

## Article

# The Role of Microplastics on Marine Pathogen Transmission: Retrospective Regression Analysis, Experimental Design, and Disease Modelling

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**1** **Abstract:** Marine wildlife and aquaculture species can accumulate large amounts of microplastic particles (<1 mm), threatening the health of marine populations and ecosystems and posing a risk to food safety and human health. The uptake of chemicals from microplastics seems to decrease the immune capacity of bivalves and corals to fight pathogenic bacteria, thereby increasing their vulnerability to disease. Moreover, major pathogens of bivalves, fish, and humans, including several *Vibrio* species, have been shown to be specifically enriched in the microbial communities adhered to marine microplastic debris (MMD). Microplastics can therefore serve as an important vector for and regulator of pathogen transmission and disease dynamics. Here, we outline a theoretical, three-perspective approach for studying the relationship between MMD and disease. First, we provide a framework for retrospective analysis of MMD and pathogen loads in marine animal tissues to assess the relationships between them, their bioaccumulation over time, and their relationship to other environmental variables. The results from such an analysis can be used to decide whether a compound or pathogen should be considered an emerging substance or organism. Second, we describe an experimental design for testing the effect of a variety of microplastics on *in vivo* pathogen removal (i.e., the phagocytic activity of hemocytes) and infection intensity in two study model species (oysters and zebrafish). Finally, we create a theoretical susceptible-infected microplastic particle and pathogen transmission model for bivalves and fish. Overall, the experiments and models we propose will pave the way for future research designed to assess the role of MMD as a vector for marine and human pathogens. This multi-faceted approach needs to be an urgent priority of the EU Strategic Research Innovation Agenda for addressing marine disease challenges related to MMD.

**22** **Keywords:** microplastics; pathogens; disease modelling; transmission

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## **23** 1. Introduction

**24** Marine microplastic debris (MMD; plastic particles <1 mm in diameter) is an emerging, human-induced threat to the world's seas and oceans [1]. Annual plastic production **25** continues to rise [2,3], and the continued degradation of larger plastic items [4] further **26** increases the abundance of MMD and therefore the risk of wildlife being exposed to it [5]. **27** Given the small size of microplastics, organisms from diverse trophic levels are capable **28**

29 of ingesting and accumulating these particles. In the marine food web, microplastics  
30 can be found in organisms ranging from zooplankton[6] to fish [7,8], including large  
31 pelagic fish [9] and whales [10]. The bioaccumulation of MMD is an emerging risk to  
32 the health of marine ecosystems, and, in turn, to food safety and human health [11–13].  
33 Marine invertebrate filter-feeders such as bivalves [12,14,15] are particularly susceptible  
34 to MMD accumulation because they process large amounts of water while feeding [16].

35 In the last decade, large-scale policy recommendations and government-sponsored  
36 programs have increased public awareness of marine MMD. At the same time, most  
37 scientific investigations have primarily focused on the distribution of MMD in seas  
38 and oceans [17,18], its presence in diverse organisms, and its toxicology [19–21]. Nev-  
39 ertheless, little is known about the virulence and disease dynamics of MMD and a  
40 comprehensive risk assessment is still far away for marine ecosystems, food safety, and  
41 public health [22]. We believe that exploring this knowledge gap should be an important  
42 component of future MMD research. In other words, across the diversity of marine biota  
43 from zooplankton to bivalves and fish, what is the role of MMD in the transmission of  
44 marine and human pathogens?

45 Answering this broad question requires research on how MMD contributes to the emer-  
46 gence of marine diseases. Marine diseases may emerge as a result of novel introductions,  
47 climate change, changes in vector populations, and the introduction of novel vectors.  
48 The assessment and management of future disease risks depends on understanding  
49 the causes of historical and contemporary disease emergence events [23]. However,  
50 because MMD is a newly recognized form of environmental pollution, there is little  
51 information on the historical prevalence of MMD. Indeed, MMD monitoring programs  
52 were non-existent until recently [24,25], mostly due to the lack of methods for routine  
53 MMD quantification [26]. Researchers have recently attempted to quantify MMD in  
54 samples collected for zooplankton analysis; the results appear to be promising and could  
55 therefore provide low-cost methods for data collection on MMD in the water column  
56 [27].

57 Data from peer-reviewed literature and publicly available repositories, as well as  
58 newly emerging data sets, suggest that the abundance and mass of MMD in the North  
59 Pacific Subtropical Gyre increased by two orders of magnitude during the period from  
60 1972 to 1987 and again between 1999 and 2010 [28]. Furthermore, North Atlantic and  
61 North Sea surface samples collected by a continuous plankton recorder suggest that the  
62 frequency with which MMD is encountered during surveys has been steadily increasing  
63 alongside the global increase in plastic production [29]. However, researchers have  
64 not yet confirmed a corresponding global increase in MMD concentrations in marine  
65 organisms.

66 One approach to obtaining such confirmation would be performing a retrospective  
67 study on the occurrence of MMD in biological samples from environmental specimen  
68 banks. Retrospective monitoring using archived samples from specimen banks can  
69 provide information on past and current trends in the exposure to and consumption of  
70 MMD by marine organisms as well as on the prevalence of major pathogens. Such a  
71 study would allow for a better evaluation not only of the concrete threat posed by MMD  
72 and major pathogens but also of the effect of MMD on disease ecology.

73 In addition, the role of MMD in the transmission of marine pathogens needs to be  
74 addressed by conducting experimental studies that explore both microplastic uptake by  
75 different organisms and disease transmission among those same organisms, based on the  
76 understanding that microplastics can be carriers of chemicals and pathogens. For exam-  
77 ple, persistent chronic pollution has been linked to pathological alterations in bivalves  
78 and a higher prevalence and intensity of parasites, including *Rickettsia/Chlamydia*-like  
79 organisms (R/CLO), in shellfish [30]. Indeed, the uptake of chemicals from ingested  
80 MMD has been suggested to decrease the capacity of bivalves to fight off pathogenic bac-  
81 teria [31]. Microplastic exposure also activates stress responses and suppresses immune  
82 function in corals [32,33].

83 Diverse pathogens have been found in the ocean's plastisphere, which is the mi-  
84 crobial community that adheres to microplastics. This microbiome is distinct from the  
85 surrounding seawater and can include humans, fish, and bivalve pathogens [34–36]. In  
86 laboratory experiments, plastisphere microbial communities form biofilms on poly-vinyl  
87 chloride surfaces during lab experiments [34]. The plastic type and particle size affects  
88 not only the biofilm formation rate [37] but also the rate at which marine organisms  
89 ingest and accumulate the plastic [12] as well the plastic's toxicity [38]. Some of the  
90 pathogens within these plastisphere biofilms, including various *Vibrio* species, are ex-  
91 tremely virulent. For example, *Vibrio cholerae* can cause cholera when they enter humans  
92 through ingested seafood [39], and *V. anguillarum* has been particularly devastating to  
93 salmonid populations [40]. *V. parahaemolyticus* causes vibriosis in marine bivalves and  
94 fish worldwide as well as sepsis, gastroenteritis, and wound infections in humans [41].  
95 Other human pathogens, including *V. alginolyticus* and *V. vulnificus*, have been found in  
96 fish [42] and shellfish samples [43].

