# scientific reports



# *Legionella* **colonization OPEN and 3D spatial location within a** *Pseudomonas* **bioflm**

**Ana Rosa Silva1,2, Luis F. Melo1,2, C. William Keevil3 & Ana Pereira1,2**\*

**Bioflms are known to be critical for** *Legionella* **settlement in engineered water systems and are often associated with Legionnaire's Disease events. One of the key features of bioflms is their heterogeneous three-dimensional structure which supports the establishment of microbial interactions and confers protection to microorganisms. This work addresses the impact of** *Legionella pneumophila* **colonization of a** *Pseudomonas fuorescens* **bioflm, as information about the interactions between** *Legionella* **and bioflm structures is scarce. It combines a set of meso- and microscale bioflm analyses (Optical Coherence Tomography, Episcopic Diferential Interference Contrast coupled with Epifuorescence Microscopy and Confocal Laser Scanning Microscopy) with PNA-FISH labelled**  *L. pneumophila* **to tackle the following questions: (a) does the bioflm structure change upon** *L. pneumophila* **bioflm colonization?; (b) what happens to** *L. pneumophila* **within the bioflm over time and (c) where is** *L. pneumophila* **preferentially located within the bioflm? Results showed that** *P. fuorescens* **structure did not signifcantly change upon** *L. pneumophila* **colonization, indicating the competitive advantage of the frst colonizer. Imaging of PNA-labelled** *L. pneumophila* **showed that compared to standard culture recovery it colonized to a greater extent the 3-day-old** *P. fuorescens* **bioflms, presumably entering in VBNC state by the end of the experiment.** *L. pneumophila* **was mostly located in the bottom regions of the bioflm, which is consistent with the physiological requirements of both bacteria and confers enhanced** *Legionella* **protection against external aggressions. The present study provides an expedited methodological approach to address specifc systematic laboratory studies concerning the interactions between** *L. pneumophila* **and bioflm structure that can provide, in the future, insights for public health** *Legionella* **management of water systems.**

**Keywords** Bioflm, Bioflm structure, *Legionella pneumophila*, *Legionella* spatial location, Stagnation, Water systems

*Legionella pneumophila* is a well-known waterborne pathogen responsible for the severe, and ofen fatal, pneu-monia named Legionnaires' Disease<sup>1,[2](#page-10-1)</sup>. *L. pneumophila* is a very intriguing and complex microorganism which exhibits multiple adaptation and survival mechanisms in the environment, according to the conditions to which it is exposed<sup>[2](#page-10-1)-4</sup>.

Protozoa and bioflms are reported as key ecological niches for *Legionella* settlement and survival in water systems<sup>5</sup>. Protozoa are known to graze the microcolonies of the biofilm, in a prey-predator relationship, and are able to shape the microbial community including the number of pathogens<sup>[1](#page-10-0),[6](#page-10-4)</sup>. However, the specific role of biofilms in *Legionella* survival and replication in biofilms is not consensually accepted among researchers<sup>[2,](#page-10-1)[4](#page-10-2)[,6](#page-10-4)</sup>. While some researchers advocate that *Legionella* growth requires a protozoan hos[t7](#page-10-5)[,8](#page-10-6) , others argue that *Legionella* is able to colonize and survive in biofilms without intracellular replication<sup>9[,10](#page-10-8)</sup>. Rogers et al.<sup>11</sup> and Wadowsky et al.<sup>12</sup> stated that the presence of non-legionellae bacteria could favor *Legionella* growth. Later, Surman et al.<sup>9</sup> while using a model water system showed that *L. pneumophila* was able to proliferate within bioflms without protozoan intracellular replication, as long as other bacterial species were present. More recently, Stewart et al.[13](#page-10-11) showed that bioflms composed of *Klebsiella pneumoniae* and *Flavobacterium* sp. allowed *Legionella* persistence for long periods.

Bioflms are complex three-dimensional (3D) heterogeneous structures of microorganisms encased in selfproduced extracellular polymeric substances (EPS[\)5](#page-10-3)[,14](#page-10-12). Engineered water systems are complex networks that

1 LEPABE ‑ Laboratory for Process Engineering, Environment, Biotechnology and Energy, Faculty of Engineering, University of Porto, Rua Dr. Roberto Frias, 4200-465 Porto, Portugal. <sup>2</sup>ALiCE - Associate Laboratory in Chemical Engineering, Faculty of Engineering, University of Porto, Rua Dr. Roberto Frias, 4200-465 Porto, Portugal. <sup>3</sup>School of Biological Sciences, University of Southampton, Southampton, UK. <sup>[2]</sup>email: aalex@fe.up.pt

ofer multiple localized conditions, including diferent temperatures, surface materials, hydrodynamics and nutrients that can favour biofilm formation<sup>15,16</sup>. Such conditions are known to affect the characteristics of the biofilms, including its microbiome<sup>17–[19](#page-11-1)</sup>, its structure<sup>[20](#page-11-2)</sup>, and how *Legionella* colonizes such biofilms<sup>[21](#page-11-3)–23</sup>. For exam-ple, biofilms grown under stagnation are usually thicker, less compact, and more susceptible to sloughing-off<sup>[20](#page-11-2),[24](#page-11-5)</sup>. Besides, water stagnation has also been reported to be critical for *Legionella* proliferation, due to repeated failures in disinfection procedures and higher accumulation of nutrients $^{23}$ .

From a public health perspective, it is important to investigate *Legionella* colonization and the spatial location within an existing biofilm structure. The risk for legionellosis will be different if *Legionella* is located on the outer regions of the bioflm, where it is more susceptible to slough-of and release into the bulk water, or if positioned closer to the bottom regions of the bioflm, where *Legionella* is expected to be more protected against disinfection procedures. Bioflm slough-of can release signifcant amounts of *Legionella* into the bulk water, which through aerosolization settings (like cooling towers or showers, etc.) can reach human lungs and trigger Legionnaire's Disease[5](#page-10-3) . Very little information is available on the role of bioflm structure on *Legionella* colonization. For example, Shen et al.[25](#page-11-6) investigated the relationship between bioflm structure and *Legionella* adhesion and detachment from biofilms. The authors reported that biofilm roughness was found to favor *L. pneumophila* adhesion to the bioflm top surface. However, most investigations have been focused on evaluating the efect of plumbing materials, temperature and microbial consortia on biofilm colonization by legionellae $11,26,27$  $11,26,27$  $11,26,27$ .

The present work uses an expedited, high-throughput and reproducible model, comprising a 12-well plate platform, a monospecies *Pseudomonas fuorescens* bioflm, in combination with molecular tracking with a specifc 16S rRNA peptide nucleic acid (PNA) probe for *L. pneumophila* detection<sup>[28](#page-11-9)</sup>, and 3D imaging techniques (Optical Coherence Tomography—OCT, Episcopic Diferential Interference Contrast with Epifuorescence—EDIC/EF microscopy, and Confocal Laser Scanning Microscopy—CLSM). Te model does not mimic bioflms, *Legionella* behaviour, nor *Legionella*-bioflms interactions in real-feld engineered water systems. Rather, the model uses a bacterium commonly found in biofilms of engineered water systems<sup>[13](#page-10-11),[21](#page-11-3)</sup> and is well characterized regarding bioflm formation[20](#page-11-2),[24](#page-11-5)[,29.](#page-11-10) It also considers the conditions that are known to favour *Pseudomonas fuorescens* bioflm build-up like temperature (30 °C) and formulated low nutrient medium (R2), that are not optimum for *Legionella* growth[30.](#page-11-11) Tis methodological approach aims to understand how *L. pneumophila* colonization of *P. fuorescens* bioflms afects the overall bioflm structure as well as the spatial location of *Legionella* within the bioflm.

# **Materials and methods**

### **Bacterial strains and culture maintenance**

The bacterium used to form the biofilms was *P. fluorescens* ATCC 13525<sup>T</sup>. Bacteria were grown overnight at 30±3 °C under agitation in 100 mL of sterile R2 (0.5 g/L peptone, 0.5 g/L glucose, 0.1 g/L magnesium sulphate · 7H2O, 0.3 g/L sodium pyruvate, 0.5 g/L yeast extract, 0.5 g/L casein hydrolysate, 0.5 g/L starch soluble and 0.393 g/L di-potassium phosphate·3H<sub>2</sub>O). All components were purchased from Merck (Darmstadt, Germany).

