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Responses of *Mytilus galloprovincialis* to challenge with environmental isolates of the potential emerging pathogen *Malaciobacter marinus*

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14 Abstract

Bacteria of the *Arcobacter*-like spp. represent emerging foodborne zoonotic pathogens in humans and animals. Their increasing presence in seafood, suggesting higher occurrence in seawater due to marine pollution, is raising some environmental concern. Although *Arcobacter* is frequently detected in diseased oysters and stressed bivalve species, no data are available so

19 far on its potential pathogenicity or interactions with the immune system of the bivalve host.

In this work, responses to challenge with two strains of *Malaciobacter marinus* IRTA-19-131 and IRTA-19-132, R1 and R2), isolated from adult *Crassostrea gigas* during a mortality event

in 2019 in Spain, were investigated in the mussel *Mytilus galloprovincialis*.

In vivo experiments were performed in larvae (48 h post-fertilization), and in adult mussels at 24 h post-injection, in order to evaluate the pathogenicity for early developmental stages, and

the hemolymph immune responses, respectively. Both R1 and R2 were moderately pathogenic

to early larvae, with significant decreases in the development of normal D-veligers from 10^4

and 10³ CFU/mL, respectively. In adults, both strains decreased hemocyte lysosomal membrane
 stability (LMS), and stimulated extracellular defense responses (ROS production and lysozyme

29 activity).

The interactions between mussel hemocytes and M. marinus were investigated in in vitro 30 short-term experiments (30-90 min) using the R1 strain (10⁶-10⁸ CFU/mL). R1 decreased LMS 31 and induced lysosomal enlargement, but not cell detachment or death, and stimulated 32 extracellular ROS production and lysozyme release, confirming in vivo data. Moreover, 33 lysosomal internalization and degradation of bacteria were observed, together with changes in 34 levels of activated mTor and LC3, indicating phagocytic activity. Overall, the results indicate 35 the activation of both extracellular and intracellular immune defenses against *M. marinus* R1. 36 Accordingly, these responses resulted in a significant hemolymph bactericidal activity, with a 37

38 large contribution of hemolymph serum.

The results represent the first data on the potential pathogenicity of *Arcobacter* isolated from a shellfish mortality to bivalve larvae and adults, and on their interactions with the immune system of the host.

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Keywords: bivalves, *Malaciobacter marinus*, mussel, larvae, hemocytes, immune response,
 mTor, LC3

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46 **1. Introduction**

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In the last decades, aquacultured bivalves have been increasingly subjected to recurrent 48 disease outbreaks resulting in mass mortality events. Although juveniles of the Pacific oyster 49 (Crassostrea gigas) are the most severely affected, the occurrence of heterogeneous mortalities 50 has been described in adults and other species such as mussels [1-3]. The causes of the disease 51 processes that lead to mass mortality are not always evident; however, it is commonly accepted 52 that these episodes are polymicrobial and multifactorial, involving both host and environmental 53 factors (e.g. bivalves species, genetics and age, temperature, food availability, microbiota, 54 pollutant exposure) [3]. Whatever the source and degree of infection, the outcome of the 55 response to potential pathogens depends on complex interactions between the immune system 56 57 of the host and the associated microbial communities [4]. Recent studies have reported the recurrent presence of bacteria of the genus Arcobacter in oysters (C. gigas) during mortality 58 59 episodes [5,6]. Similar observations were made in laboratory experiments in oysters immune-60 compromised by OsHV-1 [7] or oysters and mussels exposed to temperature stress [8,9]. In mussels (Mytilus galloprovincialis) exposed to nanoplastics, an increased abundance of 61 Arcobacter in hemolymph microbiome was observed [10]. 62 63 Arcobacter spp. are recently regarded as emerging foodborne pathogens affecting both

humans and animals, with the most common A. butzleri (reviewed in [11]). Arcobacter have 64 been shown to inhabit very diverse environments, including sewage water [12]. Even though 65 some Arcobacter species are believed to be free-living, waterborne organisms, and 66 autochthonous to aquatic environments, they are also naturally present in bivalve microbiome 67 [13,14]. While some species were found only in mussels (e.g. A. mytili) [15], the presence of 68 others seems to be due to fecally contaminated freshwater inputs, as the presence of A. butzleri 69 was correlated with the levels of Escherichia coli [16]. Since bivalves represent a cause of 70 foodborne disease in humans, available literature mainly focuses on the detection of Arcobacter 71 in edible species [11,14,16–18]. However, no data are available yet on the capacity of bivalves 72 73 to respond to infection with Arcobacter and on the interactions with their immune system. Therefore, it is not clear if Arcobacter members can represent primary or opportunistic 74 75 pathogens for different bivalves.

76 In this work, responses to challenge with two strains of *Malaciobacter marinus* isolated from C. gigas during a mortality event in 2019 in the Ebro delta in Spain (IRTA-19-131 and IRTA-77 19-132) were investigated in the Mediterranean mussel M. galloprovincialis. In vivo 78 experiments were performed in larvae (48 h post-fertilization, hpf), and in adult mussels at 24 79 h post-injection (p.i.), in order to evaluate the pathogenicity for early developmental stages, and 80 the hemolymph immune responses, respectively. The interactions with mussel hemolymph 81 components and the mechanisms involved in the immune response were investigated in *in vitro* 82 short-term experiments with IRTA-19-131. This work is part of a wider study on the 83 epidemiology of *M. marinus* in the Ebro delta, along with the screening of other bacterial and 84 viral pathogens, and on the *in vivo* pathogenicity of *M. marinus* in oysters. 85 86