97 These pathogens can be trophically transmitted even if the MMD itself is not. For ex-  
98 ample, *Vibrio* pathogens have caused extensive epizootics and mass mortalities of oysters  
99 [44]. Recent laboratory experiments suggest that MMD does not bioaccumulate in oyster  
100 tissues in the short term; however, the microorganisms assimilated via the ingestion  
101 of biofilm-coated MMD do seem to be transferred to higher trophic levels and have  
102 potential infectious capacity [45]. The transmission of MMD-carried pathogens poses a  
103 serious risk to wildlife, food safety, and human health. Understanding the relationship  
104 between MMD and bacterial pathogens in commercially harvested bivalve species is  
105 particularly important for determining the risks MMD poses to marine ecosystems and  
106 human health because (i) several marine pathogens have caused mass mortality events  
107 in bivalves [e.g. 44], and (ii) the accumulation of human pathogens in edible bivalve  
108 species poses seafood-related health risks to human consumers [46].

109 Based on these concerns, we have identified three parallel, interconnected, and  
110 urgent research objectives for better understanding the role of MMD in the transmis-  
111 sion of marine pathogens. First, researchers must explore the past and expected future  
112 trends of both MMD exposure and pathogen occurrence in marine ecosystems. Second,  
113 field and laboratory experiments should be conducted to determine the effect of the  
114 MMD-pathogen interaction on disease transmission. Finally, researchers should develop  
115 the quantitative and theoretical basis for modeling disease processes associated with  
116 MMD ingestion in marine organisms to better understand the epizootiology of these  
117 'vector-borne' disease. Here, we describe some useful experimental, statistical, and  
118 disease modelling methods that can be used to address these three research objectives.  
119 We also present some theoretical results that we discussed in relation to the potential  
120 mechanisms by which MMD ingestion affects pathogen transmission in marine organ-  
121 isms.

122

## 123 2. Materials and Methods

124 In this study, we describe the three key approaches outlined above for studying  
125 the role of MMD on marine disease transmission: (i) a retrospective analysis of the  
126 interaction between MMD and disease in the context of other environmental variables;  
127 (ii) an experimental design for studying the uptake of MMD-carrying pathogens by  
128 marine organisms and the associated effects on disease transmission; and (iii) a quanti-  
129 tative disease transmission model parameterized by data from retrospective analyses,  
130 experiments, and previously published work.

### 131 2.1. Retrospective analysis

132 Data on historical MMD concentrations and pathogen loads in bivalves, as well as  
133 data on other environmental parameters (e.g., temperature), can be used to determine the  
134 environmental factors that facilitate and limit the exposure of filter feeders to MMD and

<sup>135</sup> pathogens. In this context, the environmental parameters act as inputs in multivariate  
<sup>136</sup> regression models predicting MMD or pathogen load.

In a general way, a regression model describes the relationship between a response variable,  $Y$ , and some explanatory variables,  $\mathbf{X} = (X_1, \dots, X_p)$ . The explanatory variables are also known as covariates. Such a multivariate model is defined as:

$$Y = m(\mathbf{X}) + \varepsilon$$

<sup>137</sup> where  $m(\cdot)$  is the mean function and  $\varepsilon$  is the regression error.

The simplest form of regression analysis is a linear regression, which serves as a good jumping-off point for newer or advanced modeling approaches that generalize or extend this method. In a linear regression, the response variable is assumed to follow a normal distribution, and the effect of the covariates on the response is assumed to be linear. The problem with this simple model is that, in most real-world contexts, including in the study of MMD prevalence, the response variable is not normally distributed. Instead, the response variable might follow a discrete distribution, such as the Poisson. For these situations, generalized linear models (GLMs) [47,48] extend simple linear ones by allowing the use of other distribution families to model the response variable. In a GLM, the relationship between the mean response and the covariates is modeled by:

$$E[Y|\mathbf{X}] = \eta(\beta_0 + \beta_1 X_1 + \dots + \beta_p X_p),$$

where  $\eta(\cdot)$  is a known monotonic function (the inverse of the link function). Once the distribution of the response variable has been determined, we must also determine whether the effect of the covariates on the response is linear. Although simple and generalized linear models have been widely used, their parametric assumption of linear effects is very restrictive and, in certain circumstances, not supported by the data. If the parametric model is inappropriate for the data, the conclusions from the model will be erroneous. In this case, nonparametric regression techniques can be used to model the dependence between  $Y$  and  $\mathbf{X}$  without needing to specify in advance the function that links the covariates to the response. This family of models is called generalized additive models (GAMs) [49] and is defined by:

$$E[Y|\mathbf{X}] = \eta(\alpha + f_1(X_1) + \dots + f_p(X_p)), \quad (1)$$

<sup>138</sup> where  $\eta(\cdot)$  is a known monotonic function (the inverse of link function) and  $f_1, \dots, f_p$   
<sup>139</sup> are smooth, unknown, continuous functions. A large body of literature has been de-  
<sup>140</sup> voted to finding techniques for estimating the regression model in equation 1. Two of  
<sup>141</sup> most widely used approaches are splines [50,51] and kernel smoothers [52,53]. Spline  
<sup>142</sup> smoothing involves modeling a regression function as a piecewise polynomial, where  
<sup>143</sup> the number of pieces is relatively high compared to the sample size. The performance  
<sup>144</sup> of this technique is governed by the number and position of knots used to calculate  
<sup>145</sup> the estimator. Despite considerable research effort [54], the difficult problem of knot  
<sup>146</sup> selection has not been totally solved. Our continued research on the topic of marine  
<sup>147</sup> microplastics includes the development of a new methodology that will allow us to  
<sup>148</sup> estimate any type of unknown curve, compare the results with other existing estimation  
<sup>149</sup> procedures, and use simulations to study the performance of our method in a finite  
<sup>150</sup> sample.

<sup>151</sup> Another option for fitting GAMs is local regression based on kernel smoothers; this  
<sup>152</sup> method involves computing the fit at a point  $x_0$  using only the nearby observations.  
<sup>153</sup> A key advantage of kernel smoothers is their use of binning techniques [55], which  
<sup>154</sup> greatly reduce the computational time and thus enable the model to be adequately  
<sup>155</sup> solved in practical situations. However, kernel smoothers require the user to choose  
<sup>156</sup> the bandwidth parameters, which can have a large effect on the obtained parameter  
<sup>157</sup> estimates. Different studies have proposed various methods for choosing the optimal

158 bandwidth, including generalized cross-validation [56], plug-in methods [57], bootstrap  
159 techniques [58].

160 Variable selection is another important issue when developing a multivariate regres-  
161 sion framework, especially when the number of covariates is large enough. Inferences  
162 based on models with only a few variables can be biased; conversely, models that use too  
163 many variables may result in a lack of precision or false-positive effects. The so-called  
164 model selection problem arises from the need to ensure that a model is neither under-  
165 nor over-fitted [59]. The literature describes several procedures for solving this problem  
166 and choosing the optimal set of variables; these methods can include shrinkage regres-  
167 sion (e.g., the Lasso [60,61]), Bayesian approaches [62–64], iterative procedures such as  
168 stepwise selection based on the use of some information criteria [65–67], or the use a full  
169 information criteria-based approach [68].

170 The multivariate regression methodology described above can be easily used to  
171 investigate the abundance of MMD in bivalves, both at present and over time, with  
172 the aim of determining the environmental and food chain-associated human health  
173 risks of MMD. For example, such a regression could be applied to retrospective data  
174 on microplastic concentrations and pathogen prevalence in bivalve tissue samples from  
175 biospecimen banks spanning the last few decades. For this analysis, MMD abundance  
176 could be determined in bivalve tissues using polarized light microscopy following the  
177 recommendations of recent studies [69]. In addition, the prevalence of shellfish and  
178 human pathogens, as well as histopathological alterations, could be scored using either  
179 quantitative or semi-quantitative scales [70]. The results of this retrospective study  
180 would help assess current and historical trends in the accumulation of microplastics  
181 and pathogens in marine filter-feeders as well as the relationship between microplastic  
182 accumulation and pathogen prevalence. When combined with information on the  
183 ecotoxicology and pathogenicity of a given pathogen, these exposure and prevalence  
184 data can be helpful for deciding whether a compound or pathogen must be considered  
185 as an emerging substance or organism.

