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Poromechanics of a yeast aggregate placed under fluid constraints

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The capture of solid particles in a porous medium is critical for many processes but has a major drawback: internal fouling due to pore clogging. Clogging at pore scale is now well understood for inert and rigid particles, but the study of bio-clogging - clogging by biological objects, e.g. living cells - opens many topical research questions as living cells have particular properties that may impact the clog properties: they are deformable, endowed with specific adhesion mechanisms, and are able to proliferate. As a result, these cells can both change their shape and volume, leading to local cellular rearrangements, thus modifying the microstructure of the clog, and consequently its hydrodynamic resistance. In the literature, this change of hydraulic resistance has been extensively studied at the macroscale (the scale of a membrane, the whole clog). In particular, it has been reported that the resistance of a clog depends on the hydrodynamic pressure imposed to the filtration system. But the precise interpretation of this phenomenon is still controversial and patchy: observations are missing at the microscale (the pore, the cell). In particular, a precise understanding of displacements and rearrangements inside a yeast clog, and a link with the local microstructure is still missing.

To address this specific issue, we have developed an experimental quasi-2D microfluidic device consisting in one single pore retaining cells whose properties are well known and easily controllable: the baker's yeast Saccharomyces cerevisiae. After an initial build-up phase, the pressure driving the flow through the pore is changed in order to compress/decompress the clog cyclically, while the flow rate is measured and the clog is imaged under an epifluorescence microscope. This allows to directly measure the microstructure from nucleus fluorescence (figure, center panel), and to quantify the movements within the clog (bright field microscopy, figure, left panel), using dedicated algorithms to distinguish collective movements and local rearrangements (figure, right panel).

These results provide the first observations of the compressibility of a yeast clog at the microscale, and reveal that, in the absence of proliferation, the clogs undergo a first compression with plastic-elastic deformations, characterized by both large collective displacements and local cell rearrangements, while the following compressions are characterized by smaller deformations that are mainly elastic. The plastic deformations modify the local microstructure, as the clogs are denser after compression/decompression cycles than before. Finally, the hydraulic resistance of the clog increases with the hydraulic pressure.

Together, these results show a poromechanical fluid-structure coupling: the fluid deforms the porous medium which in turn modify the fluid percolation. They also show several quantitative differences with the predictions of poroelasticity theory. A dedicated DEM model has thus been developed, to simulate the mechanical behaviour of individual yeast cells. Simulations reproduce quantitatively well the experimental results, which suggests the discrepancies with the poroelasticity theory come from the particle/particle and particle/wall friction.

Overall, this study presents the first measurements of the poromechanical behaviour of a yeast aggregate, and suggest that it is significantly altered by the specific adhesion mechanisms of individual cells.

Participation

In-Person

References

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