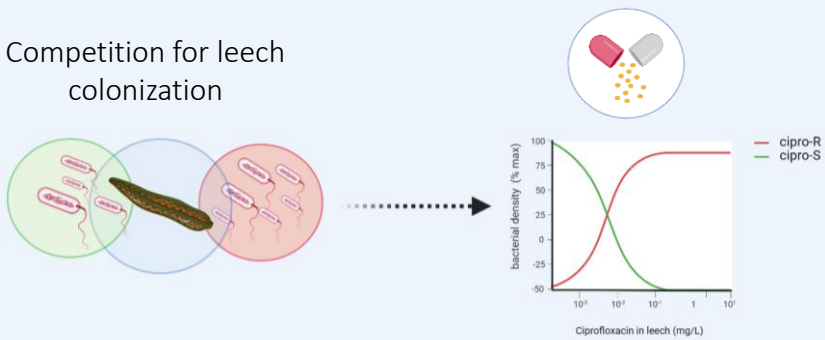
**Figure 2: *Aeromonas* in the *One Health* world, a complex network of relationships.**

The figure presents the 3 parts of the *One Health* world where aeromonads are present: environment, mainly waters (blue), animals (green), human beings and related activities (light orange) and the compartments to which they are connected are shown with red dotted connectors. The intricate and complex network in which aeromonads interface the different compartments, mostly through waters, and in which they play a role of courier is shown with blue dotted lines. Flashes highlight the compartments where aeromonads contribute to disseminate antimicrobial resistance, dark orange specific host-bacteria interactions; beneficial relationships with host (e.g., human being) are highlighted in purple while detrimental relationships are yellow highlighted. WWTP, Wastewater treatment plant. Some parts of the figure were made with biorender (<https://biorender.com>).

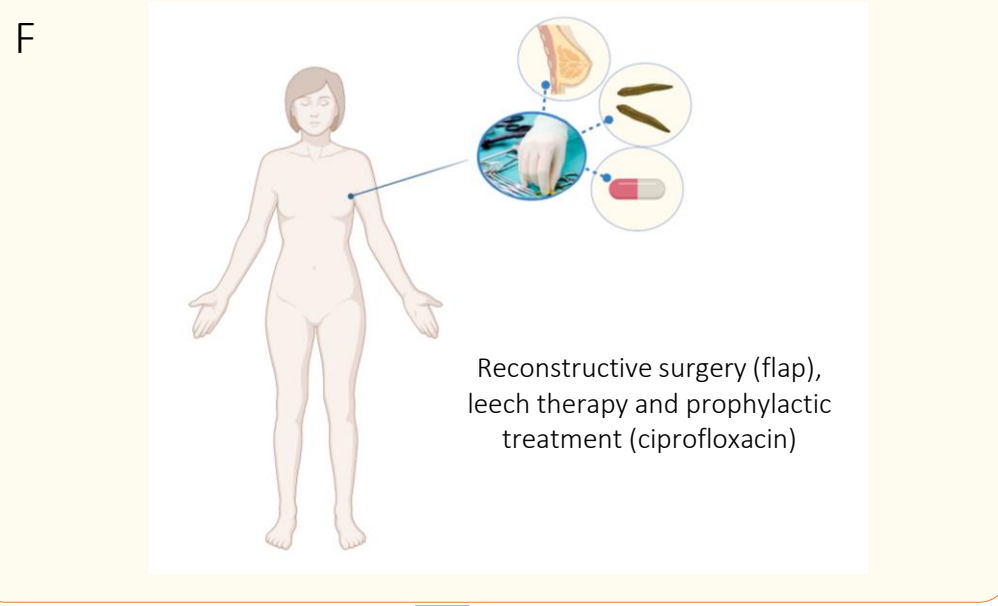
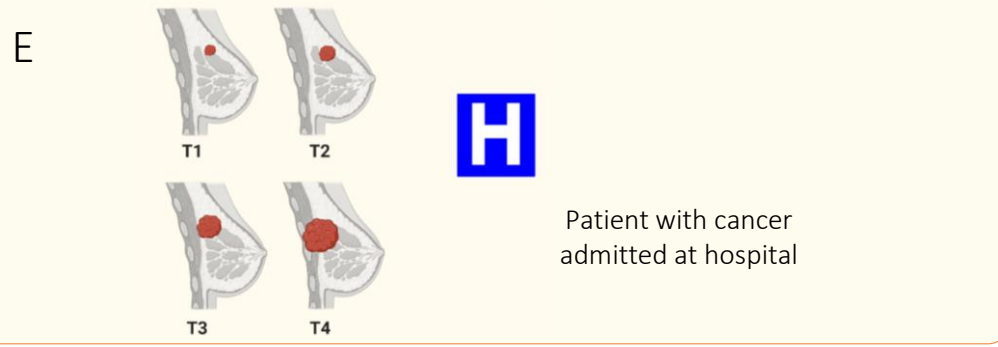




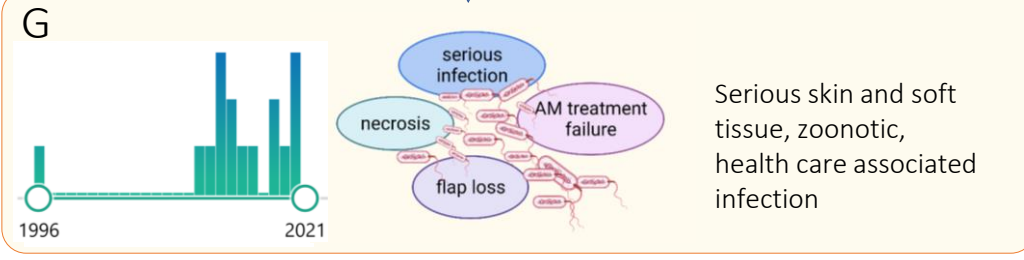
**C** Competition for leech colonization



Leech colonized with cipro-R aeromonads



Leech regurgitates (multi-) drug resistant aeromonads



**Figure 3: the *One Health* perspective of aeromonad infection following leech therapy, an emblematic health care associated zoonotic infection caused by multi-drug resistant environmental opportunistic bacteria.**

A, aeromonads are ubiquitous bacteria present primarily in waters. They usually exhibit very high rate of susceptibility to ciprofloxacin (green circles) [46]. B, Human activities with either misuse or overuse of antimicrobials, including quinolones, lead to antimicrobial selective pressure on aeromonads that can become resistant to ciprofloxacin (red circles). C, during leech colonization by *Aeromonas*, its main symbiont, ciprofloxacin resistant strains outcompete the susceptible strains when some trace of quinolones are present in the leech environment [52]. D, the leech trade is a global trade with diverse distant supplying sources, which allows the dissemination of bacteria from distanced parts of the world. E, patients with cancer are managed in hospital. F, during care pathway, cancer patients may benefit from reconstructive surgery, which may include flap surgery and may be associated with leech therapy to circumvent flap venous congestion. There is a risk of aeromonosis when leech regurgitates bacteria into the flap during bloodletting. Risk of infection is controlled with an antimicrobial prophylactic treatment, mainly ciprofloxacin [53]. G, because leeches are now frequently colonized with ciprofloxacin-resistant aeromonads, infection occurs despite prophylactic treatment and results in serious skin and soft tissue infection with flap loss and sepsis. Such event are posterior to 2010 and are regularly reported [55]. Some parts of the figure were created in biorender.com. Bibliometry histogram in G was obtained from Pubmed with keywords *Aeromonas*, leech therapy, infection and antimicrobial resistance. R: resistant. AMR: antimicrobial resistant. AM: antimicrobial.