186 In addition to the multivariate regression modelling approach predicting both  
187 MMD and pathogen loads in bivalves based on a suite of environmental variables, some  
188 industry evolution data can be included in the predictor data pool. This final model  
189 could be evaluated using a specific stepwise method; in this case, we suggest a forward  
190 stepwise-based selection procedure that both (i) selects the best combination of variables  
191 and (ii) determines the optimal number of covariates to include in the model. This type  
192 of analysis would provide valuable information for understanding which factors or  
193 variables from the plastic industry, in addition to the physiochemical environment, are  
194 involved in the temporal trends of microplastic occurrence and pathogen prevalence in  
195 marine animals. The results from such a model would also have important implications  
196 for future studies of the ecological and seafood-related risks of microplastics.

197 In this study, we present an example of this type of analysis by GAMs to analyze  
198 (i) the effect of different environmental variables on microplastic abundance (*number*  
199 *of occurrences of microplastics g<sup>-1</sup>*) and infection intensity (*number of occurrences of*  
200 *pathogens g<sup>-1</sup>*) in mussels and (ii) the relationship between microplastic abundance  
201 and infection intensity. Explanatory variables in the first model included river flow rate  
202 ( $m^3 sec^{-1}$ ), salinity, temperature (°C), dissolved oxygen (%), percent dissolved oxygen  
203 saturation), salinity stratification index, and chlorophyll concentrations ( $mg m^{-3}$ ). These  
204 data were obtained from monthly samplings from 1998 to 2015 in the Basque coast  
205 (estuaries of Bilbao and Urdaibai), N Spain (43°24.2'N 2°41.7'W), using the material  
206 and methods described in Iriarte *et al.* [71]. The response variables were constructed  
207 theoretically. We used the log function as a link and thin plate regression splines as a  
208 smoothing basis. The optimal number of degrees of freedom was chosen via (generalised)  
209 cross-validation [72], and parameter estimation was performed using the mgcv package  
210 [73] in R [74].

211 2.2. *Experimental studies*

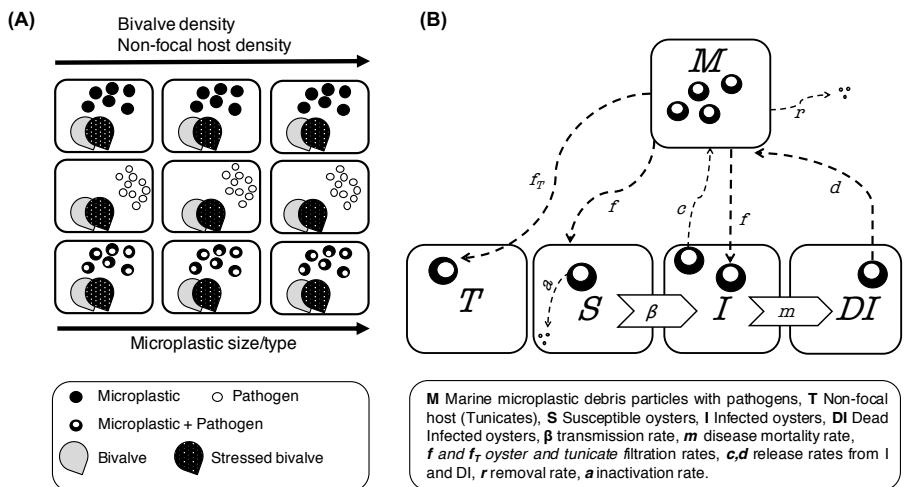
212 To better understand the global risks of MMD particles as disease vectors, basic  
213 experimental research is needed on how the MMD-pathogen interaction affects emerging  
214 marine disease dynamics. Such studies are essential for generating the knowledge  
215 needed to mitigate both marine ecosystem degradation and the human health risks of  
216 marine pathogens.

## 217 2.2.1. Oysters as an experimental model

218 In the context of MMD, bivalves and other filter-feeders are distinct because they  
219 can filter out and therefore accumulate MMD from the water column [75], making  
220 them particularly susceptible to pathogens [44]. They are also important vectors for  
221 seafood-borne human pathogens [46] that are adhered to microplastics [76]. Due to their  
222 tremendous filtration capacity (up to 8 liters of seawater per hour [16]), oysters are one  
223 of the best model organisms for experimental studies exploring how marine organisms  
224 uptake MMD and the role of microplastics on pathogen transmission.

225 The experimental setup may emphasize one or more of the following aspects of  
226 MMD (Figure 1A): (1) the role of microplastic size or type on its uptake in bivalves; the  
227 relationship of this uptake with (2) the *in vivo* accumulation or removal of pathogens  
228 (e.g., the phagocytic activity of hemocytes); and (3) the infection intensity of bivalve  
229 pathogens. Microplastic types and sizes for the experiments can be chosen from irregular  
230 polyethylene and polyethylene terephthalate fragments in the shape of fibres, spheroids,  
231 granules, pellets, flakes, or beads. Particle sizes should be in the range of 0.1-5000  $\mu\text{m}$ .

232 For the study design, oysters should be deployed in tanks and exposed to MMD  
233 for 1-5 weeks to obtain stressed oysters for subsequent trials. Stress in oysters can be  
234 assessed by studying a variety of stress responses such as tissue alteration, immune  
235 alteration, DNA damage, oxidative stress, altered lipid and glucose metabolism, and a  
236 reduced clearance rate of pathogenic organisms [77,78]. By comparing MMD-stressed  
237 and non-stressed oysters, researchers can evaluate how the uptake of chemicals adhered  
238 to the surface of MMD may affect the oysters' capacity to remove (or resist) pathogenic  
239 bacteria [31-33]. In this theoretical experimental setting, three important experimental  
240 trials can be conducted. First, oysters can be exposed to microplastics of different types  
241 and sizes at varying concentrations (e.g., 10 and 1000  $\mu\text{g L}^{-1}$ ) (Figure 1A, top panel)  
242 and for different periods of time (e.g., 1-5 weeks). This exposure would be performed  
243 under static conditions using similar protocols as [78]. Second, oysters can be exposed  
244 to different *Vibrio* spp. concentrations in the water column (from  $10^3$  to  $10^7$  cells  $\text{L}^{-1}$ )  
245 (Figure 1A, mid panel). By analyzing the bacterial load of oyster samples at the end  
246 of the exposure period (e.g., as culturable *Vibrio* counts), researchers can assess the  
247 incidence of *Vibrio* in terms of pathogen infection intensity. Third, oysters can be exposed  
248 to microplastics with adhered *Vibrio* spp. (Figure 1A, bottom panel) and then assess  
249 the incidence of *Vibrio* as in the second experiment. These three trials would ideally be  
250 conducted for both stressed and non-stressed oysters at varying temperatures and oyster  
251 densities. These trials could also be performed in systems that include non-focal hosts  
252 such as tunicates (T in Figure 1B) in order to assess the disease-diluting effect of other  
253 filter-feeders in the same ecosystem [79].

