New Bacterial Biorecognition Elements from Phage Origin

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Bacteria are responsible for numerous infections and diseases with severe implications in animal's and human's health and also causing great economic and production loss in the community. The use and misuse of broad-spectrum antibiotics has created a new problem: antimicrobial resistance which is currently the second leading cause of death worldwide and has exacerbated the number and severity of bacterial infections.

Proteins able to bind problematic bacteria present high potential in the battle against bacterial infections. They enable the development of fast and accurate bacterial detection methods allowing a sooner application of a correct and efficient therapeutic. On the other hand they can be fused to unspecific drugs to target specific bacteria increasing this way antibacterial activity and decreasing the likelihood of antimicrobial resistance.

Bacteriophages (phages) are virus that specifically infect bacteria and are innocuous to eukaryotic cells. Their specificity, which can go up to the strain level, means that they naturally present the necessary proteins/structures to recognize their bacterial hosts. Consequently, phages are a powerful source of bacterial cell binding proteins.

In this work, we have used bioinformatics to identify different proteins from phage origin with potential binding ability to cells of problematic pathogenic bacteria. The genes encoding those proteins were cloned in a frame with a green fluorescent protein (GFP) gene creating fusion proteins that were heterologous expressed in *E. coli*, purified and incubated with the target bacteria to enable decoration of the cells. After washing the unbound fusion proteins, observations at the fluorescence microscope enable to visualize the target cells and assess binding and specificity.

This functional analysis enable to identify proteins able to bind specifically to four problematic bacteria: i) *Paenibacillus larvae*, the responsible for the American foulbrood (AFB) disease in larvae bees that causes enormous economic losses in honey production; ii); *Salmonella*, the main foodborne pathogen worldwide; iii) *Staphylococcus aureus*, a major cause of bacteremia with high morbidity and mortality and responsible for food poisoning, representing an important social and economic burden worldwide and; iv) *Citrobacter koseri*, an opportunistic pathogen in a variety of human infections with serious impact in neonates.

These new bacterial biorecognition elements from phage origin will now be used to design new, fast and accurate diagnostic methods as well to design new tailor-made antimicrobials enabling the efficient control of these problematic pathogenic bacteria.