Microfluidic insights into the fibrillation of amyloids

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Historically associated with certain neurodegenerative diseases and more recently implicated in bacterial resistance and virulence, amyloid proteins are characterized by their ability to aggregate into fibers with a specific structure. This aggregation dynamics and the species formed during the process, are responsible for potentially harmful biological activities. In particular, oligomers, intermediate size fibrils, could be responsible for the cytotoxicity of some of these proteins. However, small species and the fibrillation process itself are difficult to characterize with traditionally used methods, and the relationship between amyloide structure and their effect remains poorly understood. In the aim of understanding aggregation and especially to quantify the size distribution of fibrils, we developed a microfluidic experiment based on the Taylor-dispersion analysis. This method presents the advantages of being quick (few minutes of measurements), not altering the proteins by the addition of tracers and being applicable to other polydisperse solutions or suspensions. In parallel, an aggregation – diffusion model and simulations are created to complete and explain the experimental results.