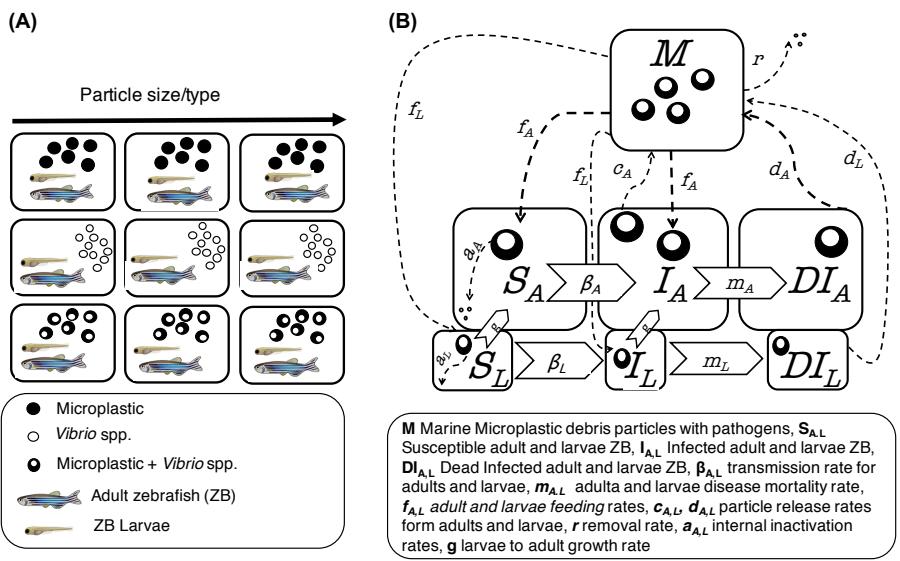


**Figure 1.** Experimental design for bivalves. The proposed experiment (A) can evaluate different microplastic types/sizes and different oyster and non-focal host densities to determine the effect of these variables on MMD uptake and accumulation in oysters and the relationships between MMD uptake and each of pathogen (i.e., *Vibrio* spp.) occurrence and disease responses. The conceptual disease model (B) represents a simplified scheme of subpopulations, parameters, and processes that will be incorporated into an ordinary differential equation system (as in [80]). This system comprises the 'bivalve-microplastic-*Vibrio*' disease model. B

### 2.3. Zebrafish as an experimental model

Another valuable model system for studying the role of microplastics in pathogen transmission is the zebrafish (*Danio rerio*). Zebrafish are already one of the most important models in environmental toxicology and developmental biology and are rapidly becoming a major model in studies of animal and human health and disease. The zebrafish has a long and extremely successful history as a model organism for many biological processes ranging from development to bacterial pathogenesis [81,82], including the pathogenesis of aquatic pathogens such as *Vibrio* spp. [41,83,84]. Other studies have also investigated the uptake and accumulation of polystyrene microplastics in zebrafish tissue [e.g. 85]. Experimentally studying the role of microplastics as vectors of aquatic pathogens in such a well-established model system is particularly valuable because the biology of zebrafish is already thoroughly understood, allowing researchers to easily identify the risks posed by these various processes. Moreover, because zebrafish larvae are transparent, researchers can visualize the *in vivo* uptake and accumulations of microplastics and pathogens using fluorescently labelled pathogens and microplastic particles. These observations may be crucial for studying the behavior of the host-microplastic-pathogen system.

Overall, studies using zebrafish could determine whether the uptake and transmission of pathogens in fish is affected by the presence of microplastics. Future experiments in the zebrafish model should address the basic but unanswered questions about host-microplastic-pathogen dynamics; for example, will microplastics alter the bioavailability, uptake route, or transmission of pathogens like *Vibrio* spp.? Will the transmission of pathogens through microplastics be similar in different types and sizes of plastic? Will it be similar in adult fish and larvae?



**Figure 2.** Experimental and model design for zebrafish. The proposed experiment (A) can evaluate different microplastic types/sizes to determine their effect on MMD uptake and accumulation in both adult fish and larvae, as well as the relationship between MMD uptake and each of pathogen (i.e., *Vibrio* spp.) occurrence and disease responses. The conceptual disease model (B) represents a simplified scheme of subpopulations, parameters, and processes that will be incorporated into an ordinary differential equation system referred to as the fish-microplastic-*Vibrio* disease model.

278 To analyze the behavior, accumulation, and transfer of microplastic-associated  
279 pathogen in adult and larval zebrafish, researchers can use different sizes and types of  
280 fluorescently labeled microplastics as well as a model pathogen (carrying a plasmid that  
281 encodes green fluorescent protein) as representative for aquatic bacterial pathogens. Six-  
282 month old zebrafish are sufficient for experiments with adult zebrafish, and zebrafish at  
283 five days post-fertilization may be suitable for the larval experiments. Microplastic accu-  
284 mulation could be assessed in the gills, gut, and intestines based on fluorescence intensity.  
285 In parallel, pathogen infection levels can be assessed with histological analyses in adults  
286 and fluorescence tracking in larvae. By taking advantage of the transparency of zebrafish  
287 larvae and using a genetically engineered fluorescent model pathogen, researchers can  
288 observe the active uptake and colonization of MMD-associated pathogens.

289 As in the oyster model, the zebrafish model could use a similar combination of  
290 microplastic types/sizes, microplastic concentrations, experimental durations, treatment  
291 types, and pathogen concentrations (Figure 2A). As a result, the zebrafish experiment will  
292 investigate the role of microplastic size and type on the plastic uptake and accumulation  
293 rate as well as the relationships between microplastic uptake, pathogen accumulation,  
294 and infection intensity in both adults and larvae. Alternative experiments could in-  
295 vestigate the transmission of MMD and pathogens through the food chain by feeding  
296 zebrafish with brine shrimp (*Artemia nauplii*) that have already accumulated MMD and  
297 pathogens.

#### 298 2.4. Disease transmission modelling

299 The results obtained from these controlled experimental studies, in combination  
300 with previously published data, would provide the empirical and theoretical information  
301 needed to understand the role of microplastics as a transmission vector for bivalve, fish,  
302 and human pathogens. Specifically, this data can be used to develop and parameterize  
303 epizootiological and epidemiological models. In this study, we use continuous-time  
304 compartmental models adapted from previous susceptible-infected-particle-filtration-  
305 type disease dynamic models [e.g. 79,86]. Note that, by using a combination of empirical

306 data and disease transmission models, researchers can also build relationship models  
 307 to describe the links between microplastic pollution, microplastic uptake, toxicological  
 308 effects, and *Vibrio* infections.

309 2.4.1. Model schemes

310  
 311 Figure 1B and Figure 2B show flow diagrams of the disease transmission models for  
 312 suspension bivalves and fish, respectively, highlighting the important processes involved  
 313 in disease transmission. We refer to these models as the bivalve-microplastic-*Vibrio* and  
 314 fish-microplastic-*Vibrio* disease transmission models, respectively.

315 In both compartmental susceptible/infected-type models, the pathogen is attached  
 316 to particles of *MMD*; these particles are represented by  $M$  in the models. The pathogen  
 317 is then transmitted to the susceptible population  $S$  at a rate  $\beta$  through either filtration or  
 318 ingestion of  $M$  at a rate  $f$ . Infected animals  $I$  die according to a disease mortality rate  $m$ .  
 319 Particles are removed *in vivo* from individuals in each population at a rate  $a$  by internal  
 320 inactivation processes, and particles are removed from the water column at a rate  $r$  by  
 321 diffusion/advection and decay processes. The bivalve model includes a non-target host  
 322 population ( $T$ ) that is immune to and importantly inactivates pathogens. The zebrafish  
 323 model includes adult (subindex  $A$ ) and larvae (subindex  $L$ ) subpopulations. A detailed  
 324 description of the variables, parameters, and units for each model can be found in Table  
 325 1 and Table 2.