*L. pneumophila* serogroup 1 (WDCM00107), an environmental isolate, was used throughout this work. The choice relied on the fact that *L. pneumophila* is responsible for approximately 90% of the reported cases of legionellosis[21](#page-11-3). Bacteria was grown on bufered charcoal-yeast extract (BCYE) agar (Merck, Portugal) at 37 °C for 2 days.

# **Preparation of the bioflm set‑up**

In this study, polyvinyl chloride (PVC) coupons placed inside 12-well plates were used to grow bioflms. PVC was selected since it is ofen found in water engineered systems and past studies showed that it supports bioflms colonized by *Legionella*[11](#page-10-9). Coupons were sonicated in a 10% sodium dodecyl sulphate (VWR International, Portugal) solution for 5 min. To remove any remaining detergent, coupons were rinsed with tap water and then sonicated again in ultrapure water. Aferwards, the surfaces were rinsed in ultrapure water, air dried, and sterilized with ultraviolet (UV) radiation (254 nm) for 60 min each side. Double-sided adhesive tape was placed in each plate well, sterilized with UV radiation for 60 min, and fnally, the sterile coupons were glued in place.

#### **Bioflm formation and** *Legionella* **spiking**

An overnight culture of *P. fluorescens* ATCC 13525<sup>T</sup> was harvested by centrifugation at 4000 rpm for 10 min at 25 °C (MegaStar 600R, VWR International, Portugal). Cell concentration was adjusted to an optical density  $(OD_{610}$  nm) of 0.7 in fresh R2, which is equivalent to approximately 10<sup>8</sup> colony-forming units per mL (CFU/mL).

Each well was filled with 3 mL of the prepared bacterial suspension. The plates were then incubated for 14 days at 30 °C under stagnation. Tree days afer starting bioflm formation, bioflms were spiked with a suspension of *L. pneumophila* containing 10<sup>9</sup> CFU/mL and incubated again under the same conditions. Culture media was replaced by fresh R2 every 2 days.

#### **Bioflm sampling**

Coupons were sampled afer 3, 4, 7, 9, 11 and 14 days for bioflm analysis. In the 12-well plates, the bulk media was gently removed and rinsed with sterile saline solution (8.5 g/L) to remove planktonic cells. Coupons were kept in saline solution or let to air dry for imaging (detailed procedures described in ["Optical coherence tomog](#page-2-0)[raphy \(OCT\)"](#page-2-0) and "[Peptide nucleic acid \(PNA\) – Fluorescence in situ hybridization \(FISH\)"](#page-2-1) sections). For quantifcation of the sessile cells in the bioflms, coupons were gently removed from the 12-well plates, and were transferred to 15 mL centrifuge tubes (VWR, Portugal), containing 2 mL of saline solution. To disaggregate the bioflms and resuspend the cells, the tubes were submitted to three alternate cycles of 30 s sonication (Ultrasonic Cleaner USC-T, 45 kHz, VWR International, Portugal), followed by 30 s of vortexing.

# **Bioflm analysis**

### <span id="page-2-0"></span>*Optical coherence tomography (OCT)*

Bioflms were imaged as described by Silva et al.[29,](#page-11-10) directly from the 12-well plates with sterile saline solution, using spectral-domain Optical Coherence Tomography (OCT; Thorlabs Ganymede, Thorlabs GmbH, Germany) with a central wavelength of 930 nm<sup>29</sup>. The captured volume was  $2.49 \times 2.13 \times 1.52$  mm (y×z×x), consisting of  $509 \times 313 \times 1024$  $509 \times 313 \times 1024$  $509 \times 313 \times 1024$  pixels<sup>3</sup>. For each coupon, 2D and 3D imaging were performed with a minimum of five and three different fields of view (FoV), respectively. The acquired OCT images were processed with the software Biofilm Imaging and Structure Classifcation Automatic Processor (BISCAP)[31](#page-11-12), available at [https://github.com/diogonarci](https://github.com/diogonarciso/BISCAP) [so/BISCAP](https://github.com/diogonarciso/BISCAP). In brief, for each 2D-OCT image, the pixels at the substratum were identifed, and a threshold for the pixel intensity was calculated, enabling binarization of pixels as biomass or background, thereby distinguishing the biofilm from the liquid bulk phase<sup>[32](#page-11-13)</sup>. The 2D image processing was extended to the 3D-OCT images, which correspond to 509 2D-OCT images as described by Narciso et al.<sup>31</sup>. BISCAP software was used to quantify the biofilm average thickness, compaction parameter and porosity. The specific definitions of the average thickness, compaction parameter and porosity can be found in Narciso et al.<sup>31,[32](#page-11-13)</sup>. Briefly, the average thickness refers to the total length between the bottom and top of the biofilm. The compaction parameter, proposed by Narciso et al.[32,](#page-11-13) measures the compactness of the bioflm; it represents the ratio between the continuous biomass pixels to the total number of pixels (biomass + water) between the bottom and top interfaces. The delivered values range from 0 to 1, where values closer to 1 correspond to very compact biofilms (with low empty spaces). The porosity was defned as the fraction of background voxels in the bioflm region, and varies between 0 and 1, as proposed by Narciso et al.<sup>[31](#page-11-12)</sup>.

# <span id="page-2-1"></span>*Peptide nucleic acid (PNA)—fuorescence in situ hybridization (FISH)*

To track the spatial position of *L. pneumophila* inside bioflms, the PNA probe PLPNE620 (5′-CTG ACC GTC CCA GGT-3′) (Cambridge Research Biochemicals United Kingdom) was used, since it was successfully applied to detect the pathogen in past studies<sup>28</sup>. After rinsing with saline solution, coupons were allowed to air dry at room temperature. The PNA hybridization and washing step were performed according to Wilks et al.<sup>[28](#page-11-9)</sup>. Control experiments were carried at each sampling timepoint to ensure that no cross-staining between *P. fuorescens* and *L. pneumophila* occurred, nor EPS staining. For that, control bioflms of *P. fuorescens* were hybridized with the PNA probe in the same conditions formerly described.

#### *Episcopic diferential interference contrast (EDIC)/epifuorescence (EF) microscopy*

The stained coupons were examined using a Nikon Eclipse CFI60 episcopic differential interference contrast (EDIC) coupled with epifuorescence (EF) microscope, using a 50×Plan APO objective (Best Scientifc, UK). The EDIC channel was used to visualize the microscale structure of biofilms, while the TRITC channel was used to visualize and track the red labelled *L. pneumophila*. Representative images were taken over 20 felds of view and processed using ImagePro image capture software. The images were obtained with equal exposure times and gain values.

#### <span id="page-2-2"></span>*Confocal laser scanning microscopy (CLSM)*

The stained coupons were also observed with a white light laser (WLL) at excitation wavelength of 565 nm and a 405-diode laser at excitation wavelength of 398 nm, using a 40×glycerol objective lens in a Leica STELLARIS (Leica Stellaris, Leica Microsystems, Germany). A minimum of six stacks of horizontal plane images (512×512 pixels, corresponding to 387.5×387.5 µm) with a z-step of 0.36 µm were acquired for each sample. IMARIS 9.1 software (Bitplane, Switzerland) was used to create 3D projections of biofilm structures. The plugin COMSTAT2 from ImageJ was used to quantify the biovolume  $(\mu m^3/\mu m^2)^{33}$  $(\mu m^3/\mu m^2)^{33}$  $(\mu m^3/\mu m^2)^{33}$ . The biovolume was defined as the overall volume of cells ( $\mu$ m<sup>3</sup>) divided by the substratum area, and it can be used to estimate how much biomass is in a biofilm<sup>33</sup>.

