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Title:	Design of Aqueous-Liquid Crystal Interfaces To Monitor Protein Aggregation at Nanomolar Concentrations
Authors:	Pani, I. (/jspui/browse?type=author&value=Pani%2C+I.) Hemaswathi, M. (/jspui/browse?type=author&value=Hemaswathi%2C+M.) Mukhopadhyay, S. (/jspui/browse?type=author&value=Mukhopadhyay%2C+S.) Pal, S.K. (/jspui/browse?type=author&value=Pal%2C+S.K.)
Keywords:	Amyloids Proteinaceous Aggregates
Issue Date:	2019
Citation:	Journal of Physical Chemistry C, 123(2), 1305-1312.
Abstract:	<p>Amyloids are proteinaceous aggregates, the deposition of which is associated with neurodegenerative diseases, such as Alzheimer's disease. In vitro protein aggregation requires high protein concentration, which is generally far from physiological concentration. Here, we utilize the interfacial properties of liquid crystals (LCs) to monitor the membrane-induced aggregation of a bacterial functional amyloid, curli, at nanomolar concentration. The binding event triggers an orientational transition of the LC, which is accompanied by the appearance of dynamic spatial patterns enabling sensitive detection of lipopolysaccharide (LPS)-mediated protein aggregation. Quantification of LC response shows a sigmoidal time profile, typical of a protein fibrillation assay. Curli is composed of two subunits (CsgA and CsgB) and is expressed on the outer membrane of Gram-negative bacteria containing LPSs endotoxin. CsgA forms the major subunit of curli, which is nucleated by the membrane-tethered minor subunit CsgB. Using an array of complementary tools, such as polarizing optical microscopy, fluorescence, and atomic force microscopy imaging, we found that the patterned orientation of the LC in response to the binding of curli subunits with LPS corresponds to amyloid fibril formation. Furthermore, using the curli amyloid system, we have successfully demonstrated that membrane-decorated interfaces of LC can be used to study heterotypic cross-seeding in amyloidogenesis. We believe that the LC-based system can be used as a probe to monitor mechanistic details of lipid-induced protein aggregation in the low-concentration regime.</p>
URI:	https://pubs.acs.org/doi/10.1021/acs.jpcc.8b10863 (https://pubs.acs.org/doi/10.1021/acs.jpcc.8b10863) http://hdl.handle.net/123456789/2261 (http://hdl.handle.net/123456789/2261)
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