Variable	Definition	Unit
$S, S_A, S_L$	Susceptible hosts in the population	Number of individuals
$I, I_A, I_L$	Infected individuals in the population	Number of individuals
$DI, DI_A, DI_L$	Dead infected individuals in the population	Number of individuals
$M$	Marine microplastic debris particles with adhered pathogens	Number of particles
$T$	Alternate non-competent reservoir hosts	Number of individuals

Table 1: Variables in the bivalve- and fish-microplastic-*Vibrio* models. There is no subindex for the oyster population, whereas the A and L subindexes in the fish model represent adult and larvae subpopulations, respectively. Note that the model has an implicit surface area for the host subpopulations and an implicit volume for the pathogens.

326 The two theoretical models described here (bivalve and zebrafish) are different from  
 327 each other because they include the differentiated mechanisms and processes involved  
 328 in disease transmission in each organism. The main differences are the following: (1) In  
 329 the bivalve model (Figure 1), an alternative host, tunicsates  $T$ , competes for waterborne  
 330 pathogens with the susceptible host. This alternative host is resistant to the disease  
 331 and does not release particles to the water. Pathogens filtered by  $T$  are assumed to be  
 332 inactivated by the immune system or by diapedesis. (2) In the zebrafish model (Figure 2),  
 333 populations are subdivided into adults and larvae. The modeled processes are allowed  
 334 to occur at different rates for fish adults (subindex A) and larvae (subindex L), and larvae  
 335 mature into adults at a rate  $g$ .

336 2.4.2. Model assumptions

337  
 338 The two disease transmission models track waterborne environmental pathogens  
 339 attached to microplastic particles. The pathogen-microplastic complex drifts through

Parameter	Definition	Unit
$\beta$	Transmission rate in oysters	individual <sup>-1</sup> day <sup>-1</sup>
$\beta_A, \beta_L$	Transmission rates in fish	individual <sup>-1</sup> day <sup>-1</sup>
$m$	Disease mortality rate in oysters	day <sup>-1</sup>
$m_A, m_L$	Disease mortality rate in fish	day <sup>-1</sup>
$g$	Growth rate from larvae to adult	day <sup>-1</sup>
$d, d_A, d_L$	Removal rate of dead individuals by scavengers or decay	day <sup>-1</sup>
$b_I, b_{I_A}, b_{I_L}$	Average number of MMD per $I$	MMD particles
$b_T$	Average number of MMD per $T$	MMD particles
$b_{DI}$	Average MMD per $DI$	MMD particles
$c, c_{A,L}$	Release rate of particles from $I$	day <sup>-1</sup>
$c_T$	Release rate of particles from $T$	day <sup>-1</sup>
$c_{DI}, c_{DI_A}, c_{DI_L}$	Release rate of particles from $DI$	day <sup>-1</sup>
$r$	Loss rate of MMD particles from the local environment	day <sup>-1</sup>
$f, f_A, f_L$	Filtration/feeding rate of $S$ and $I$	$m^3$ individual <sup>-1</sup> day <sup>-1</sup>
$f_T$	Filtration/feeding rate of $T$	$m^3$ individual <sup>-1</sup> day <sup>-1</sup>
$a, a_A, a_L$	Inactivation of pathogens in $S$ and $I$	day <sup>-1</sup>
$a_T$	Inactivation of pathogens in $T$	day <sup>-1</sup>

Table 2: Parameters of the bivalve- and fish-microplastic-*Vibrio* disease transmission models. Note that the models implicitly include a surface area (in  $m^2$ ) for oysters and volume (in  $m^3$ ) for fish and microplastic particles. In the fish model, the subindex A represents adult fish and the subindex L represents fish larvae.

340 the water and is either filtered (by bivalves) or ingested (by fish). For simplicity, the  
 341 model assumes no natural mortality for hosts; infected individuals only die due to  
 342 disease. Background mortality could be incorporated in more complex models for slow-  
 343 progression diseases. The model also assumes no natural mortality and total inactivation  
 344 of particles in the non-focal hosts  $T$ ,

345 The models also assume that populations are closed (i.e., demographic turnover  
 346 processes, like reproduction and migration, are not included in either model). In addition,  
 347 the models assume that no animals recover from the disease once infected. Indeed,  
 348 there are only a few examples of disease recovery in the marine realm [87–89]. Finally,  
 349 parameterization of the model is standardized to represent (i) a square meter of the  
 350 environment for bivalves and (ii) a cubic meter of the environment for particles and  
 351 fishes. As a result, units in the bivalve model are individuals per square meter and  
 352 units for population size are individuals per cubic meter, as in [86]. The variables and  
 353 parameters of the model related to the host can be adapted to experimental formation  
 354 as the level of stress of oysters in the case these have been exposed to microplastics  
 355 before microplastic with pathogen exposure.

### 356 3. Results

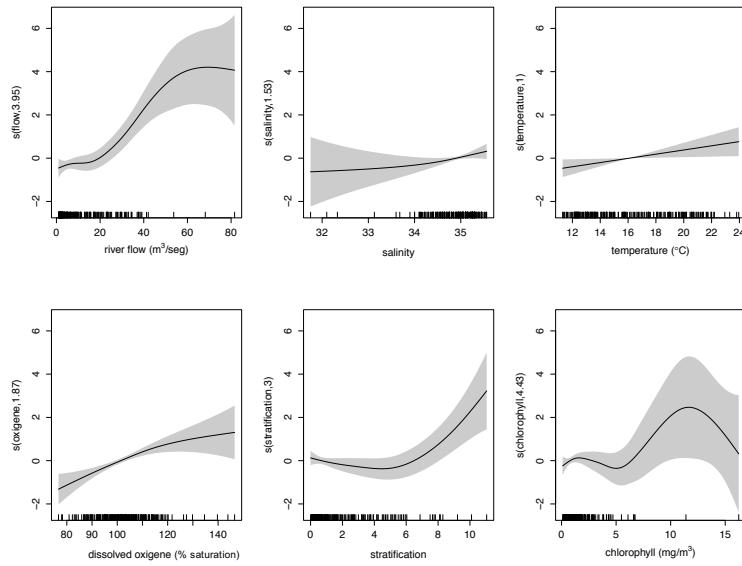
#### 357 3.1. Retrospective multivariate modeling

358 Figures 3 - 5 show the response plots from our theoretical GAM examples. The  
 359 output shown in these figures allows researchers to study the relationship between the  
 360 various environmental variables and the response variables (either the abundance of  
 361 microplastics in the organisms (Figure 3) or infection intensity (Figure 4). In our models,  
 362 salinity, temperature, dissolved oxygen, and especially the stratification index showed  
 363 a positive relationship with microplastic abundance (Figure 3). River flow rate and  
 364 chlorophyll concentrations also had an overall positive effect on microplastic abundance,  
 365 with relative maximums or minimums observed along the measured ranges of the two  
 366 variables (Figure 3).