#### *Quantifcation of sessile cells*

To assess *P. fuorescens* culturability, serial dilutions were performed and plated in triplicate in plate count agar (PCA) (Oxoid, Portugal). Plates were incubated at 30 °C for 24 h for colony-forming units (CFU) enumeration. Afer assessing *P. fuorescens* culturability, bioflm suspensions were thermal treated (50 °C for 30 min) to eliminate *P. fluorescens* from the sample. The treated suspensions were spread onto the selective media BCYE-GVPC (bufered charcoal yeast extract supplemented with glycine, vancomycin, polymyxin and cycloheximide) agar and incubated at 37 °C up to 10 days to assess *Legionella* culturability.

#### *L. pneumophila migration within the bioflm during the initial 24 h*

The migration of *L. pneumophila* within the biofilm was followed over time during the first 24 h after spiking. Bioflm was sampled, labelled with the 16S rRNA PNA probe and imaged using CLSM, according to the previously described methods (["Peptide nucleic acid \(PNA\)—fuorescence in situ hybridization \(FISH\)](#page-2-1)" and "[Confocal](#page-2-2) [laser scanning microscopy \(CLSM\)"](#page-2-2) sections). The biofilms were analysed at 5 min, 15 min, 30 min, 2 h, 4 h, 6 h, 10 h, 20 h and 24 h afer *Legionella* spiking.

# **Statistical analysis**

The experimental data were analysed using the software GraphPad Prism 9.0 for Windows (GraphPad Software, USA). Three independent experiments were performed. The mean and standard deviation (SD) for each set of results were calculated. Results were compared using an ANOVA single-factor statistical analysis and Student's t-test. The level of significance was set for  $p$ -values < 0.05.

# **Results**

# *P. fuorescens* **and** *L. pneumophila* **culturability**

*P. fuorescens* culturability per volume of bioflm did not show statistically signifcant diferences over time between the control bioflm (*P. fuorescens* alone—*Pf*) and those spiked at day 3 with *L. pneumophila* (*Pf*+*Lp*)— Fig. [1a](#page-3-0). In both cases, the amount of *P. fluorescens* (~9  $\log_{10}$  CFU/cm<sup>3</sup>) did not significantly change between days 3 and 14 ( $p > 0.05$ ). On the other hand, *L. pneumophila* was recovered for 11 days from the mixed biofilm of *Pseudomonas* and *Legionella*, but as shown in Fig. [1](#page-3-0)b, the culturable numbers of *L. pneumophila* per bioflm volume had 1-log reduction ( $p$  < 0.0001) between days 4 and 7 and maintained around 5  $\log_{10}$  CFU/cm<sup>3</sup> until the end of each experiment. Tis reinforces the notion that *L. pneumophila* is able to colonize and persist (at least for 11 days) in *P. fluorescens* biofilms, confirming the previous work from Stewart et al.<sup>[13](#page-10-11)</sup>.

#### **Bioflm mesoscale structure**

Te mesoscale structures of the control bioflms of *P. fuorescens* (*Pf*—without *L. pneumophila*) were compared with those spiked with *L. pneumophila* (*Pf*+*Lp*) on day 3. Figure [2](#page-4-0) depicts representative 2D-OCT bioflm images for both conditions (*Pf* and *Pf*+*Lp* bioflms).

When analyzing the control *P. fuorescens* bioflm mesoscale structure over time, it can be seen that the regular and fat structure observed on day 3 (Fig. [2A](#page-4-0)) is similar to the one found on day 4 (Fig. [2](#page-4-0)B). Over time, *P. fuorescens* control bioflms (Fig. [2](#page-4-0)C and D) tend to become more irregular and exhibit more empty spaces (colored in blue). A similar behavior is observed for the *P. fuorescens* bioflms spiked with *L. pneumophila*, except that, for longer incubation periods, the spiked bioflms (Fig. [2](#page-4-0)F and G) tend to be signifcantly thicker than the control bioflms, and show increased empty channels. Not surprisingly, the area occupied by the empty channels is more pronounced in the top of the bioflm than in the bottom, for the control and spiked bioflms.

Based on the 3D-OCT biofilm images and using the BISCAP software<sup>31</sup> the following biofilm structural parameters were quantifed: thickness (Fig. [3a](#page-5-0)), porosity (Fig. [3b](#page-5-0)) and compaction parameter (Fig. [3c](#page-5-0)).

No signifcant changes were observed in the thickness profle of the *P. fuorescens* control bioflms (Fig. [3](#page-5-0)a, green bars) which was found to be  $61 \pm 11$  µm over the 14 days experimental period. The other mesoscale parameters showed significant changes from days 3 to 4 ( $p$  < 0.05): while porosity (Fig. [3b](#page-5-0)) increased, the compactness of the bioflm has been reduced (Fig. [3](#page-5-0)c). From day 4 until the end of the experiment, the above mentioned parameters remained stable, suggesting the biofilm structure reached the plateau<sup>[34](#page-11-15)</sup>.

Upon *L. pneumophila* spiking to the *P. fuorescens* bioflms (*Pf*+*Lp*), no signifcant changes in thickness were noticeable between days 3 and 4, as shown in Fig. [3a](#page-5-0) (orange bars). However, from days 7 to 14, bioflms with *L. pneumophila* became signifcantly thicker than the ones of *P. fuorescens* alone (*p*<0.0001), reaching the highest thickness of 90  $\mu$ m by day 11. The porosity and compactness did not change ( $p > 0.05$ ) between days 3 and 4 (*Pf*+*Lp*, orange bars). Changes were only noticeable later, by day 7, as the porosity increased (*p*<0.05) and the compaction decreased ( $p$  < 0.05), to values like the ones from the non-spiked biofilms ( $Pf$ ).

#### *Legionella* **spatial location**

To study the spatial location of *L. pneumophila* within the *P. fuorescens* bioflms, the microscale structure of the spiked bioflms was characterized by episcopic diferential interference contrast microscopy (EDIC) with epifuorescence (EF) and by Confocal Laser Scanning Microscopy (CLSM). *L. pneumophila* is labelled red through the specifc 16S rRNA PNA probe (PLPNE620). Representative images of *P. fuorescens* bioflms stained with the same PNA probe and visualized at the EDIC/EF (Fig. S1) and CLSM (Fig. S2) are provided in the Supplementary Information. These images show that there is no cross-staining between the bacteria nor any interaction with



<span id="page-3-0"></span>Figure 1. Bacteria culturability expressed per volume of biofilm (log<sub>10</sub> CFU/cm<sup>3</sup>) (a) *P. fluorescens* and (b) *L*. *pneumophila* recovered from biofilm over time. The mean ± standard deviation is shown. Statistically significant differences are represented for  $p < 0.0001$  by \*\*\*\*; ns: not statistically significant.

Day 3 - Before the spiking





<span id="page-4-0"></span>**Figure 2.** Representative images obtained by 2D-Optical Coherence Tomography (OCT) of 3-, 4-, 7- and 14-day bioflms not spiked (lef side) and spiked (right side) with *L. pneumophila*. White scale bars are 100 µm. Specific areas of Fig. 2D (D1) and 2G (G1), marked with a white rectangle, were × 12 enlarged. The empty spaces within the bioflm structure are colored in blue.

the bioflm EPS (no red signal is observed). Figures [4](#page-6-0) and [5](#page-7-0) show representative EDIC/EF and CLSM images of the spiked bioflms, respectively, and show that *L. pneumophila* was widespread within the coupons, and also emphasize the success of bacteria in colonizing the *P. fuorescens* bioflm.

The EDIC/EF microscopy images allowed to qualitatively characterize the biofilm microscale structure and to visualize the predominant location of *L. pneumophila* within it. Direct observation of bioflms 24 h afer the *L. pneumophila* (day 4) spiking, EDIC/EF imaging revealed the presence of microcolonies (Fig. [4—](#page-6-0)white arrows) and the diffuse fluorescence surrounding them is indicative of eDNA in the accumulating EPS. The presence of microcolonies was further confrmed with the OCT since each of the individual black dots are too large to be individual bacteria and more likely to be microcolonies (approximately 10–20 microns in diameter). In general, from days 4 to 14, there were some highly colonized areas (Fig. [4](#page-6-0)—yellow arrows) separated by others with less bioflm density, showing the heterogeneous nature of bioflms. Bioflms showed increased thickness with time, which is particularly noticeable by day 14 (Fig. [4E](#page-6-0)). In this figure, biofilm microcolonies seem to be brighter and more well-defned than in previous days, which refects the growth of the microcolonies and the expected higher rRNA content present in the bioflm.