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2. Methods

89 2.1 Bacterial isolation and identification

Bacterial strains (IRTA-19-131 and IRTA-19-132) for challenge experiments were isolated from adult diseased oysters (*C. gigas*) collected during a mortality event that occurred in Fangar here $(40^\circ, 46.506'N; 0^\circ, 44.246'E, Ehro Dolta, Spain)$ in June 2010. Briefly, alignets (1 mL) of

bay (40° 46.506'N; 0° 44.246'E, Ebro Delta, Spain) in June 2019. Briefly, aliquots (1 mL) of
whole oyster tissue homogenates (from a pool of 5 oysters) were added with 9 mL of *Arcobacter*

- whole oyster ussue homogenates (from a poor of 5 oysters) were added with 9 mL of Arcobacter
 broth (Sigma-Aldrich, CM0965, Steinheim, Germany) supplemented with CAT [(C.A.T)
- broth (Sigma-Aldrich, CN10965, Steinheim, Germany) supplemented with CAT [(C.A

selective supplement: Cefoperazone-Amphotericin B-Teicoplanin) OxoidTM, SR0174E, 95 Hampshire, UK] and 50% artificial seawater [19] and incubated aerobically at 23 °C in static 96 97 conditions. After 48 h the tubes were vortexed for 10 sec and aliquots of 100 µL were transferred to Marine Agar (MA) (Scharlab, 109352, Sentmenat, Spain) plates overlaid with 98 0.45 µm nitrocellulose membrane filters of (Millipore, Ref # HAWP04700, Tullagreen, Ireland) 99 to retain larger bacteria. After 30 min, the filters were removed, and the plates were incubated 100 aerobically at 23 °C for 48 h. Arcobacter-like spp. (i.e., small, transparent/translucent, beige, or 101 off-white colonies) were sub-cultured on MA medium and incubated in the conditions 102 mentioned above. Genomic DNA (gDNA) was extracted from bacterial isolates using QIAGEN 103 DNeasy® Blood & Tissue Kit (QIAGEN, Ref # 69506, Hilden, Germany). Identification of the 104 isolates was conducted by Arcobacter 23S genus specific qPCR and amplification and 105 sequencing of the *rpoB* phylogenetic marker gene as previously described (GenBank accession 106 numbers rpoB: OP441048 and OP441049) [15, 20, 21]. Two bacterial isolates were identified 107 as belonging to the species *M. marinus* (IRTA-19-131 and IRTA-19-132). 108

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110 2.2 Bacterial cultures and inoculum preparation

111 IRTA-19-131 and IRTA-19-132 strains (henceforth indicated as R1 and R2, respectively) 112 were cultured in *Arcobacter* broth (conventional broth media containing peptone 18 g/L, yeast 113 extract 1g/L, NaCl 5g/L modified with the addition of 50% artificial seawater-ASW) at 30 °C 114 in a water bath with continuous agitation. After 24 h growth, the inoculum was centrifuged 115 $(4500 \times g, 20 \text{ min})$, and the pellet was resuspended to obtain a concentration of about 10⁸ colony 116 forming units CFU/mL (determined spectrophotometrically as an Abs₆₀₀=0.20). MA was used 117 throughout the experiments.

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119 2.3. Effects of M. marinus R1 and R2 strains on mussel early larval development

Sexually mature mussels (M. galloprovincialis), 4–5 cm long, purchased in February 2021 120 from an aquaculture farm (La Spezia, Liguria, Italy) were acclimated in tanks with aerated 121 artificial seawater (ASW), salinity 35 ppt (1 L/mussel) at 18 °C and utilized within 2 days for 122 gamete collection [22]. The 48 h embryotoxicity assay was carried out in 96-microwell plates 123 as in Balbi et al. (2019) [23]. At 30 min post-fertilization, aliquots of R1 and R2, from a 10⁸ 124 CFU/mL stock suspension, were tenfold serially diluted in ASW and added to fertilized eggs 125 in each microwell to reach the desired nominal final concentrations (from 10^2 to 10^7 CFU/mL) 126 in a 200 μ L volume. Microplates were then incubated for 48 h at 18 °C ± 1 °C, with a 16:8 h 127 light: dark photoperiod. All the procedures were carried out following ASTM [24]. At the end 128 of incubation, each sample was fixed with buffered formalin (4%) and all larvae examined by 129 optical microscopy using an inverted Olympus IX53 microscope (Olympus, Milano, Italy) at 130 $40 \times$, equipped with a CCD UC30 camera and a digital image acquisition software (cellSens 131 Entry). A D-shaped (straight hinge) larva with no protruding mantle was considered normal; if 132 the typical stage at 48 hpf was not reached (trochophore or earlier stages) or when some 133 developmental impairments were observed (concave, malformed or damaged shell, protruding 134 mantle), the larva was considered malformed. The acceptability of test results was based on 135 controls for a percentage of normal D-shell larvae >75% [24]. 136

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138 2.4 In vivo challenge of adult mussels with M. marinus R1 and R2 strains

Adult mussels (*M. galloprovincialis*), 4–5 cm long, were purchased in summer 2021 and acclimated in tanks with aerated artificial seawater (ASW) for 24 h, salinity 35 ppt (1 L/mussel) at 18 °C. Animals (20 mussels per condition) were injected into the posterior adductor muscle as previously described [23] utilizing 50 μ L of live bacterial suspensions (*M. marinus* R1 or R2) containing 10⁸ CFU/mL in PBS+NaCl (phosphate-buffered solution isotonic with

hemolymph, PBS+NaCl: 2 mM KH2HPO4, 10 mM Na2HPO4, 3 mM KCl, 600 mM NaCl in 144 distilled water, pH 7.4), in order to obtain a nominal concentration of 5×10^6 CFU/mL 145 hemolymph. Control mussels were injected with PBS+NaCl. No mortality was observed during 146 the experiments. At 24 h post-injection (p.i.), hemolymph was collected from the posterior 147 adductor muscle of 4 pools of 4 mussels each. Hemocyte LMS, reactive oxygen species (ROS) 148 production, and soluble lysozyme activity were determined in whole hemolymph samples from 149 control and exposed groups. Hemolymph collection and assays were performed as previously 150 described [23,25,26]. 151

