



Nonlocal dynamics of biofilm clogging in a porous microfluidic device

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Bacteria constitute about 15% of the global biomass on Earth [1]. The success of bacteria in colonizing a wide range of ecosystems is mainly due to biofilms, a sessile form of microbial life [2]. Biofilms are communities of interacting microbes that adhere to each other and to structures in their environment [3], making them more resistant to stress. Biofilms regulate critical processes in porous ecosystems [5], such as soils and groundwater systems, and are also key actors in bioengineering applications, such as biofilters [4]. These porous systems generally have a complex architecture, with structures that are connected, heterogeneous and exhibit strong couplings between flow and transport phenomena. Understanding the fundamental mechanisms of the colonization process in such systems may provide important insight into environmental processes and yield new approaches to bioengineering.

In this work, we study biofilm growth in porous media using microfluidics. The setup consists in a glass/PMDS honeycomb channel network, colonized by *Pseudomonas aeruginosa*, a known biofilm model bacteria [3]. Using microscopy techniques, image analysis and particle tracking velocimetry (PTV), we obtain both the distribution of biomass and the velocity field within the network. This allows us to study the coupling mechanisms between flow and biofilm growth. We further study how this evolves over a range of flow rates. Results show a spatial distribution of biofilm that is strongly correlated to the flow rate within each channel. For the low flow rates, the biofilm colonization at short times is rather homogeneous, while at long times the clogging of channels due to biofilm creates preferential flow paths. These paths are unstable with cycles of clogging/declogging due to a competition between growth and flow-induced detachment. Signal analysis of pressure and fluorescence signals show that these events have a characteristic frequency, and we propose a model taking into account the flow rate, the cross-section surface of the channel and the doubling time for the bacteria population.

References

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