*L. pneumophila* red fuorescing cells can also be seen (under the TRITC flter), evidencing its widespread distribution within the bioflm. Regions, where the coupon was scratched or with some more prominent bioflm aggregates, had massive *L. pneumophila* clumps. Some water channels were also observed in the bioflm, but no significant amounts of *L. pneumophila* were observed near such water channels. The intensity of the red fluorescing cells (Fig. [4](#page-6-0)B, D and F) seems to become faint over time (particularly by day 14).

The detailed investigation of the *L. pneumophila* spatial position within the *P. fluorescens* biofilm was estab-lished via confocal imaging. The three-dimensional reconstructions of the biofilms—Fig. [5](#page-7-0)—revealed the presence of *P. fluorescens* (observed as green due to the autofluorescence conferred by self-produced pigments<sup>35[,36](#page-11-17)</sup>) and *L. pneumophila* in very similar proportions. Furthermore, *L. pneumophila* was mostly located in the bottom layers of the biofilm. This was observed for the whole experimental period.

# **Quantifcation of the bioflm microscale structure**

The biovolume of *P. fluorescens* and *L. pneumophila* in the spiked biofilms (Fig. [6](#page-7-1)) were determined by CLSM from days 4 to 14.





b)

 $\Box$  Pf

 $Pf+Lp$ 

<span id="page-5-0"></span>**Figure 3.** Tickness (**a**), porosity (**b**) and compaction parameter (**c**) of the control (*Pf*) – green bars and spiked (*Pf*+*Lp*) – orange bars bioflms over 14 days. Values were extracted from 3D-OCT images with the BISCAP software. The mean  $\pm$  standard deviation is shown. Statistically significant differences are represented for  $p$ <0.05 by \*,<0.01 by \*\*,<0.0005 by \*\*\* and<0.0001 by \*\*\*\*. Error bars in black, green and orange refer to signifcant diferences between control and spiked bioflms, between the control bioflms and between the spiked bioflms, respectively. *L. pneumophila* spiking is indicated by an arrow.

The biovolume of *P. fluorescens* in the mixed  $Pf + Lp$  biofilms remained constant ( $12 \pm 2 \mu m^3/\mu m^2$ ) from days 4 to 14 (*p* > 0.05), while the biovolume of *L. pneumophila* increased (not statistically signifcant) until day 9  $(11 \pm 1 \mu m^3/\mu m^2)$  and became significantly lower ( $p < 0.05$ ) at day 11 ( $7 \pm 2 \mu m^3/\mu m^2$ ).

# *L. pneumophila* **migration within the bioflm during the initial 24 h**

The migration of *L. pneumophila* within the *P. fluorescens* biofilm was monitored over a 24 h period after *L. pneumophila* spiking, using confocal imaging (Fig. [7\)](#page-8-0). No *L. pneumophila* was observed in the 5 initial minutes afer the spiking. A thin layer of *L. pneumophila* was detected on the top surface of the bioflm 15 min afer spiking. Over time, an increase in *L. pneumophila* on the top of the bioflm was observed, suggesting an accumulation of the bacteria. By the 4 h mark, a signifcant amount of *L. pneumophila* started to appear in the bottom layers of the bioflm, simultaneously with a bacterial decrease on the top. Tis migration continued progressively, with *L. pneumophila* becoming predominantly located at the bottom of the bioflm by the end of the 24 h observation period.

# **Discussion**

*L. pneumophila* entrance in the 3-days *P. fuorescens* bioflm was evaluated regarding the impact on the bioflm structure and on the bacteria positioning over 11 days.



<span id="page-6-0"></span>**Figure 4.** Representative EDIC/EF images of 4-, 7- and 14-days bioflms spiked with *L. pneumophila*; the latter were stained with a PNA probe (in red). Bioflms were visualized using the EDIC channel (images **A**, **C** and **E**) and using a TRITC flter for fuorescence (images **B**, **D**, and **F**). White arrows indicate microcolonies and yellow arrows indicate areas highly colonized. Bars represent 10  $\mu$ m. Magnification × 500. A representative image of the control of *P. fuorescens* bioflm stained with the PNA probe is provided in Supplementary Information (Fig. S1).

# *L. pneumophila* **colonization of the** *P. fuorescens* **bioflm—impact on the bioflm structure**

When *L. pneumophila* colonizes the *P. fuorescens* bioflms, they maintained their mesoscale structure (quantifed through thickness, porosity, and compaction parameter of the 3D-OCT images) as no signifcant diferences were found between days 3 and 4 (before and 24 h afer *L. pneumophila* spiking, respectively)—Fig. [3](#page-5-0) (orange bars). Diferences in the *Legionella* spiked bioflms structure were only noticeable later (when sampling the bioflm at day 7), as they tended to rearrange into similar characteristics as those from the control (*P. fuorescens* alone) biofilms. Lee et al.<sup>37</sup> reported a delay in biofilm development, concluding that the development of mixed-species is slower (1- or 2-day delay) than single-species biofilms. The control biofilm (*P. fluorescens* only) rearranged structurally between days 3 and 4 (Fig. [3,](#page-5-0) green bars), and then remained stable, suggesting that the bioflm development reached its plateau by day 4.

However, thickness followed a diferent trend: from days 7 to 14, the spiked bioflms became progressively thicker ( $\sim$ 30%) than the *Pf* controls (Fig. [3a](#page-5-0), green bars). A similar behaviour was found by Koh et al.<sup>38</sup> who described that the thickness of *P. aeruginosa* bioflms exposed to a waterborne pathogen, *Cryptosporidium parvum*, increased when compared to the control biofilms. Also, Puga and colleagues<sup>39</sup> reported that spiking *Listeria monocytogenes* to pre-established *P. fuorescens* bioflms led to an EPS matrix over-production. According to other authors, mixed-species biofilms might have an increased biomass production $37,40$  $37,40$ , which can be related to events of space optimization due to different bacterial interactions<sup>[41](#page-11-22)</sup>.

The other mesoscale characteristics of the biofilms (including porosity and compaction parameter) suggest that regardless of the *Legionella* presence, the dominant bioflm structure is the one from the *P. fuorescens—*the frst colonizer. In addition, the present results show that the cell density of *P. fuorescens* (Fig. [1a](#page-3-0)) was not signifcantly afected by the presence of *L. pneumophila*. Pang et al.[42](#page-11-23) while studying the colonization of *P. fuorescens*



<span id="page-7-0"></span>Figure 5. Representative CLSM images of 4-, 7- and 14-days biofilms spiked with *L. pneumophila*; The latter was stained with a PNA probe (in red). The confocal images are 3D projections obtained using IMARIS, and the white scale bars are 50 µm. A representative image of the control *P. fuorescens* bioflm stained with the PNA probe is provided in Supplementary Information (Fig. S2).



<span id="page-7-1"></span>

bioflms by *L. monocytogenes* also concluded that *P. fuorescens* cell density did not change with the presence of *L. monocytogenes*.

Te observed dominance of *P. fuorescens* over *L. pneumophila* in the bioflm may be related with the fact that *P. fluorescens* is a well-known EPS producer strain<sup>[20,](#page-11-2)[42,](#page-11-23)43</sup>. It has been previously reported that microorganism producers of EPS have competitive advantages over other bacteria if they are the first colonizers<sup>[44](#page-11-25)</sup>. Some authors argue that *Legionella* is able to form biofilms on its own under very well-defined laboratory conditions<sup>45[,46](#page-11-27)</sup>, but with no signifcant amounts of EP[S46](#page-11-27). However, under real environmental scenarios, *Legionella* colonizes preestablished bioflms, as a secondary colonizer[5](#page-10-3) . Furthermore, the large amounts of EPS produced by *P. fuorescens* might enhance the physical fxation/entrapment of *L. pneumophila* and will allow the establishment of more robust biofilms with increased cohesion<sup>[39](#page-11-20),[47](#page-11-28)</sup>, arguably more difficult to suffer slough-off.