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153 2.5 In vitro challenge of Mytilus hemocytes with M. marinus R1 strain

154 2.5.1 Hemolymph sampling and monolayer preparation

Using a sterile 1 mL syringe with an 18 G1/2" needle, the hemolymph was extracted from the 155 posterior adductor muscle. The hemolymph, with the needle prior removed, was filtered 156 through sterile gauze and pooled at 18 °C. For hemocyte monolayers preparation, 20 µL drops 157 of the whole hemolymph were deposited on microscope slides and the cells were let to adhere 158 159 for 20 min before removing the excess of hemolymph. To obtain hemolymph serum-HS, the whole hemolymph was centrifuged at $100 \times g$ for 10 min, and the supernatant was sterilized 160 through a 0.22 µm-pore filter. Hemocyte monolayers or whole hemolymph (according to the 161 endpoint, see details in the next sections) were incubated with M. marinus R1 suspension 162 suitably diluted in ASW or HS at different concentrations (10⁶, 10⁷, 10⁸ CFU/mL) from 30 to 163 90 min, depending on the endpoint measured. Untreated samples in ASW or HS were run in 164 parallel. Filter-sterilized ASW was utilized in all experiments. 165

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167 *2.5.2 Determination of functional parameters*

All assays were carried out as previously described [23,25,26]. Lysosomal membrane stability 168 (LMS) was evaluated in hemocytes monolayers by the Neutral Red Retention Time (NRRT). 169 Hemocyte monolayers were pre-incubated for 30 min with different concentrations (10⁶, 10⁷, 170 10⁸ CFU/mL) of *M. marinus* in ASW or HS. Samples were washed out and incubated with a 171 neutral red (NR) (Sigma-Aldrich, Milan, Italy) solution (40 µg/mL in ASW). After 15 min, after 172 removal of excess dye, a drop of ASW was added, and slides were observed under an optical 173 microscope from time zero every 15 min, and the percentage of cells showing loss of dye from 174 lysosomes in each field (10 fields each containing 8-10 cells) was evaluated until 50% of the 175 cells showed sign of lysosomal leaking, i.e., the cytosol becoming red, and the cells rounded. 176 177 All incubations were carried out at 18 °C.

For the determination of Lysozyme release and ROS production, aliquots of 400 µl of whole 178 hemolymph were incubated with suspensions of M. marinus in ASW or HS (final 179 concentrations 10⁶ and 10⁷ CFU/mL) for different times. Lysozyme activity in the extracellular 180 medium after incubation with bacteria for 0, 30 and 60 min. was evaluated 181 spectrophotometrically at 450 nm using a suspension of *Micrococcus lysodeikticus* (15 mg/100 182 mL in 66 mM phosphate buffer, pH 6.4). Hen egg white (HEW) lysozyme was used as a 183 standard and lysozyme activity was expressed as HEW lysozyme equivalents (U/mg 184 protein/mL). Extracellular ROS generation was measured by the reduction of cytochrome c. 185 Hemolymph samples were incubated for 30 min with a cytochrome c solution (75 μ M 186 ferricytochrome c in TBS (0.05M Tris-HCl buffer, pH 7.6, containing 2% NaCl)). Cytochrome 187 c in TBS was used as a blank. Samples were read at 550 nm against cytochrome c in TBS as a 188 189 blank and the results were expressed as changes in OD per mg protein. All data are reported as

percentage of control values. Protein content was determined using the Bradford method withbovine serum albumin (BSA) as a standard.

- For *in vivo* experiments, functional parameters were evaluated directly on hemolymph samplesafter challenge with R1 or R2.
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195 2.5.3 Giemsa Staining

Hemocyte monolayers on microscope slides were incubated for 30 and 90 min with M. *marinus* R1. Samples were washed out, fixed in >50% methanol, and stained with a Giemsa kit (Diff-QuikTM, Medion Grifols Diagnostics AG, Switzerland), following the manufacturer instructions.

200 2.5.4. Electrophoresis and Western blotting

Hemocyte monolayers were incubated with bacterial suspensions in ASW (10⁷ CFU/mL) at 201 18 °C for 30 and 90 min. Control samples were run in parallel. All procedures were carried out 202 as previously described [26]. Supernatants from each culture dish were discarded and the 203 204 hemocytes were lysed with 0.1 vol of ice-cold lysis buffer (50 mM Tris-HCl pH 7.8, 0.25 M sucrose, 1% SDS, 2 mM sodium orthovanadate, 0.1% Nonidet-P40, 5 mM M DTT) with 205 protease inhibitors cocktail and phosphatase inhibitors cocktail (Roche, Basel, Switzerland). 206 207 Samples were boiled for 4 min. and then centrifuged for 20 min. at $14,000 \times g$ to remove insoluble debris. Levels of target proteins were determined by SDS-PAGE and Western blotting 208 using specific antibodies as previously described [26]. Samples were probed with rabbit 209 polyclonal anti-LC3 (Sigma-Aldrich, L8918) antibodies (1:500), rabbit polyclonal mTor 210 (phospho S2481) (www.abcam.com, ab137133) (1:1000) and rabbit polyclonal anti-actin 211 antibody (Sigma-Aldrich, A5060) (1:500) as primary antibodies, and with horseradish 212 peroxidase-conjugated goat anti-rabbit IgG (Invitrogen G21234) (1:3000) as secondary 213 antibodies. Immune complexes were visualized using an enhanced chemiluminescence Western 214 blotting analysis system (PURECL-Chemiluminescence Substrate Vilber) following the 215 manufacturer's specifications. Western blotting films were digitized (Chemidoc-Biorad) and 216 band optical densities (arbitrary units) were quantified using a computerized imaging system 217 (QuantityOne). 218