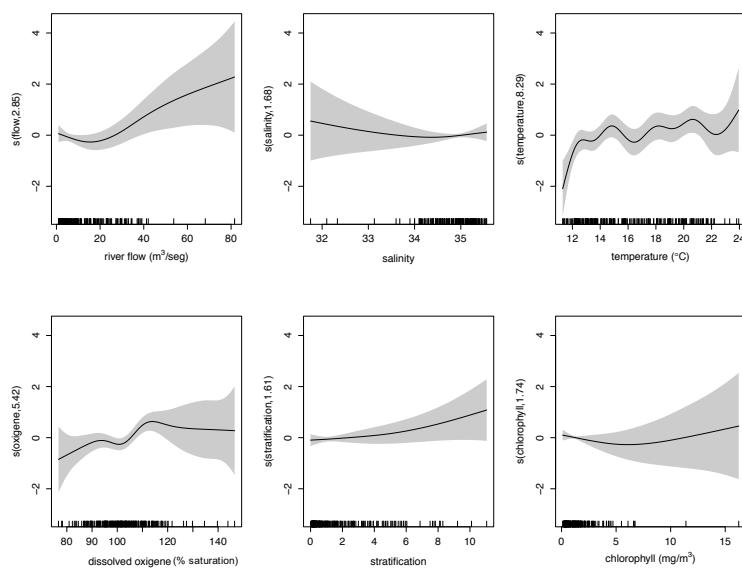
367 With the exception of salinity, all the explanatory variables that we considered  
 368 also had a positive effect on infection intensity. In the case of dissolved oxygen and

369 temperature, infection intensity increased as these variables increased but then reached a  
 370 maximum beyond which it remained within a range of high values with little oscillation  
 371 (Figure 4).

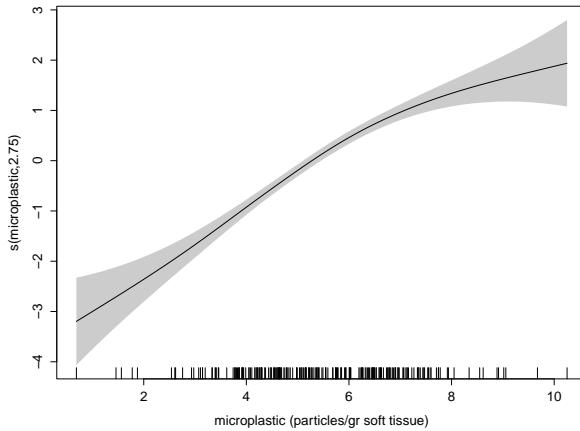
372 Lastly, we analyzed the relationship between the two response variables (microplas-  
 373 tic abundance and infection intensity) (Figure 5). This relationship was significantly  
 374 positive, with infection intensity increasing alongside microplastic abundance, though  
 375 the relationship was weaker at higher values of microplastic abundance. Continued  
 376 empirical, retrospective studies of this relationship are critical for gaining further insight  
 377 into the emergence of diseases due to the transmission of pathogens adhered to MMD.



**Figure 3.** Partial effects from the fitted GAM predicting microplastic abundance (*number of occurrences of microplastics g<sup>-1</sup>*) in an organism (for example bivalves or oysters) as a function of river flow ( $m^3 sec^{-1}$ ), salinity, temperature (°C), dissolved oxygen (%), percent dissolved oxygen saturation), salinity stratification index, and chlorophyll concentration ( $mg m^{-3}$ ). The degrees of freedom for smoothed fits are indicated in parentheses on the y-axis. Tick marks above the x-axis indicate the distribution of observations. The shaded area represents the 95% confidence intervals of partial effects.



**Figure 4.** Partial effects from the fitted GAM predicting infection intensity (number of occurrences of the pathogen  $g^{-1}$ ) as a function of river flow ( $m^3 sec^{-1}$ ), salinity, temperature ( $^{\circ}C$ ), dissolved oxygen (%), percent dissolved oxygen saturation), salinity stratification index, and chlorophyll concentration ( $mg m^{-3}$ ). The degrees of freedom for smoothed fits are indicated in parentheses on the y-axis. Tick marks above the x-axis indicate the distribution of observations. The shaded area represents the 95% confidence intervals of partial effects.



**Figure 5.** Partial effect from the fitted GAM predicting infection intensity (number of occurrences of the pathogen  $g^{-1}$ ) as a function of microplastic abundance (number of occurrences of microplastics  $g^{-1}$ ). The degrees of freedom for smoothed fits are indicated in parentheses on the y-axis. Tick marks above the x-axis indicate the distribution of observations. The shaded area represents the 95% confidence interval.

### 378 3.2. Pathogen transmission modelling

379 The host and pathogen states or subpopulations (variables) of bivalve- and fish-  
 380 microplastic-*Vibrio* models satisfy a system of ordinary differential equations describing  
 381 the dynamics of the host-pathogen association. The variables and parameters for these  
 382 models are described in Tables 1-2. We programmed the numerical models for these  
 383 systems in Matlab and solved them with a 4<sup>th</sup>-order predictor corrector scheme using the

<sup>384</sup> Adams-Basforth predictor and the Adams-Moulton corrector. The system of differential  
<sup>385</sup> equations in each of the two models comprises the following differential equations:

<sup>386</sup> 3.2.1. Bivalve-microplastic-*Vibrio* disease model

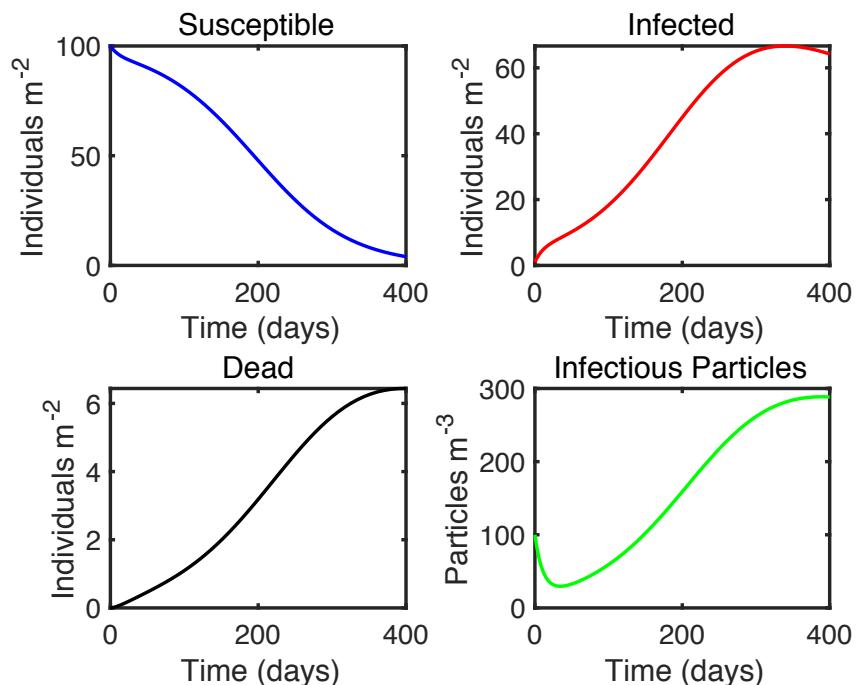
$$\frac{dS}{dt} = -\beta f MS + SRC_S \quad (2)$$

$$\frac{dI}{dt} = (\beta - a) f MS - m I \quad (3)$$

$$\frac{dDI}{dt} = m I - d DI \quad (4)$$

$$\frac{dM}{dt} = (1 - a) c b_I I + (1 - a_T) c_T b_T T + b_{DI} d DI - f M (S + I) - f_T M T - r M + SRC_M \quad (5)$$

$$\frac{dT}{dt} = T + SRC_T \quad (6)$$



**Figure 6.** Pathogen transmission simulation involving oysters (as a representative filter-feeder) and microplastics with adhered pathogens (infectious particles). Oysters were divided into three subpopulations (susceptible, infected, and dead/infected), and simulations were run based on an initial population of 100 susceptible oysters, one infected oyster, and 100 infectious particles. Parameter values for the simulations were as follows:  $\beta=5 \times 10^{-5}$ ,  $f=2.5 \times 10^{-4}$ ,  $m=2 \times 10^{-3}$ ,  $d=2 \times 10^{-2}$ ,  $c=2.5 \times 10^{-2}$ ,  $r=5 \times 10^{-2}$ ,  $b_I=10$ ,  $b_{DI}=20$ ,  $a=0$ ,  $a_T = 1$ ,  $SRC_S=0$ ,  $SRC_T=0$ , and  $SRC_M=1$ . For this example, all rates associated with the non-competent host ( $T$ ), such as particle uptake and pathogen inactivation, were considered null.