# *L. pneumophila* **location within the** *P. fuorescens* **bioflm**

Results showed that *L. pneumophila* successfully colonized and persisted in a *P. fuorescens* bioflm at least for 11 days.



<span id="page-8-0"></span>**Figure 7.** Representative CLSM images of bioflms 5 min, 15 min, 2 h, 4 h, 10 h, 20 h and 24 h afer *L. pneumophila* spiking; The confocal images are 3D projections obtained using IMARIS, and the white scale bars are  $50 \mu m$ .

The EDIC images showed that PNA-L. pneumophila signal became faint over time, which seems to be consistent with the *Legionella* biovolume (Fig. [6](#page-7-1)) and culturability (Fig. [1](#page-3-0)b) decrease over time. In all situations this might be a consequence of *L. pneumophila* entering a non-culturable but viable state (VBNC). It is reported that

VBNC cells have lower metabolic activity and lower levels of rRNA[48](#page-11-29),[49](#page-11-30). If the amount of rRNA decreases, and since the PNA probe binds specifcally to 16S rRNA molecules, one might expect that the intensity of the signal (observed as a red color) will also decrease<sup>[48,](#page-11-29)50</sup>. Former studies showed that there are a vast number of 16S rRNA molecules per bacterium compared to copies of the gene<sup>[51](#page-11-32),52</sup>. Thus, the bright and further decrease in the PNA-FISH signal is arguably due to decreasing 16S rRNA content and not from the very low number of copies of the 16S rRNA chromosomal gene. The ability of *Legionella* to enter into the VBNC state has been demonstrated by several author[s53](#page-11-34)[–55.](#page-11-35) Gião et al.[56](#page-11-36) and Alleron et al[.57](#page-11-37) induced *L. pneumophila* cells into VBNC state through chlorine and monochloramine exposure, respectively. Indeed, the former remained infective in an *Acanthamoeba* animal model. Other studies also concluded that under a low nutrient environment, *Legionella* would lose its culturability<sup>58</sup>, and that VBNC cells exhibit smaller cell sizes<sup>59,60</sup>. An alternative explanation for the faint signal might be that, over time*, L. pneumophila* is washed-of of the bioflm, as the medium is replaced every 2 days.

Regarding the spatial positioning of the bacteria, the CLSM images (Fig. [5\)](#page-7-0) show that bacteria were essentially positioned in two distinct layers. While *L. pneumophila* was positioned in the bottom of the bioflm, *P. fuorescens* was located in the upper layers (Fig. [5](#page-7-0)). Two distinctive physiological aspects between both bacteria are related to the oxygen consumption and nutrients uptake. While *P. fluorescens* metabolizes carbon sources and is aerophilic<sup>[61](#page-12-3)</sup>, *L. pneumophila* has very specific nutritional requirements and behaves as a microaerophilic microorganism<sup>62</sup>, thus growing in the presence of oxygen but better at lower oxygen levels. Since the transport of nutrients and oxygen is higher at the bioflm top interface[63,](#page-12-5) the relative positioning of *Pseudomonas* and *Legionella* inside the bioflm is a win–win situation for both bacterial species. Tis also explains why *L. pneumophila* is not placed around water channels (observed in the EDIC/EF imaging—Fig. [4](#page-6-0)), as the primarily function of water channels is to favor mass transport (nutrients, oxygen, waste-products, etc.) between the bioflm and the surrounding liquid<sup>64</sup>. And expectedly higher oxygen and nutrients concentrations might be found on those areas<sup>[11](#page-10-9)</sup>. It is not surprising though that *Legionella* is located at the bottom layers of the bioflm where micro-environments with lower oxygen levels can be found. Additionally, it has been demonstrated that the EPS producer cells and their descendants (in the case of the present study—*P. fuorescens*) will be positioned in the bioflm top layers, keeping privileged access to nutrients and oxygen and allowing such bacteria to dominate the biofilm<sup>65</sup>. Indeed, the OCT imaging (Fig. [2](#page-4-0)) demonstrated that most of the empty spaces—that are linked to events of mass transfer—are located in the upper layers of the biofilm<sup>66</sup>. This also supports the former conclusions of the present work that by the middle of the experimental bioflms colonized by *L. pneumophila* presents the same mesoscale structure properties (except for thickness) as the one from the *P. fuorescens* control bioflm.

Finally, from the *Legionella* perspective, being at the bottom of the bioflm (the EDIC/EF imaging showed that many cells were in the scratches of substratum material), *Legionella* will be more protected than in the top layers against external harshness like biocides or thermal shocks. There are several studies demonstrating the ability of *P. fluorescens* biofilms to shield pathogens<sup>39[,67](#page-12-9),[68](#page-12-10)</sup>.

#### **How long does** *L. pneumophila* **need to reach the bottom of the** *P. fuorescens* **bioflm?**

The time-lapse representative CLSM images of *L. pneumophila* colonization of the pre-established *P. fluorescens* bioflm over the initial 24 h afer *L. pneumophila* spiking (Fig. [7\)](#page-8-0) show that *L. pneumophila* starts to adhere, to a greater extent, to the top of the bioflm within 15 min afer spiking. It is somehow surprising that no *L. pneumophila* was observed in the first 5 min, as the experiment was conducted under stagnation (no flow) conditions. Former work demonstrated that sedimentation signifcantly afects bacterial attachment and mass transfer, even under low flow conditions<sup>[69](#page-12-11),[70](#page-12-12)</sup>. Under no-flow conditions, the sedimentation effect is even higher, and the entire biofilm was surrounded by *Legionella*. Therefore, the fact that *L. pneumophila* took between 5 and 15 min to adhere to the top layer of the *P. fuorescens* (Fig. [7](#page-8-0), Top, 15 min), is likely due to the multiple adaptation strategies that *Legionella* can undergo. Several studies show that the morphological changes of *Legionella* appendages are critical to the interactions within host-protozoa and allow the bacteria to switch between the replicative and transmissive phases<sup>71</sup>. The study from Abdel-Nour et al.<sup>72</sup> also shows that adhesins, in particular, collagen-like adhesin is important for *Legionella* attachment to surface, bioflm formation and auto-aggregation.

Once *L. pneumophila* interacts with the top layer of the bioflm it quickly (between 2 and 4 h) reaches the bottom of the *P. fuorescens* bioflm. Considering that the pre-established 3 days bioflm have an average thickness of  $\sim$  58  $\mu$ m, the average linear migration speed of *L. pneumophila* across the biofilm is  $\sim$  22  $\mu$ m/ h. This migration speed is consistent with the range proposed by Picioreanu et al[.73](#page-12-15) for the computational model simulation of *P. aeruginosa* bioflm formation, which accounted with many factors, including cells motility and twitching motility. Albeit it is important to remark that in the present study, *L. pneumophila* was not the frst colonizer and already encountered a pre-established thick biofilm, with high cellular density ( $\sim$ 9 log $_{10}$  CFU/cm<sup>3</sup>) and a very well organized mesoscale structure (Fig. [2A](#page-4-0)), which could have been a constraint to *L. pneumophila* and migration. Puga et al.[39](#page-11-20) attributed the diferences between the colonization of 48 h pre-established *P. fuorescens* bioflms by *L. monocytogenes* formed under diferent conditions to the physical impediment bacteria face when entering diferent structures of the already established bioflms. It seems that apart from the hypotheses already discussed regarding the distinctive physiological aspects between the two bacteria species (nutrient and oxygen requirements), *L. pneumophila* might had also taken advantage of the empty spaces found in the *P. fuorescens* bioflm (Fig. [2A](#page-4-0)—colored in blue) to quickly move across the bioflm and reach its bottom. As previously discussed, no signifcant changes were observed at the mesoscale structure of the bioflm (Figs. [2](#page-4-0) and [3\)](#page-5-0) reinforcing the idea that *L. pneumophila* took advantage of the already existing bioflm structure rather than creating transient bioflm structures (like pores or channels) as reported in other works $74$ .