219 2.5.5. Bactericidal activity

In vitro bactericidal activity of hemocyte monolayers was evaluated as previously described 220 [23,25]. Hemocytes were incubated with *M. marinus* R1 (5 \times 10⁶ CFU/mL) at 18 °C in ASW 221 or HS for different periods of time (0, 30 and 90 min). The bactericidal activity of HS was also 222 evaluated. M. marinus in ASW was used as a control for bacterial growth over the experimental 223 time. Immediately after the inoculum (T = 0) and after 30 and 90 min of incubation, 224 supernatants were collected and hemocytes were lysed by adding filter-sterilized ASW 225 supplemented with 0.05% Triton x-100 and by 10 sec agitation. Supernatants and lysates were 226 pooled and tenfold serial diluted in ASW. Aliquots (100 µL) of the diluted samples were plated 227 onto MA. Samples of *M. marinus* suspensions in ASW or HS at the same concentrations were 228 directly diluted and plated. After 48 h incubation at 30 °C, the number of CFU per hemocyte 229 monolayer (representing live, culturable bacteria) was determined. Percentages of killing were 230 determined in comparison to values obtained at zero time. The number of CFU in control 231 hemocytes never exceeded 0.1% of those enumerated in experimental samples. 232

233 2.6. Data analysis

234 Data from *in vitro* and *in vivo* experiments on hemocyte and hemolymph functional parameters are the mean \pm SD of at least 4 independent experiments, with each assay performed in 235 triplicate. Statistical analyses were performed by the non-parametric Kruskal-Wallis test 236 followed by Dunn's test ($p \le 0.05$). Embryotoxicity test data, representing the mean \pm SD of 237 4 independent experiments, carried out in 6 replicate samples in 96-microwell plates, were 238 analyzed by ANOVA plus Tukey's post-test. Data from WB were analyzed by non parametric 239 Mann-Whitney U test. All statistical calculations were performed using the GraphPad Prism 240 version 7.03 for Windows, GraphPad Software, San Diego, CA, USA. 241

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243 **3. Results**

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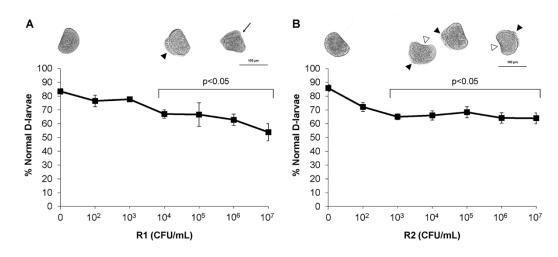
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245 3.1 Effects of M. marinus strains R1 and R2 on mussel early larval development

Fertilized eggs were exposed to either R1 or R2 in a wide concentration range (from 10^2 to 247 10⁷ CFU/mL) and the percentage of normal D-larvae at 48 hpf was evaluated as previously 248 described [5,23]. The results are reported in Fig. 1. Exposure to both strains moderately affected 249 normal development, with significant effects for R1 from 10⁴ CFU/mL and for R2 from 10³ 250 CFU/mL. At the maximal concentration tested, the effect of R1 was slightly stronger than that 251 of R2 (with a -38% and -25% decrease in normal larvae, respectively). Interestingly, as shown 252 by representative images, R1 mainly induced a delayed larval phenotype (immature veligers 253 with protruding mantle and incomplete shell formation), whereas exposure to R2 mainly 254 resulted in shell malformations (convex shell hinge). 255

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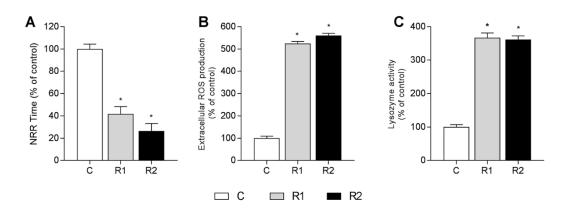
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Figure 1. Effects of different concentrations of *M. marinus* strains R1 and R2 on *M. galloprovincialis* larval development at 48 hpf. Percentage of normal D-shaped larvae with respect to controls after exposure to R1 (A) and R2 (B). Data, representing the mean \pm SD of 4 experiments carried out in 96-multiwell plates, were analyzed by ANOVA plus Tukey's post-test (p < 0.05). Representative images of control larvae and of the main larval phenotypes (lateral view) observed in different experimental conditions at 48 hpf are reported (scale bar: 100 µm). Black arrowhead = protruding mantle; arrow = immature larva (pre-veligers); white arrowhead = convex hinge.

266 3.2 Effects of in vivo challenge of adult mussels with two M. marinus strains R1 and R2

The effects of *in vivo* challenge of mussels with *M. marinus* R1 and R2 were compared. Bacteria were injected into the posterior adductor muscle to reach a final nominal concentration of 5×10^6 CFU/mL in hemolymph. After 24 h p.i. the hemolymph was collected and functional immune parameters were evaluated (Fig. 2). Similar responses were observed with both strains. A significant decrease in LMS, evaluated as a marker of cellular stress, was observed (about -60 and -73% with respect to controls for R1 and R2, respectively) (Fig. 2A). This effect was accompanied by a large stimulation of extracellular ROS production (about +400% with respect to controls) (Fig. 2B) and of soluble lysozyme activity (+280% with respect to controls) (Fig. 2C) for both R1 and R2.

