Colloids And Surfaces B Biointerfaces Template

Marcia

In the present study a small reduction in charge (10% arginine modification with 1,2-cyclohexanedione (CHD), was hypothesized to result in different interactions with model monolayers composed of PE, phosphatidylethanolamie, 79 mole%:PG, phosphatidlyglycerol, 17 mole%: and CL, cardiolipin, 4 mole%), and model bilayer membranes composed of DPPC, : PE:PG:CL (79:17:4 mole%).

# 1. Introduction

There is a growing research interest into the use of natural cationic antimicrobial peptides (CAPs) including peptides for use in food preservation [1]. Long use of antibiotics has led to resistance in some food pathogens [2]. However, cationic antimicrobial peptides have exhibited broad spectrum inhibitory activity against several foodborne pathogens and there have only been a few reports of developed resistance  [3]. These properties of CAPs have resented an opportunity for considering them as natural food preservatives. In addition, some of these candidate compounds can be extracted cheaply from waste streams ([4]. Clupeine is a CAP that is extracted from the milt (sperm) of commercially caught fish including salmon (salmine) and herring (clupeine).

Previous work has shown native clupeine to be active against a range of pathogenic and spoilage bacteria ([5] [6] [7] but non-specific binding of the peptide to anionic food surfaces limits the availability of the peptide to interact with the anionic surfaces of target bacteria. However, these non-specific interactions can be overcome by using, 1,2-cyclohexanedione (CHD) to modify charged arginine moieties of clupeine (CHD-treated clupeine). Unlike the native peptide, CHD-treated clupeine has shown significant reduction of Gram-negative spoilage bacteria (*Enterobacteriaceae*) in ground beef and milk [8].  This finding was significant since Gram-negative bacteria are surrounded by two lipid bilayers: (1) an inner cytoplasmic membrane, (2) an outer asymmetric membrane, the latter protects the bacteria from harmful compounds in the environment, a property which makes Gram-negative bacteria intrinsically more resistant to most antimicrobial agents (Hancock and Rozek, 2002). Most of the literature that has examined clupeine’s mode of interaction with Gram-negative spoilage organisms has focused on the interactions of the native peptide. Inspite of the improved antimicrobial activity observed for the CHD-treated peptide, the structural details related to the modified peptide’s mode of interaction with Gram-negative organisms is not clearly defined.  Further studies on the mode of interaction of the CHD-treated clupeine on bacterial targets are needed as the cause of the increased antimicrobial effect in not known.

Neutron reflectometry (NR) and X-ray reflectometry (XRR) are complementary biophysical techniques that have been used to investigate peptide-lipid interactions to understand changes  in membrane structures in model biomembranes (Dabkowska et al., 2009; Fernandez et al., 2012;  Abuillan et al., 2013).  At this time, these complementary techniques have not been applied to understand how native and CHD-treated clupeine would interact with mixed lipid mono-and bilayer membranes representing Gram-negative bacteria. In the work presented here, model monolayer membranes were prepared based on the lipid composition present in the inner membrane of the Gram-negative bacteria *Escherichia coli* (*E. coli*). NR and XRR  techniques were used to examine the interactions of native and CHD-treated clupeine (with 10% arginine modification) in PE, (phosphatidlyethanoylamine, 79 mole%):PG, (phosphatidylglycerol, 17 mole%): CL, (cardiolipin 4 mole%) monolayers.  In addition to the monolayer studies, bilayer membranes that more accurately represent the asymmetry of the Gram-negative inner membrane, were constructed using dipalmitoyl-phosphatidyl-choline (DPPC) and PE:PG:CL.  For the bilayer studies, NR was used to characterize the changes in the structure and composition of the bilayer in the presence of the native or CHD-treated clupeine.



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# 2. Materials and Method

# Materials

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# Results andDiscussions

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# Acknowledgements

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# References

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