Biophysical characterization of pore forming peptides

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Pore forming peptides from bacteriophages constitute a class of small membrane-embedded peptides that mediate cell lysis during the bacteriophage life cycle. Bacteriophages have evolved different mechanisms for cell membrane penetration to release active endolysins and enable the digestion of the peptidoglycan envelope[1]: Canonical holins form very large undefined pores (88 - 1200 nm) that leads to the direct release of cytoplasmic endolysin into the periplasm[2] while pinholins lead to the formation of small defined pores (~2 nm) that first depolarize the inner bacterial plasma membrane and in turn leads to the release of membrane-anchored SAR-endolysins[3]. Although those pathways vary in their lytic strategy, both contain a delay mechanism that precisely controls the formation of pores in the inner membrane[4]. To understand the different mechanisms of peptide dependent pore formation, the structural determinants of both large and small pore forming peptides will be characterized using a combination of structure-guided mutagenesis and genetic selection followed by their detail biophysical characterization.

References

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