Afer 4 h, the signifcant decrease of *L. pneumophila* in the top layer of the bioflm is arguably related to sedimentation and with the fact that *L. pneumophila* keeps moving across the bioflm since a signifcant increase of red stained *L. pneumophila* cells is observed in the bottom of the bioflm. Between 20 and 24 h all the *L.* 

*pneumophila* is positioned in the bottom layer of the *P. fuorescens* bioflm (Fig. [7](#page-8-0)), in a very high concentration  $(\sim$ 7 log<sub>10</sub> CFU/cm<sup>3</sup>, Fig. [1b](#page-3-0)). The 24 h *L. pneumophila* concentration in the biofilm and in the bulk ( $\sim$ 8 log<sub>10</sub> CFU/ mL), raises the question of whether *L. pneumophila* is or not able to replicate within a mono-specie bioflm even if it is over a small timespan. A proper answer to this question requires further investigation. Of note is that the *L. pneumophila* numbers provided were obtained by culturability, thus likely refecting an underestimation the true amounts of bacteria in the system.

The present work brings new insights for the discussion about *Legionella* and biofilms interactions concerning the structural changes and relative location of *L. pneumophila* within the *P. fuorescens* bioflm. Although the experimental design does not aim to mimic the interactions of bioflm-*Legionella* in engineered water systems, it provides an expedite approach to tackle some fundamental questions regarding such interactions. The combination of micro and mesoscale techniques provided signifcant and complementary information that can be used in future works and in real studies. In this scope, it worth to highlight that OCT imaging showed to be a powerful non-staining technique that rapidly describes the bioflm 3D meso-scale structure, microcolonies accumulation and water flled areas.

It is important to remark that the results obtained in the present study might be diferent concerning the pre-established bioflm species used or the *Legionella* species/strains considered or the introduction of host cells.

Finally, the proposed experimental model offers to the scientific community a platform to study, in a systematic way, several questions related to mechanistic and physiological aspects of *Legionella*-bioflms interactions, including virulence, transmission, the behaviour of mutants (among many others) which might allow, in the future, to better understand the bacteria dynamics in the complexity and variability of real systems.

Future work is focused on answering to some of the questions raised during this study regarding whether *L. pneumophila* replicates or not in the bioflm and whether it enters VBNC states or wash-of from the bioflm over time. Since bioflm detachment is critical from a public health perspective of legionellosis prevention the model will also be revised to consider this aspect in future works.

# **Conclusions**

Bioflms are a key ecological niche for *Legionella* persistence in water systems, although the microbial interactions between them are still poorly understood. The laboratory model developed in this study deciphered some of the interactions of *L. pneumophila* and *P. fluorescens* biofilms. The main findings of this work are: (a) the overall dominant bioflm structure is the one provided by *P. fuorescens*, regardless of the *L. pneumophila* colonization; (b) the spiked bioflms are thicker than the ones from *P. fuorescens* alone; (c) *L. pneumophila* reaches in 2–4 h the bottom of the bioflm, were it is preferentially positioned over the 11 days of the trial, thus being more protected from external stressors, and (d) both PNA-labelling and *L. pneumophila* culturability suggest that by the end of the experiment *Legionella* might be entering a VBNC state for stress survival.

#### **Data availability**

The datasets that support the findings of this study are available from the corresponding author on reasonable request.

