

A synthetic receptor architecture for the detection of pathogens with small peptides

C. Hüttl^{1,2}, L. Danckert¹, W.F.M. Stöcklein¹, C. Hettrich¹, F.F. Bier^{1,3}

¹ Fraunhofer Institute for Biomedical Engineering (IBMT) · Potsdam · Germany ² University of Potsdam · Institute for Nutrition Science · Nuthetal · Germany ³ University of Potsdam · Institute for Biochemistry and Biology · Potsdam · Germany, christine.huettl@ibmt.fraunhofer.de

Objectives

- development of a specific detection unit for influenza virus
- optimization of the peptide arrangement for signal amplification
- design of a detection platform and immobilisation method

background

- the membrane protein hemagglutinin (HA) is located on the surface of influenza virus type A
- Matsubara et al. [1] identified HA-binding peptides (Tab. 1 bottom)
- multiple simultaneous interactions are relevant for the attachment – also for the influenza host cell interaction and detection [2]

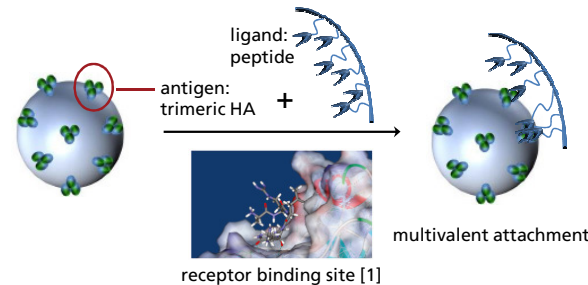


Fig. 1 cartoon demonstrating the binding of influenza virus to a multivalent peptide receptor; docking simulation of the complex between peptide S1 and the receptor binding site of HA

micelle characterization

- peptides were coupled to palmitic acid
- micelle formation in solution (Fig.2)
- determination of the critical micelle concentration (CMC) with drop and bubble shape tensiometer (Fig. 3)
- measurements of micelle size via dynamic light scattering (DLS)

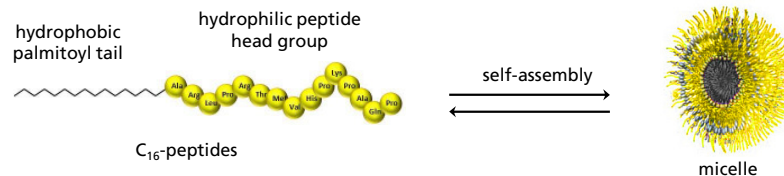


Fig. 2 schematic presentation of the micellar peptide assembly

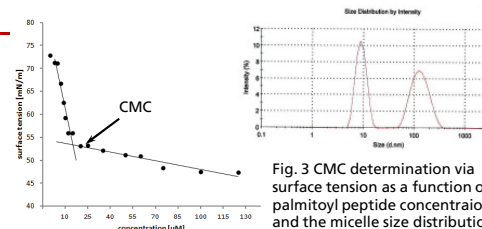


Fig. 3 CMC determination via surface tension as a function of palmitoyl peptide concentration and the micelle size distribution

binding studies by SPR

- immobilisation of the antigen: hemagglutinin protein H5 HA1 domain via amine coupling
- analyte: peptide micelle buffer solution
- 100fold signal amplification in comparison to the single peptide (Fig. 4)
- inhibition test with the single peptide (Fig. 5) → specificity of the palmitoyl-peptide H5 interaction

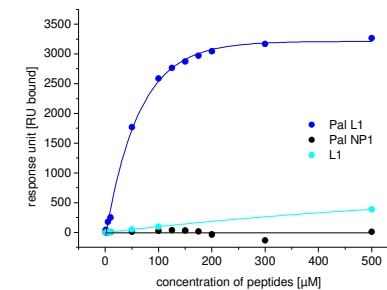


Fig. 4 binding curve of Pal L1 and single L1 and the negative control (Pal NP1) as a function of the peptide concentration

Tab. 1 peptide samples

palmitoyl peptides	sequence
Pal L1	C ₁₆ -ARLPRTMVHPKPAQP
Pal M1	C ₁₆ -ARLPRTMV
Pal S1	C ₁₆ -ARLPR
Pal NP1	C ₁₆ -GSWGEW
non-palmitoyl peptides	sequence
L1 (large)	ARLPRTMVHPKPAQP
M1 (middle)	ARLPRTMV
S1 (short)	ARLPR
NP1 (negative control)	GSWGEW

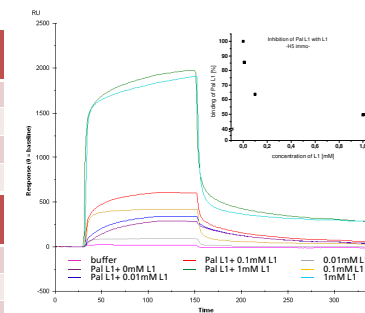
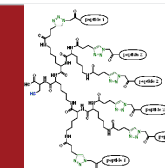


Fig. 5 sensorgram of the inhibition test of Pal L1 with L1, up to 50 % inhibition at 1 mM L1

Outlook

- assembly of a lysine dendron to provide the multivalent architecture
- arrangement of peptides in selected distances by click chemistry
- immobilisation on a SPR chip for kinetic studies



[1] T. Matsubara et al., J Med Chem 53:4441-4449
[2] M. Whitesides et al., Angew Chem 37:2754-2794