A reaction-diffusion model to describe *Listeria monocytoges* biofilms life cycle

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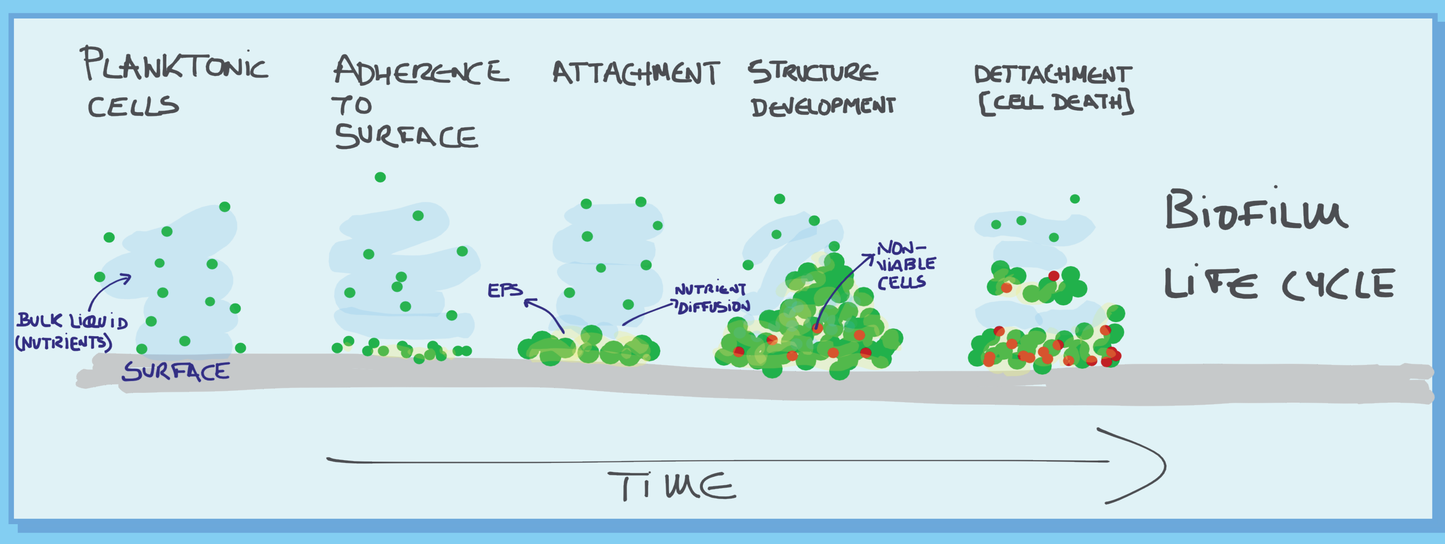
MOTIVATION



Listeria monocytogenes is a pathogenic bacteria responsible for outbreaks of listeriosis. The main mode of transmission to humans is the consumption of contaminated food. This contamination frequently occurs by cross contamination in unhygienic work surfaces and facilities where *L. monocytogenes* can form **biofilms**.

Biofilm **life cycle** characterization is critical to design cost effective and environmentally friendly disinfection techniques.

This work combines quantitative confocal laser scanner microscopy image analysis and mathematical modeling to understand and explain the life cycle of the biofilms formed by the L1A1 strain.

MATERIALS AND METHODS

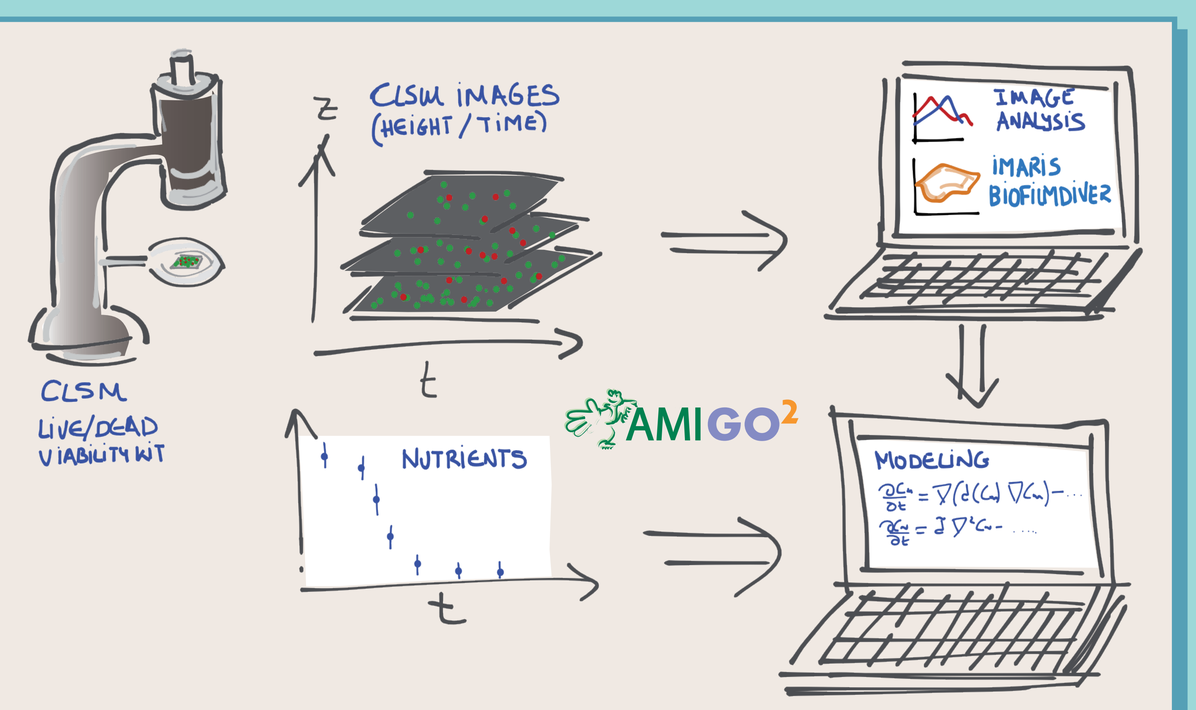
Biofilms were formed in polystyrene microtiter plates under static conditions.