<sup>387</sup> Our bivalve-microplastic-*Vibrio* model simulations (Figure 6) detected the effect  
<sup>388</sup> of MMD-adhered pathogens on disease transmission. The size of the susceptible sub-

389 population decreased as more individuals became infected by filtering infectious MMD,  
 390 thereby increasing the size of the infected population. The size of the dead/infected  
 391 subpopulation increased, in turn, as individuals from the infected pool died (Figure 6; S,  
 392 I, D plots). The number of MMD particles with adhered pathogens initially decreased  
 393 as the susceptible and infected populations filtered MMD out of the seawater (Figure 6;  
 394 infectious particle plot); however, this initial decrease was followed by a rapid increase  
 395 as more MMD particles entered the water column from external water masses and from  
 396 the infected and dead subpopulations. The overall infection rate for this model (Figure 7)  
 397 shows an initial decrease as MMD particles are filtered out of the water column, followed  
 398 by an increase due to the release of particles from infected and dead subpopulations. The  
 399 infection rate decreases to zero once all susceptible individuals have become infected,  
 400 and infected individuals continue to die out.

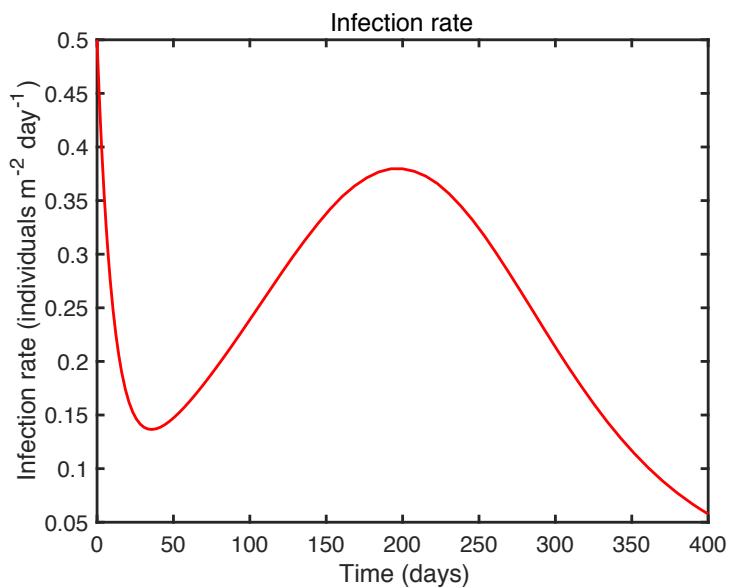


Figure 7. Infection rate dynamics for a simulated oyster population (as an example of filter-feeders) filtering infectious microplastic particles. The simulation began with an initial population of 100 susceptible oysters, one infected oyster, and 100 infectious particles. Parameter values for the simulation were the same as for Figure 6.

401 3.2.2. Fish-microplastic-Vibrio disease model

$$\frac{dS_L}{dt} = -\beta_L f_L M S_L - g S_L + SRC_{S_L} \quad (7)$$

$$\frac{dS_A}{dt} = -\beta_A f_A M S_A + g S_L + SRC_{S_A} \quad (8)$$

$$\frac{dI_L}{dt} = (\beta_L - a_L) f_L M S_L - g I_L - m_L I_L \quad (9)$$

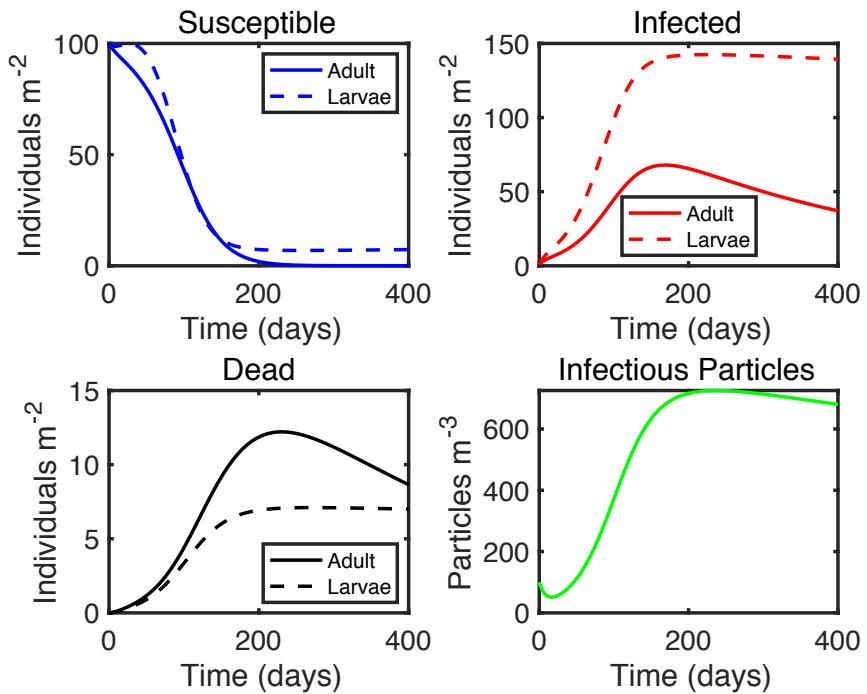
$$\frac{dI_A}{dt} = (\beta_A - a_A) f_A M S_A + g I_L - m_A I_A \quad (10)$$

$$\frac{dDI_L}{dt} = m_L I_L - d_A DI_L \quad (11)$$

$$\frac{dDI_A}{dt} = m_A I_A - d_L DI_A \quad (12)$$

$$\frac{dM}{dt} = (1 - a_L) c_L b_{I_L} I_L + (1 - a_A) c_A b_{I_A} I_A + b_{DI_L} d_L D_{I_L} + b_{DI_A} d_A D_{I_A} - f_L M (S_L + I_L) - f_A M (S_A + I_A) - r M + SRC_M \quad (13)$$