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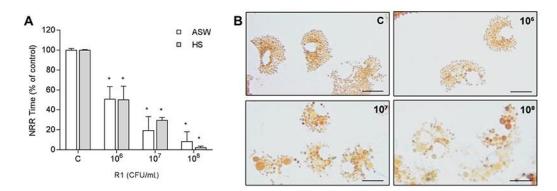
Figure 2. *In vivo* effects of two *M. marinus* strains R1 and R2 on hemolymph parameters of *M. galloprovincialis*. Hemocyte lysosomal membrane stability-LMS (A), ROS production (B) and serum lysozyme activity (C) were evaluated in hemolymph sampled from mussels challenged with either R1 or R2 at 24 h p.i. Data are the mean \pm SD of 4 independent experiments performed in triplicate. Statistical analyses were performed by non-parametric Kruskal–Wallis followed by Dunn's multiple comparisons test (p < 0.05).

284 *3.3 Effects of in vitro challenge of Mytilus hemocytes with M. marinus R1*

The effects of *in vitro* short-term incubation (30 min) with different concentrations of the M. 285 marinus strain R1 on hemocyte LMS were compared utilizing bacterial suspensions in different 286 media, ASW or HS, and the results are reported in Fig. 3. A dose-dependent decrease in LMS 287 was recorded in both media (Fig. 3A). Significant effects were observed from the lowest 288 concentration tested (10⁶ CFU/mL), with a -45% decrease in LMS with respect to control, until 289 almost complete destabilization (> 95%) at the highest concentration tested (10^8 CFU/mL). The 290 effects of R1 on hemocyte LMS were compared with those of the R2 strain in similar 291 experimental conditions. Since similar dose-dependent effects were observed (Fig. S1), 292 subsequent in vitro experiments were carried out only with R1. 293

Early lysosomal changes induced by R1 in live hemocytes could be appreciated from the 294 beginning of the NRR assay (see representative images in Fig. 3B obtained at time 0, after 295 incubation with bacteria, washing and NR loading). In control samples (C), healthy hemocytes 296 297 were characterized by the presence of numerous small NR loaded vesicles, representing individual lysosomes. In samples challenged with R1, lysosomal enlargement and fusion were 298 observed at increasing concentrations of bacteria. Interestingly, at the end of the assay, when 299 lysosomal destabilization was observed in > 50% of hemocytes (corresponding to data shown 300 in Fig. 3A), the cells remained fully adherent to the substrate, with no appreciable cell 301 detachment and rounding typical of dying cells (Fig.S2). 302

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305 Figure 3. In vitro effects of M. marinus R1 strain on hemocyte lysosomal membrane stability-LMS.

A) LMS evaluated in different media (ASW or HS). Data, expressed as percent values with respect to controls and representing the mean \pm SD of 4 experiments in triplicate. Statistical analyses were performed by non-parametric Kruskal–Wallis followed by Dunn's multiple comparisons test (* = p < 0.05).

B) Representative images of control hemocytes (C) and of hemocytes exposed to different concentrations of bacteria (10^6 , 10^7 , 10^8 CFU/mL in ASW) after loading with NR (time 0). Lysosomes are stained in red, nuclei and intact cytoplasm appear transparent (Scale bar: $10 \,\mu$ m).

Data on functional immune parameters, ROS production and lysozyme release, are reported in Fig. 4. Hemocyte exposure to *M. marinus* R1 suspensions in ASW did not elicit significant extracellular ROS production; however, in the presence of HS, a large increase in ROS was observed at both 10⁶ and 10⁷ CFU/mL (+350% to +480% respectively, with respect to controls) (Fig. 4A). Lysozyme activity showed small increases (+20-+50% with respect to controls), depending on the time of incubation (30 and 60 min) and exposure medium (Fig. 4B and 4C).

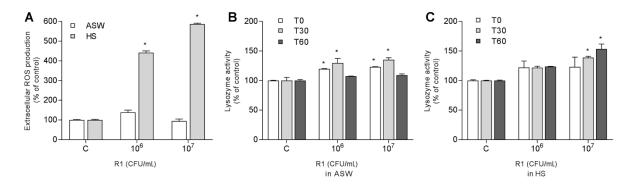




Figure 4. *In vitro* effects of *M. marinus* R1 on immune responses of *M. galloprovincialis* hemocytes. Extracellular ROS production (A) and lysosomal enzyme release (B-C) were evaluated after incubation with R1 at 10^6 and 10^7 CFU/mL in ASW or HS. Hemocytes were incubated for different periods of time (30 min for ROS production and 30 and 60 min for lysozyme release). Data are the mean \pm SD of at least 4 experiments performed in triplicate. Statistical analyses were performed by non-parametric Kruskal–Wallis followed by Dunn's multiple comparisons test (* = p < 0.05).

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Hemocyte monolayers incubated with different concentrations of R1 (10⁶ - 10⁸ CFU/mL) in 327 ASW for 30 or 90 min, were stained with Giemsa (Fig. 5). At both 30 and 90 min incubation, 328 control hemocytes were well spread on the support, showing different cytoplasmic extensions, 329 with the nuclei colored in dark violet, the cytosol in pink, and intracellular vacuoles and 330 331 lysosomes (mainly located in the perinuclear region) in pink-yellowish (Fig. 5A and 5 E). After 30 min incubation with R1 (Fig. 5, B-D), an increasing number of bacteria were observed within 332 the hemocytes, on cellular membranes and in the extracellular medium at increasing 333 concentrations. Intracellular bacteria were mainly localized within enlarged lysosomal vesicles, 334

indicating phagocytosis (black arrowhead). Similar observations were made after 90 min
incubation (Fig. 5, F-H), showing still adherent hemocytes with enlarged lysosomes. Moreover,
at the highest concentration tested, enlarged vacuoles stained in dark violet were observed at
both 30 and 90 min, containing bacteria. Similar results were obtained using bacterial
suspensions in HS (not shown).