Received: 8 May 2024; Accepted: 15 July 2024 Published online: 22 July 2024

#### **References**

- <span id="page-10-0"></span>1. Berjeaud, J.-M. *et al. Legionella pneumophila*: Te paradox of a highly sensitive opportunistic waterborne pathogen able to persist in the environment. *Front. Microbiol.* **7**, 486 (2016).
- <span id="page-10-1"></span>2. Pereira, A., Silva, A. R. & Melo, L. F. *Legionella* and bioflms—Integrated surveillance to bridge science and real-feld demands. *Microorganisms* **9**, 1212 (2021).
- <span id="page-10-15"></span>3. Borella, P., Guerrieri, E., Marchesi, I., Bondi, M. & Messi, P. Water ecology of *Legionella* and protozoan: Environmental and public health perspectives. *Biotechnol. Annu. Rev.* **11**, 355–380 (2005).
- <span id="page-10-2"></span>4. Taylor, M., Ross, K. & Bentham, R. *Legionella*, protozoa, and bioflms: Interactions within complex microbial systems. *Microb. Ecol.* **58**, 538–547 (2009).
- <span id="page-10-3"></span>5. Declerck, P. Bioflms: Te environmental playground of *Legionella pneumophila*. *Environ. Microbiol.* **12**, 557–566 (2010).
- <span id="page-10-4"></span>6. Lau, H. Y. & Ashbolt, N. J. Te role of bioflms and protozoa in *Legionella* pathogenesis: Implications for drinking water. *J. Appl. Microbiol.* **107**, 368–378 (2009).
- <span id="page-10-6"></span><span id="page-10-5"></span>7. Declerck, P. *et al.* Replication of *Legionella pneumophila* in bioflms of water distribution pipes. *Microbiol. Res.* **164**, 593–603 (2009). 8. Wadowsky, R. M. *et al.* Growth-supporting activity for *Legionella pneumophila* in tap water cultures and implication of hartman-
- <span id="page-10-7"></span>nellid amoebae as growth factors. *Appl. Environ. Microbiol.* **54**, 2677–2682 (1988). 9. Surman, S., Morton, G., Keevil, B. & Fitzgeorge, R. *Legionella pneumophila* proliferation is not dependent on intracellular replication. *Legionella* **70**, 86–89 (2001).
- <span id="page-10-8"></span>10. Murga, R. *et al.* Role of bioflms in the survival of *Legionella pneumophila* in a model potable-water system. *Microbiology* **147**, 3121–3126 (2001).
- <span id="page-10-9"></span>11. Rogers, J., Dowsett, A. B., Dennis, P. J., Lee, J. V. & Keevil, C. W. Infuence of plumbing materials on bioflm formation and growth of *Legionella pneumophila* in potable water systems. *Appl. Environ. Microbiol.* **60**, 1842–1851 (1994).
- <span id="page-10-10"></span>12. Wadowsky, R. M. & Yee, R. B. Satellite growth of *Legionella pneumophila* with an environmental isolate of *Flavobacterium breve*. *Appl. Environ. Microbiol.* **46**, 1447–1449 (1983).
- <span id="page-10-11"></span>13. Stewart, C. R., Muthye, V. & Cianciotto, N. P. Legionella pneumophila persists within bioflms formed by *Klebsiella pneumoniae*, *Flavobacterium* sp., and *Pseudomonas fuorescens* under dynamic fow conditions. *PLoS One* **7**, e50560 (2012).
- <span id="page-10-12"></span>14. Donlan, R. M. Bioflms: microbial life on surfaces. *Emerg. Infect. Dis.* **8**, 881–890 (2002).
- <span id="page-10-13"></span>15. Di Pippo, F., Di Gregorio, L., Congestri, R., Tandoi, V. & Rossetti, S. Bioflm growth and control in cooling water industrial systems. *FEMS Microbiol. Ecol.* **94**, fy044 (2018).
- <span id="page-10-14"></span>16. Wang, H. *et al.* Bioflms controlling in industrial cooling water systems: A mini-review of strategies and best practices. *ACS Appl. Bio Mater.* **6**, 3213–3220 (2023).
- <span id="page-11-0"></span>17. Pinel, I., Biškauskaitė, R., Pal'ová, E., Vrouwenvelder, H. & van Loosdrecht, M. Assessment of the impact of temperature on bioflm composition with a laboratory heat exchanger module. *Microorganisms* **9**, 1185 (2021).
- 18. Di Gregorio, L., Tandoi, V., Congestri, R., Rossetti, S. & Di Pippo, F. Unravelling the core microbiome of bioflms in cooling tower systems. *Biofouling* **33**, 793–806 (2017).
- <span id="page-11-1"></span>19. Paniagua, A. T., Paranjape, K., Hu, M., Bédard, E. & Faucher, S. P. Impact of temperature on *Legionella pneumophila*, its protozoan host cells, and the microbial diversity of the bioflm community of a pilot cooling tower. *Sci. Total Environ.* **712**, 136131 (2020).
- <span id="page-11-2"></span>20. Pereira, M. O., Kuehn, M., Wuertz, S., Neu, T. & Melo, L. F. Efect of fow regime on the architecture of a *Pseudomonas fuorescens* bioflm. *Biotechnol. Bioeng.* **78**, 164–171 (2002).
- <span id="page-11-3"></span>21. Abu Khweek, A. & Amer, A. O. Factors mediating environmental bioflm formation by *Legionella pneumophila*. *Front. Cell. Infect. Microbiol.* **8**, 38 (2018).
- 22. Abdel-Nour, M., Duncan, C., Low, D. E. & Guyard, C. Bioflms: the stronghold of *Legionella pneumophila*. *Int. J. Mol. Sci.* **14**, 21660–21675 (2013).
- <span id="page-11-4"></span>23. Nisar, M. A., Ross, K. E., Brown, M. H., Bentham, R. & Whiley, H. Water stagnation and fow obstruction reduces the quality of potable water and increases the risk of legionellosis. *Front. Environ Sci.* <https://doi.org/10.3389/fenvs.2020.611611>(2020).
- <span id="page-11-5"></span>24. Vieira, M., Melo, L. & Pinheiro, M. Bioflm formation: Hydrodynamic efects on internal difusion and structure. *Biofouling* **7**, 67–80 (1993).
- <span id="page-11-6"></span>25. Shen, Y. *et al.* Role of bioflm roughness and hydrodynamic conditions in *Legionella pneumophila* adhesion to and detachment from simulated drinking water bioflms. *Environ. Sci. Technol.* **49**, 4274–4282 (2015).
- <span id="page-11-7"></span>26. Gião, M. S., Wilks, S. A. & Keevil, C. W. Infuence of copper surfaces on bioflm formation by *Legionella pneumophila i*n potable water. *BioMetals* **28**, 329–339 (2015).
- <span id="page-11-8"></span>27. Rogers, J., Dowsett, A. B., Dennis, P. J., Lee, J. V. & Keevil, C. W. Infuence of temperature and plumbing material selection on bioflm formation and growth of *Legionella pneumophila* in a model potable water system containing complex microbial fora. *Appl. Environ. Microbiol.* **60**, 1585–1592 (1994).
- <span id="page-11-9"></span>28. Wilks, S. A. & William, K. C. Targeting species-specifc low-afnity 16S rRNA binding sites by using peptide nucleic acids for detection of *Legionellae* in bioflms. *Appl. Environ. Microbiol.* **72**, 5453–5462 (2006).
- <span id="page-11-10"></span>29. Silva, A. R. *et al.* Proof-of-concept approach to assess the impact of thermal disinfection on bioflm structure in hot water networks. *J. Water Process Eng.* **53**, 103595 (2023).
- <span id="page-11-11"></span>30. Surman, S. B., Morton, L. H. G. & Keevil, C. W. Te dependence of *Legionella pneumophila* on other aquatic bacteria for survival on R2A medium. *Int. Biodeterior. Biodegrad.* **33**, 223–236 (1994).
- <span id="page-11-12"></span>31. Narciso, D. A. C. *et al.* 3D optical coherence tomography image processing in BISCAP: characterization of bioflm structure and properties. *Bioinformatics* **40**, btae041 (2024).
- <span id="page-11-13"></span>32. Narciso, D. A. C., Pereira, A., Dias, N. O., Melo, L. F. & Martins, F. G. Characterization of bioflm structure and properties via processing of 2D optical coherence tomography images in BISCAP. *Bioinformatics* **38**, 1708–1715 (2022).
- <span id="page-11-14"></span>33. Heydorn, A. *et al.* Quantifcation of bioflm structures by the novel computer program COMSTAT. *Microbiology* **146**, 2395–2407  $(2000)$ .
- <span id="page-11-15"></span>34. Melo, L. F. & Bott, T. R. Biofouling in water systems. *Exp. Therm. Fluid Sci.* 14, 375-381 (1997).
- <span id="page-11-16"></span>35. Xiao, R. & Kisaalita, W. S. Purifcation of pyoverdines of pseudomonas fuorescens 2–79 by copper-chelate chromatography. *Appl. Environ. Microbiol.* **61**, 3769–3774 (1995).
- <span id="page-11-17"></span>36. Meyer, J. M. & Abdallah, M. A. Te fuorescent pigment of *Pseudomonas fuorescens*: Biosynthesis, purifcation and physicochemical properties. *Microbiology* **107**, 319–328 (1978).
- <span id="page-11-18"></span>37. Lee, K. W. K. *et al.* Bioflm development and enhanced stress resistance of a model, mixed-species community bioflm. *ISME J.* **8**, 894–907 (2014).
- <span id="page-11-19"></span>38. Koh, W., Clode, P. L., Monis, P. & Tompson, R. C. A. Multiplication of the waterborne pathogen *Cryptosporidium parvum* in an aquatic bioflm system. *Parasit. Vectors* **6**, 270 (2013).
- <span id="page-11-20"></span>39. Puga, C. H., Dahdouh, E., SanJose, C. & Orgaz, B. *Listeria monocytogenes* Colonizes *Pseudomonas fuorescens* bioflms and induces matrix over-production. *Front. Microbiol.* <https://doi.org/10.3389/fmicb.2018.01706> (2018).
- <span id="page-11-21"></span>40. Rao, Y., Shang, W., Yang, Y., Zhou, R. & Rao, X. Fighting mixed-species microbial bioflms with cold atmospheric plasma. *Front. Microbiol.* <https://doi.org/10.3389/fmicb.2020.01000> (2020).
- <span id="page-11-22"></span>41. Liu, W. *et al.* Deciphering links between bacterial interactions and spatial organization in multispecies bioflms. *ISME J.* **13**, 3054–3066 (2019).
- <span id="page-11-23"></span>42. Pang, X. & Yuk, H.-G. Efects of the colonization sequence of *Listeria monocytogenes* and *Pseudomonas fuorescens* on survival of bioflm cells under food-related stresses and transfer to salmon. *Food Microbiol.* **82**, 142–150 (2019).
- <span id="page-11-24"></span>43. Kives, J., Orgaz, B. & SanJosé, C. Polysaccharide diferences between planktonic and bioflm-associated EPS from *Pseudomonas fuorescens* B52. *Colloids Surf. B. Biointerfaces* **52**, 123–127 (2006).
- <span id="page-11-25"></span>44. Jayathilake, P. G. *et al.* Extracellular polymeric substance production and aggregated bacteria colonization infuence the competition of microbes in bioflms. *Front. Microbiol.* **8**, 1865 (2017).
- <span id="page-11-26"></span>45. Mampel, J. *et al.* Planktonic replication is essential for bioflm formation by *Legionella pneumophila* in a complex medium under static and dynamic fow conditions. *Appl. Environ. Microbiol.* **72**, 2885–2895 (2006).
- <span id="page-11-27"></span>46. Piao, Z., Sze, C. C., Barysheva, O., Iida, K. & Yoshida, S. Temperature-regulated formation of mycelial mat-like bioflms by *Legionella pneumophila*. *Appl. Environ. Microbiol.* **72**, 1613–1622 (2006).
- <span id="page-11-28"></span>47. Gomes, L. C., Piard, J.-C., Briandet, R. & Mergulhão, F. J. *Pseudomonas grimontii* bioflm protects food contact surfaces from *Escherichia coli* colonization. *LWT Food Sci. Technol.* **85**, 309–315 (2017).
- <span id="page-11-29"></span>48. Nisar, M. A. *et al.* Detection and quantifcation of viable but non-culturable *Legionella pneumophila* from water samples using fow cytometry-cell sorting and quantitative PCR. *Front. Microbiol.* **14**, 1094877 (2023).
- <span id="page-11-30"></span>49. Lee, S. & Bae, S. Molecular viability testing of viable but non-culturable bacteria induced by antibiotic exposure. *Microb. Biotechnol.* **11**, 1008–1016 (2018).
- <span id="page-11-31"></span>50. Gião, M. S., Azevedo, N. F., Wilks, S. A., Vieira, M. J. & Keevil, C. W. Interaction of *Legionella pneumophila* and *Helicobacter pylori* with bacterial species isolated from drinking water bioflms. *BMC Microbiol.* **11**, 57 (2011).
- <span id="page-11-32"></span>51. Leskelä, T., Tilsala-Timisjärvi, A., Kusnetsov, J., Neubauer, P. & Breitenstein, A. Sensitive genus-specifc detection of *Legionella* by a 16S rRNA based sandwich hybridization assay. *J. Microbiol. Methods* **62**, 167–179 (2005).
- <span id="page-11-33"></span>52. Větrovský, T. & Baldrian, P. The variability of the 16S rRNA gene in bacterial genomes and its consequences for bacterial community analyses. *PLoS One* **8**, e57923 (2013).
- <span id="page-11-34"></span>53. Dietersdorfer, E. *et al.* Starved viable but non-culturable (VBNC) *Legionella* strains can infect and replicate in amoebae and human macrophages. *Water Res.* **141**, 428–438 (2018).
- <span id="page-11-35"></span>54. Alleron, L. *et al.* VBNC *Legionella pneumophila* cells are still able to produce virulence proteins. *Water Res.* **47**, 6606–6617 (2013). 55. Cervero-Aragó, S. *et al.* Viability and infectivity of viable but nonculturable *Legionella pneumophila* strains induced at high temperatures. *Water Res.* **158**, 268–279 (2019).
- <span id="page-11-36"></span>56. Gião, M. S., Wilks, S. A., Azevedo, N. F., Vieira, M. J. & Keevil, C. W. Validation of SYTO 9/propidium iodide uptake for rapid detection of viable but noncultivable *Legionella pneumophila*. *Microb. Ecol.* **58**, 56–62 (2009).
- <span id="page-11-37"></span>57. Alleron, L., Merlet, N., Lacombe, C. & Frère, J. Long-term survival of *Legionella pneumophila* in the viable but nonculturable state afer monochloramine treatment. *Curr. Microbiol.* **57**, 497–502 (2008).
- <span id="page-12-0"></span>58. Schrammel, B. *et al.* Diferential development of *Legionella* sub-populations during short- and long-term starvation. *Water Res.* **141**, 417–427 (2018).
- <span id="page-12-1"></span>59. Su, X. *et al.* Identifcation, characterization and molecular analysis of the viable but nonculturable *Rhodococcus biphenylivorans*. *Sci. Rep.* **5**, 18590 (2015).
- <span id="page-12-2"></span>60. Nowakowska, J. & Oliver, J. D. Resistance to environmental stresses by *Vibrio vulnifcus* in the viable but nonculturable state. *FEMS Microbiol. Ecol.* **84**, 213–222 (2013).
- <span id="page-12-3"></span>61. Montone, A. M. *et al.* Lactoferrin, quercetin, and hydroxyapatite act synergistically against *Pseudomonas fuorescens*. *Int. J. Mol. Sci.* **22**, 9247 (2021).
- <span id="page-12-4"></span>62. Mauchline, W. S. *et al.* Physiology and morphology of *Legionella pneumophila* in continuous culture at low oxygen concentration. *Microbiology* **138**, 2371–2380 (1992).
- <span id="page-12-5"></span>63. Dufour, D., Leung, V. & Lévesque, C. M. Bacterial bioflm: Structure, function, and antimicrobial resistance. *Endod. Top.* **22**, 2–16  $(2010)$
- <span id="page-12-6"></span>64. Neu, T. R. & Lawrence, J. R. Development and structure of microbial bioflms in river water studied by confocal laser scanning microscopy. *FEMS Microbiol. Ecol.* **24**, 11–25 (1997).
- <span id="page-12-7"></span>65. Xavier, J. B. & Foster, K. R. Cooperation and confict in microbial bioflms. *Proc. Natl. Acad. Sci.* **104**, 876–881 (2007).
- <span id="page-12-8"></span>66. Zhang, T. C. & Bishop, P. L. Density, porosity, and pore structure of bioflms. *Water Res.* **28**, 2267–2277 (1994).
- <span id="page-12-9"></span>67. Haddad, S. *et al.* Variations in bioflms harbouring *Listeria monocytogenes* in dual and triplex cultures with *Pseudomonas fuorescens* and *Lactobacillus plantarum* produced under a model system of simulated meat processing conditions, and their resistance to benzalkonium chlo. *Food Control* **123**, 107720 (2021).
- <span id="page-12-10"></span>68. Ripolles-Avila, C., Guitan-Santamaria, M., Pizarro-Giménez, K., Mazaheri, T. & Rodríguez-Jerez, J. J. Dual-species bioflms formation between dominant microbiota isolated from a meat processing industry with *Listeria monocytogenes* and *Salmonella enterica*: Unraveling their ecological interactions. *Food Microbiol.* **105**, 104026 (2022).
- <span id="page-12-11"></span>69. Li, J., Busscher, H. J., Norde, W. & Sjollema, J. Analysis of the contribution of sedimentation to bacterial mass transport in a parallel plate fow chamber. *Colloids Surf. B. Biointerfaces* **84**, 76–81 (2011).
- <span id="page-12-12"></span>70. Li, J. *et al.* Analysis of the contribution of sedimentation to bacterial mass transport in a parallel plate fow chamber: Part II: Use of fuorescence imaging. *Colloids Surf. B Biointerfaces* **87**, 427–432 (2011).
- <span id="page-12-13"></span>71. Oliva, G., Sahr, T. & Buchrieser, C. Te life cycle of *L. pneumophila*: Cellular diferentiation is linked to virulence and metabolism. *Front. Cell. Infect. Microbiol.* **8**, 3 (2018).
- <span id="page-12-14"></span>72. Abdel-Nour, M. *et al.* Polymorphisms of a collagen-like adhesin contributes to *Legionella pneumophila* adhesion, bioflm formation capacity and clinical prevalence. *Front. Microbiol.* <https://doi.org/10.3389/fmicb.2019.00604> (2019).
- <span id="page-12-15"></span>73. Picioreanu, C. *et al.* Microbial motility involvement in bioflm structure formation - a 3D modelling study. *Water Sci. Technol.* **55**, 337–343 (2007).
- <span id="page-12-16"></span>74. Houry, A. *et al.* Bacterial swimmers that infltrate and take over the bioflm matrix. *Proc. Natl. Acad. Sci.* **109**, 13088–13093 (2012).