Images were acquired using a high throughput method based on CLSM at several sampling times. Eight stacks per sampling time were randomly chosen for the image analysis. Consumption of glucose was also meassured in every sampling time.

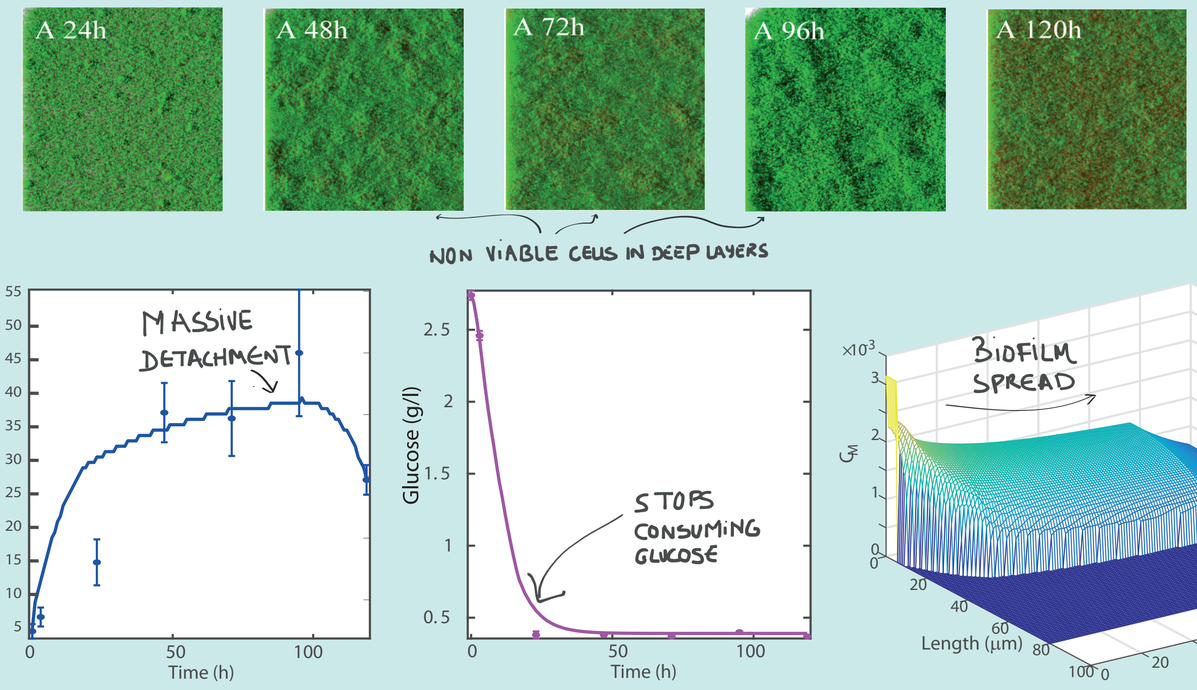
The biofilms maximum thickness (MxT) was obtained using IMARIS for all stacks. 2D parameters, maximum diffusion distance and areal porosity were obtained with BIOFILMDIVER, for all images in each stack.

Model was simulated using the numerical method of lines (a finite differences scheme in space together with an implicit time integrator).

Parameters of the model were computed using AMIGO2 toolbox to fit MxT and nutrientes data using a log-likelihood based approach.



RESULTS



The model:

$$\frac{\partial C_N}{\partial t} = d_1 \nabla^2 C_N - K_1 \frac{C_M C_N}{K_2 + C_N}$$

$$\frac{\partial C_M}{\partial t} = \nabla \cdot (d_2(C_M) \nabla C_M) + K_3 \frac{C_M C_N}{K_2 + C_N} - F_D(C_M, C_N)$$

$$d_2(C_M) = m_{\max}^{b-a} \left(\frac{\in}{1 - C_M} \right)^a C_M^b$$

C_N and C_M: nutrient and microbial biomass concentrations.

Tested decay hypotheses (F_D): i) linear decay; ii) non-linear decay due to starvation; iii) non-linear decay due to biofilm aging and iv) non-linear decay due to impaired glucose uptake.

CONCLUSIONS

This work combined **quantitative microscopy image analysis** and **mathematical modeling** to understand and explain the life cycle of **L1A1 *L. monocytogenes* biofilms**.

CLSM and quantitative image analysis were used to characterize the structure of biofilms. The 2D analysis revealed that L1A1 biofilms are rather flat; while the 3D analysis was used to compute the biofilm thickness through time.

A reaction-diffusion model was then proposed to describe L1A1 biofilm life cycle in batch culture. The model describes biomass and nutrients evolution incorporating several mechanisms such as biomass growth and spread, nutrients diffusion and consumption, and microbial decay. Unknown model parameters were estimated by means of data fitting with AMIGO2 toolbox.

The model is able to explain the data. Remarkably the mechanisms of microbial decay are critical to get satisfactory model predictions.

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