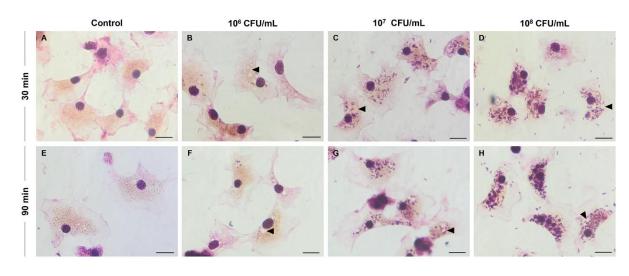


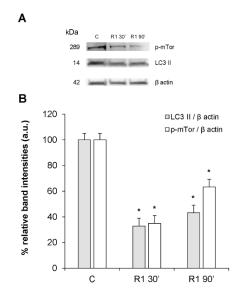
Figure 5. Giemsa staining of control hemocytes and hemocytes incubated with different concentrations of *M. marinus* **R1**.

Hemocytes were incubated with R1 10⁶, 10⁷ and 10⁸ CFU/mL in ASW for 30 (A-D) and 90 min (E-H). A and E)
Controls, B and F) 10⁶ CFU/mL, C and G) 10⁷ CFU/mL and D and H) 10⁸ CFU/mL. Black arrowheads: enlarged
lysosomes. Scale bar: 10 μm.

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The possible mechanisms involved in M. marinus R1-induced lysosomal enlargement and 348 internalization were investigated by evaluating the expression of the autophagic markers LC3 349 (microtubule-associated protein 1A/1B-light chain 3) and phosphorylated of mTor (mammalian 350 target of rapamycin mTOR) by electrophoresis and Western Blotting [26], and the results are 351 shown in Fig. 6. With regards to LC3, although the antibody can recognize both the LC3-I and 352 353 LC-II forms, only the band corresponding to the lipidated LC3-II form could be identified in all samples (Fig. 6A). Although we previously identified both bands in mussel hemocytes collected 354 in autumn (October) [26], in the present work, experiments were performed in mussels sampled 355 356 in early summer. The presence of the LC3-II form only is often observed in different marine invertebrate models ([27] and refs therein); therefore, the differences in results obtained in 357 hemocytes from mussels sampled at different times of the year may reflect seasonal variations 358 in LC expression. The results of the densitometric analysis showed that challenge with R1 359 induced a large decrease in expression of LC3-II at both 30 and 90 min (about -60% with respect 360 to controls at 30 min). A similar decrease was observed in the level of p-mTor (Fig. 6B). As 361 previously reported [26], no changes in expression of LC3-II or p-mTor were observed in 362 control samples at different times of incubation (not shown). 363 364



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Figure 6. Effects of *M. marinus* R1 on expression levels of LC3 and phosphorylated mTor in *M. galloprovincialis* hemocytes.

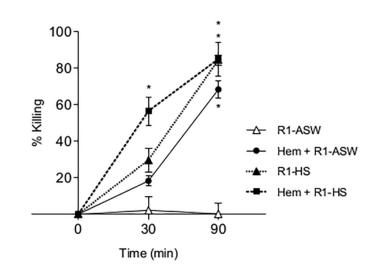
368 Expression of LC3-II and p-mTor in control hemocytes and hemocytes incubated for 30 and 90 min with R1 (10^7 **369** CFU/mL). A) Representative blots, with β actin as a loading control. B) Densitometric analysis of blots from four

independent experiments (mean \pm SD). * $p \le 0.05$, Mann-Whitney U test.

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372 Finally, the bactericidal activity of mussel hemocytes towards M. marinus R1 (5 \times 10⁶ CFU/mL) was evaluated in the presence of ASW or HS, as well as in HS and ASW alone, at 373 30 and 90 min incubation, and data are expressed as the percentage of killed bacteria with 374 375 respect time zero (Fig. 7). Hemocytes in ASW showed a significant and time-dependent bactericidal activity (20% and 75%, respectively, at 30 and 90 min). A similar effect was 376 observed using HS alone (30% and 80%). Accordingly, the bactericidal activity was highest in 377 samples of hemocytes in the presence of HS, in particular at shorter times of incubation (60% 378 379 and 85%, at 30 and 90 min, respectively). No bacterial killing was observed in ASW alone.

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384 Figure 7. In vitro bactericidal activity of mussel hemocytes and serum towards M. marinus R1.

Hemocytes were incubated for 30 and 90 min with *M. marinus* R1, at 5×10^{6} CFU/mL resuspended in either ASW (Hem + R1-ASW) or hemolymph serum (Hem + R1-HS). In parallel, *M. marinus* R1 were incubated in ASW (R1-ASW) or HS (R1-HS) alone. At each time point, the number of viable, cultivable bacteria (CFU) per monolayer was evaluated, and the results are expressed as percentage values with respect to time zero. Statistical analyses

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392 **4. Discussion**

all treatments vs control (R1 in ASW).