# **Acknowledgements**

This work was financially supported by national funds through FCT/MCTES (PIDDAC): LEPABE, UIDB/00511/2020 (DOI: 10.54499/UIDB/00511/2020) and UIDP/00511/2020 (DOI: 10.54499/ UIDP/00511/2020) and ALiCE, LA/P/0045/2020 (DOI: 10.54499/LA/P/0045/2020); by national funds through the FCT/MCTES (PIDDAC), under the project 2022.03523. PTDC-LegioFilms-Understanding the Role of Bioflm Architecture in *Legionella* Colonization and Risk of Detachment in hospital networks using an Integrated Monitoring Approach, with DOI 10.54499/2022.03523.PTDC ([https://doi.org/10.54499/2022.03523.PTDC\)](https://doi.org/10.54499/2022.03523.PTDC). Ana Rosa Silva thanks the Portuguese Foundation for Science and Technology (FCT) for the fnancial support of the PhD grant (2020.08539.BD).

# **Author contributions**

Conceptualization, A.P. and A.R.S; supervision, A.P., L. F. M., C. W. K.; laboratory experiments, A. R. S.; writing—original draf, A. R. S. and A. P.; writing—review and editing, all authors; funding, L. F. M. and A. P. All authors have read and agreed to the published version of the manuscript.

# **Competing interests**

The authors declare no competing interests.

# **Additional information**

**Supplementary Information** The online version contains supplementary material available at [https://doi.org/](https://doi.org/10.1038/s41598-024-67712-4) [10.1038/s41598-024-67712-4](https://doi.org/10.1038/s41598-024-67712-4).

**Correspondence** and requests for materials should be addressed to A.P.

**Reprints and permissions information** is available at [www.nature.com/reprints.](www.nature.com/reprints)

**Publisher's note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional afliations.

**Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit<http://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2024