Membrane-active peptides, IUPAB/EBSA symposium, Edinburgh

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As we strive to confront some of the grand challenges that face society in the early twenty-first century, such as increasing levels of resistance to existing antibiotics and the rising incidence of debilitating neuropathological conditions, for example Alzheimer's disease, the study of membrane-active peptides plays a crucial role. Peptides, whether by evolution or by design, exhibit a diverse range of activity in membranes. In eukaryotes, for example, membrane disruption by bacterial toxins is a complex process involving cell surface binding, followed by toxin insertion and assembly and ultimately membrane poration (Huang and Charron 2017; Pridmore et al. 2016). In a different context, peptide conformational changes induced by interfacial membrane interactions are at the heart of amyloidogenesis, leading ultimately to the formation of amyloid fibrils. In the case of prokaryotes, membrane lysis by antimicrobial peptides is a vital defence mechanism for many species, and is at the core of the human innate immune system. At the molecular level, understanding how these activities are produced and controlled is a significant challenge for biophysicists (Bechinger and Gorr 2017; Sani and Separovic 2016).

The *Membrane-Active Peptides* session at the IUPAB/EBSA/BBS symposium in Edinburgh reflects the global effort to meet this challenge.

Li et al. use single-molecule tracking to probe the insertion and diffusion of the antimicrobial peptide LL-37 into

supported lipid bilayers, and are able to resolve five different penetration depths for the peptide (Li et al. 2016).

Shai et al. use a range of methods to understand the properties of antimicrobial peptides that induce genetic changes that can lead to the development of resistance. They also provide insights into the biophysical properties of peptides that control activity at different stages of the life cycle of bacteria in biofilms (Nuri et al. 2015).

Wollman et al. have also used single-molecule methods, in this case total internal reflection fluorescence microscopy, to study the binding, dynamics and assembly of a bacterial toxin (LukS/F) in live mammalian cells. They find that the protein assembles as an octamer and provide new insights into the kinetics of protein binding and assembly (Haapasalo-Tuomainen et al. 2016).

Aguilar et al. report the use of dual polarisation interferometry on supported membranes to probe molecular details of antimicrobial peptide activity, membrane-mediated amyloid aggregation, and apoptotic protein-induced mitochondrial membrane permeabilization (Lee et al. 2016).

Matsuzaki et al. describe a form of the amyloid β -protein (A β) that binds to clusters of ganglioside GM1 which form in the presence of cholesterol. This form of A β changes from being mostly helical at low concentrations to mostly β -sheet at higher concentrations, and is able to act as a template for amyloid formation (Matsuzaki 2014).

Favero et al. have also studied the interaction of A β peptides with membranes enriched in glycolipids and cholesterol, and report that interactions of A β depend on the lipid composition of the membrane and the aggregation state of the peptide. The N-terminal sections of the peptide were found to have specific interactions with membrane lipids, which may drive bilayer penetration (Rondelli et al. 2016).

The work presented in this session demonstrates the efforts of biophysicists to gain significant insights into membrane-

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active peptides that will drive the development of a new generation of antibiotics and new approaches to treating disease.

Compliance with ethical standards

Conflicts of interest John M. Sanderson declares that he has no conflicts of interest. Frances Separovic declares that she has no conflicts of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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