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The results represent the first data on the interactions of environmental strains of *Arcobacter*like spp. with marine bivalves. Two strains of *M. marinus* (IRTA-19-131 and IRTA-19-132) isolated from adult diseased oysters collected during a mortality event in the Ebro delta (Spain) were utilized.

were performed by non-parametric Kruskal–Wallis followed by Dunn's multiple comparisons test, * = p < 0.05,

Bivalve early developmental stages are likely to be more susceptible to pathogens than adults, 398 since the immune system has not fully developed [28,29]. Therefore, we first tested the effects 399 of *M. marinus* strains R1 and R2 in mussel early larvae utilizing the 48 h embryotoxicity assay. 400 The results show that both strains affected normal larval development in a wide concentration 401 range. Slight differences were observed between the two strains in terms of minimal effective 402 concentrations (with significant effects observed from 10³ to 10⁴ CFU/mL, respectively, for R1 403 and R2), extent of the effects at the highest concentration tested (with R1 higher than R2), and 404 main phenotypical changes (developmental delay for R1 and larval malformations for R2). 405 Overall, the results indicate that both *M. marinus* strains are moderately pathogenic for early 406 mussel larvae. In the same experimental conditions, stronger effects were observed with 407 408 different pathogenic vibrios, such as Vibrio corallilyticus [23], V. tasmaniensis LGP32, V. bathopelagicus sp. nov. [30]. 409

Responses to challenge with *M. marinus* were then investigated in adult mussels *in vivo*, injected with either R1 or R2 (5×10^6 CFU/mL hemolymph) where functional hemolymph parameters were evaluated at 24 h p.i.. The results show that both strains induced similar lysosomal stress in hemocytes (evaluated as a decrease in LMS); however, a large stimulation of extracellular defenses (ROS production and lysozyme activity) was observed, indicating that hemolymph components of adult mussels are able to mount an efficient defense response against *M. marinus* infection.

The mechanisms involved in immune interactions with *M. marinus* were subsequently 417 investigated in *in vitro* short-term experiments in isolated hemocytes exposed for 30 - 90 min 418 419 in the absence and presence of hemolymph serum (ASW or HS). Since both strains induced a similar concentration dependent effect on hemocyte LMS in a wide concentration range, we 420 chose to utilize only R1 (10⁶ - 10⁸ CFU/mL) for further investigations. Lysosomal membrane 421 destabilization was similar in the absence and presence of HS, and the effect was accompanied 422 by lysosomal enlargement. However, no hemocyte rounding or detachment, indicating cell 423 death, was observed. R1 induced a large and concentration dependent stimulation of 424 extracellular ROS production in the presence of HS, but not in ASW, indicating a role for 425 soluble components in the recognition of this strain and subsequent activation of membrane 426 NADPH oxidase, the enzyme responsible for ROS production. R1 moderately stimulated the 427 428 release of lysozyme release in both media, with differences in the extent and time course of the response. The results obtained in vitro thus confirm in vivo observations, showing that induction 429 of lysosomal stress in the hemocytes was associated with stimulation of extracellular defense 430 mechanisms. 431

432 Interactions of *M. marinus* with hemocytes were also investigated in Giemsa stained samples.

433 After 30 min incubation, an increasing number of bacteria were visible inside the hemocytes at

434 increasing concentrations, that were mainly localized within enlarged intracellular vesicles.

435 Although optical microscopy does not allow for the identification of localization of bacteria,

the results suggest their phagocytosis and subsequent lysosomal degradation.

With regards to the intracellular mechanisms involved in the response of hemocytes to R1 (lysosomal stress and enlargement, phagocytosis and lysosomal degradation of bacteria in the absence of cytotoxicity), the possible role of autophagic processes was investigated. In mussel hemocytes, we have previously demonstrated a protective role of autophagy against the pathogen *V. tapetis* [26]. *V. tapetis* induced a rapid stimulation of autophagy (induction of autophagosomes, and increase in autophagic markers LC3-II, p-mTor and p62), in the absence of phagocytosis and lysosomal degradation [26].

The results here obtained show that challenge with *M. marinus* resulted in contrasting effects 444 on hemocyte autophagy markers. Although a decrease in mTor phosphorylation, indicating 445 stimulation of autophagy, was observed, a similar effect was also recorded for LC3-II, the 446 activated, lipidated form of LC3, whose increase is considered as an early marker of autophagy. 447 Moreover, no changes in expression of p62 were observed (not shown). Overall, the results do 448 not support an induction of the autophagic flux in mussel hemocytes by this strain of M. 449 marinus. However, these data could be explained when considering by the multiple roles of 450 mTor and LC3 in immune response. mTOR is a master kinase that also regulates lysosome 451 452 structure and function and innate immunity; in macrophages, V. vulnificus induces mTor activation and inflammatory responses [31]. LC3 is also involved in LAP (LC3-associated 453 phagocytosis), a form of non-canonical autophagy, best characterized in the clearance of 454 455 pathogens by macrophages [32]. Briefly, in LAP, LC3 is conjugated to phagosome membranes while the bacterium is captured in the phagosome, thus acting as an innate immune response 456 mechanism [32,33]. Unlike autophagy, LAP involves single-membrane structures, and a 457 458 distinct rate of activation of LC3. Accordingly, in macrophages stimulated with Candida albicans, activated LC3 was increased at the peak of phagocytosis, and decreased at later times, 459 when the process was completed [34]. In the present work, a similar condition is observed in 460 461 mussel hemocytes during phagocytosis of M. marinus R1, indicating a decrease in LC3-II at 30-90 min, when the phagocytic process is well advanced or completed. These data provide the 462 first indication for LAP, a unique process that links the ancient pathways of phagocytosis and 463 autophagy in invertebrate immunocytes [35]. 464