$$-f_L M (S_L + I_L) - f_A M (S_A + I_A) - r M + SRC_M$$

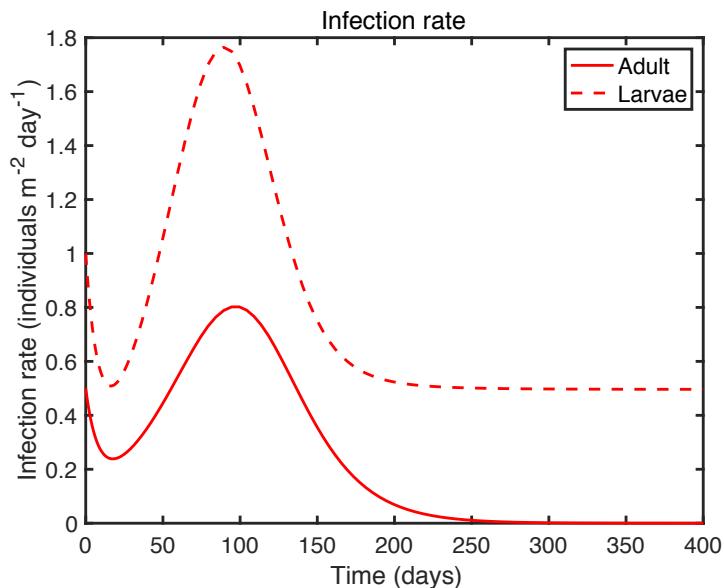


**Figure 8.** Pathogen transmission simulation involving zebrafish and microplastics with adhered pathogens (infectious particles). Zebrafish were divided into subpopulations that were further divided into adult and larval populations (i.e., susceptible adults and larvae, infected adults and larvae, and dead/infected adults and larvae). Simulations were run based on an initial population of 100 susceptible adults, 100 susceptible larvae, one infected adult, one infected larva, and 100 infectious particles. Parameter values for simulations were as follows:  $\beta_A=5 \times 10^{-5}$ ,  $\beta_L=10 \times 10^{-5}$ ,  $g=0.001$ ,  $f_A=2.5 \times 10^{-4}$ ,  $f_L=1.25 \times 10^{-4}$ ,  $m_A=2 \times 10^{-3}$ ,  $m_L=4 \times 10^{-3}$ ,  $d_A=2 \times 10^{-2}$ ,  $d_L=4 \times 10^{-2}$ ,  $c_A$  and  $c_L=2.5 \times 10^{-2}$ ,  $r=5 \times 10^{-2}$ ,  $b_{I_A}$  and  $b_{I_L}=10$ ,  $b_{DI_A}$  and  $b_{DI_L}=20$ ,  $a=0$ ,  $SRC_{S_A}=0$ ,  $SRC_{S_L}=0.5$ ,  $SRC_M=2$ .

Like the bivalve models, the fish-microplastic-*Vibrio* model simulations (Figure 8) also detected the effect of MMD-adhered pathogens on disease transmission in fish adults and larvae. The size of the susceptible adult and larvae subpopulations decreased as individuals became infected by feeding on infectious particles; infected individuals were transferred to the infected subpopulation, causing the size of the infected adult and larval populations to increase. The infected larvae population increased more rapidly due to the higher infection rate for larvae (Figure 8).

The plot for the susceptible population also shows the effect of a continuous source of larvae coming from other regions ( $SRC_{S_L}=0.5$ ) (Figure 8, S plot, in blue). By day 200, all susceptible adults had become infected, but new susceptible larvae enter the system from external sources. The dead adult subpopulation increased to a higher level than the dead larvae population because the dead larvae decay rate is faster than the decay rate for adults. At the same time, the concentration of MMD particles increased to a maximum as particles are both released from and entering the system from external sources (Figure 8, particle plot, in green). After reaching this maximum, the concentration of MMD

417 particles then decreased, as all susceptible individuals had become infected; as infected  
 418 individuals start dying, MMD particles are removed from the system through decay  
 419 processes.



**Figure 9.** Infection rate dynamics for fish (as an example of filter-feeder) filtering infectious microplastic particles. This simulation used an initial population of 100 susceptible oysters, one infected oyster, and 100 infectious particles. Parameter values for this simulation were the same as for Figure 6.

420 The behavior of the infection rate for this model is similar to that observed for the  
 421 bivalve model (Figure 9). In the fish model, the curve of the larvae infection rate is well  
 422 above the curve of the adult infection rate, adequately mirroring the higher infection rate  
 423 considered for the larvae respect to adult fish.

#### 424 4. Discussion and conclusions

425 The three-part analytical approach described here (retrospective regression analysis,  
 426 *in vivo* experiments, and disease modelling) provides a suitable framework for thor-  
 427oughly exploring the role of microplastics on marine pathogen transmission. Using this  
 428 approach to further researcher will build a body of knowledge essential for addressing  
 429 marine disease and food safety challenges related to MMD. This research is an urgent  
 430 priority of the EU Strategic Research Innovation Agenda [90]. The theoretical results  
 431 from the retrospective analysis described here demonstrate that a retrospective regres-  
 432sion analysis can offer a valuable perspective on the past and expected future trends of  
 433 MMD exposure in different marine organisms, as well as the relationship between MMD  
 434 exposure and pathogen prevalence. However, despite the importance of these analysis  
 435 for understanding the evolution of emerging pathogens, such analyses of microplastic  
 436 trends remain scarce [91].

437 Based on the results of retrospective regressions and the relationships among  
 438 modeled variables, organisms with higher MMD exposure and a higher incidence  
 439 of pathogens can be considered for *in vivo* experiments and disease modelling. For  
 440 example, the experimental approach outlined here is designed to determine the effect of  
 441 the MMD-pathogen interaction on disease transmission. To achieve this, our proposed  
 442 experimental design includes treatments with non-infectious microplastics, microplastics  
 443 with adhered pathogens, and free-floating pathogens. Such an experimental approach is  
 444 particularly timely because recent experiments have used microplastics with adhered

445 pathogens to assess whether microplastics may facilitate pathogen entry into marine  
446 food webs [92].

447 Together, retrospective analysis and *in vivo* experimental results can provide essen-  
448 tial information on the key parameters involved in the mechanisms and processes of  
449 disease transmission through microplastic exposure. In this study, as in [80], we devel-  
450 oped the theoretical basis for modeling these MMD-pathogen systems for bivalves and  
451 fishes. Our models can be parameterized with realistic values obtained from previous  
452 retrospective and experimental analyses, and our model results conform to the expecta-  
453 tions of mathematical theory and behavior and population dynamics. Most importantly,  
454 our models incorporate the effect of microplastic particles with adhered pathogens on  
455 disease transmission and mortality. In the age-dependent fish-microplastic-*Vibrio* model,  
456 the effect of infectious microplastics could be observed separately for both adult and  
457 larval zebrafish. In the future, models based on the experimental design and models  
458 described here can be developed to further explore the role of microplastic-derived stress  
459 on the transmission of both free-living and MMD-adhered pathogens [32].

460 Studying the combined risks from microplastic pollution and disease represents a  
461 novel approach to the study of marine disease ecology. Future studies along this line of  
462 research could involve a linked experimental-disease modelling approach that would  
463 allow us to understand the complex organism-microplastic-pathogen system from a pre-  
464 dictive and epizootiological perspective. This perspective is inherently interdisciplinary,  
465 with research teams possessing a unique mixture of expertise in bivalve and zebrafish  
466 microplastic toxicology, histopathology, immunology, and marine disease modelling.  
467 Moreover, the interdisciplinary and predictive aspects of this project are essential for  
468 making progress towards the long-term objectives of this research, which focus on un-  
469 derstanding the rate at which organisms encounter microplastics (e.g., via ocean models)  
470 and the physical, chemical, biological, and interactive risks these encounters pose to  
471 different organisms at different spatial scales and, through bioaccumulation, different  
472 trophic levels. Overall, this proposed study will generate the knowledge needed to  
473 guide advanced seafood safety studies in commercial bivalves, and it will be applicable  
474 to other ecologically relevant suspension-feeders such as corals.

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477 draft preparation, G.B., M.S., P.L.L., I.U., A.I. and F.V.; review and editing, G.B., M.S., P.L.L., I.U.,  
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