Finally, the bactericidal activity of hemolymph components was quantified by evaluating the 465 percentage of killed bacteria in different experimental conditions, utilizing a concentration of 466 R1 (5 \times 10⁶ CFU/mL) that induced both lysosomal stress and induction of extracellular 467 468 defenses. After 30 min, a small bactericidal activity was shown by both hemocytes and HS alone (20% and 30% respectively). This activity could be ascribed to the extracellular release 469 of ROS and enzymatic defenses (lysozyme) from hemocytes (Fig. 4) and to the direct effects 470 471 of soluble serum components. A cumulative effect was observed for hemocytes in the presence of HS. Hemocytes alone showed a stronger bactericidal activity at longer incubation times (90 472 min), (up to 75%) this increase probably reflects the time needed for recognition of R1 in 473 absence of HS, and consequent phagocytosis and lysosomal degradation. Maximal killing 474 activity was observed with hemocytes in the presence of HS (85%). Although the components 475 of HS involved in mediating immune defenses towards M. marinus strains were not identified, 476 the results support the hypothesis that *Mytilus* hemolymph contains specific soluble factors that 477 contribute to the general killing of many bacteria that are strongly pathogenic for other bivalve 478 species [36,37]. 479

The results obtained in *in vitro* experiments on the interactions between *M. marinus* strains and mussel hemocytes can be compared with previous data with other potentially pathogenic marine bacteria from the genus *Vibrio* tested in the same experimental conditions (Table 1). Among the most pathogenic vibrios for bivalves, *V. coralliilyticus* ATCC BAA-450 and *V. tasmaniensis* LGP32 induced strong cellular stress in the absence of efficient immune response and bactericidal activity [23,25]. Responses to *V. tapetis* consisted in absence or inhibition of immune responses [26]. *V. aestuarianus* 01/032 induced moderate stress in hemocytes where it 487 was rapidly internalized and degraded by phagocytosis [25]. Environmental isolates of V. parahaemolyticus and V. alginolyticus elicited efficient immune responses, whereas V. 488 vulnificus induced slower and minor responses with apoptosis [38]. The results obtained so far 489 demonstrate that mussel hemocytes show different susceptibilities to different potential 490 pathogens, according to the species and strain, reflecting specificities in pathogen recognition, 491 492 binding and consequent activation of extracellular and intracellular defenses. Although the mechanisms involved in these specific interactions can be easily identified *in vitro*, the observed 493 outcome of the response is generally observed also in vivo ([25], this work). 494

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	LMS	ROS	Lyso. act	Killing
M. marinus R1	$\downarrow\downarrow\downarrow\downarrow$	$\uparrow\uparrow\uparrow$	↑	$\uparrow\uparrow\uparrow$
V. coralliilyticus ¹	$\downarrow\downarrow\downarrow\downarrow$	\approx	nd	\approx
V. tasmaniensis ²	$\downarrow\downarrow\downarrow\downarrow$	nd	$\uparrow\uparrow$	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
V. aestuarianus ²	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	nd	\uparrow	\uparrow
V. tapetis ³	\downarrow	\downarrow	*	22
V. parahaemolyticus ⁴	$\downarrow\downarrow$	1	\uparrow	nd

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Table 1. Summary of *in vitro* data on immune parameters in *M. galloprovincialis* hemocytes challenged with *M. marinus* R1 and different *Vibrio* (10⁷ CFU/mL) in the presence of HS. The parameters reported include: lysosomal membrane stability (LMS), extracellular ROS production and lysozyme release, expressed as % of control values.
 Bactericidal activity is reported as % of killed bacteria with respect to the inoculum.

V. coralliilyticus ATCC BAA-450 [23], ²V. tasmaniensis LGP32 and V. aestuarianus 01/032 [25], ³V. tapetis LP2
 [26]. ⁴V. parahaemolyticus Conero 80 [38]. nd: not determined. ↓: decreased; ↑: increase; ≈ no effect.

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505 On the basis of the overall data, the *M. marinus* strain R1 utilized in the present work is among the less pathogenic to mussels under laboratory conditions. However, the increased in vivo 506 abundance of members of the Arcobacter-like spp. in stressed or diseased bivalve species, often 507 508 in association with more pathogenic Vibrio [4], indicates that the interactions with the immune system of the host are extremely sensitive to perturbations by environmental factors or 509 concomitant infections with pathogens, resulting in a strongly opportunistic behavior of 510 Arcobacter. In this light, the role of the non-virulent microbiota should not be neglected, as 511 non-virulent Vibrio strains have the potential to dramatically increase the host damages caused 512 by virulent strains [4]. Data from co-challenge experiments with pathogenic and opportunistic 513 bacteria may help understanding these interactions. Moreover, edible bivalves can vehiculate 514 Arcobacter-like species up to humans, as shown by a recently reported case of human 515 bacteremia induced by M. mytili [39]. Further information is also needed on the interactions of 516 Arcobacter strains with the immune system of other bivalves; in particular research is in 517 progress on the interactions between *M. marinus* strains and immune system of the oyster *C.* 518 519 gigas. 520

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522 Supplementary Materials

Figure S1: Effects of different concentrations of two *M. marinus* strains R1 and R2 on hemocyte lysosomal membrane stability (LMS).

Figure S2. Representative images of hemocytes exposed to *M. marinus* strains R1 at the end
of the NRR assay (120 min).

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536 **CRediT authorship contribution statement**

- 537 Manon Auguste: Conceptualization; Data curation; Formal analysis; Investigation;
 538 Roles/Writing original draft; Writing review & editing.
- **Faiz Ur Rahman** : Methodology; Formal analysis
- 540 Teresa Balbi : Conceptualization; Data curation; Software
- 541 Martina Leonessi : Data curation; Formal analysis; Investigation
- 542 Caterina Oliveri : Data curation; Formal analysis; Investigation
- 543 Grazia Bellese : Formal analysis
- 544 Luigi Vezzulli : Conceptualization; Resources; Supervision; Writing review & editing.
- 545 **Dolors Furones** : Resources; Supervision; Writing review & editing.
- 546 Laura Canesi : Conceptualization; Supervision; Roles/Writing original draft; Writing review
- 547 & editing.
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