Effect of single versus antibiotic combinations on Staphylococcus epidermidis biofilm viability and on genetic expression of some virulence genes
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In this study five clinical isolates strains were used, and nine antibiotics at breakpoint concentrations: vancomycin, tetracycline, rifampicin, gentamicin, cefazolin, cephalothin, levofloxacine, daptomycin and clindamycin were tested. 48 hours biofilms were grown on Calgary Biofilm Device (CBD) and challenged overnight with antibiotics alone and in combination. Biofilm cells viability was determined by colony forming units (cfu). Afterwards, the effect of the most active antibiotics combinations against S. epidermidis biofilm on genetic expression of some genes of interest such as: icaA, icaR, sarA and rsbU was determined by real-time PCR.

Although biofilms were generally insensitive to individual antibiotics, they were more susceptible to combinations. Levofloxacine was a constituent of almost all the combinations active against S. epidermidis biofilm pointing to be part of any antibiotic therapy directed against biofilms of these organisms.

Reduction of marine biofouling by complex communities of micro-organisms on organic polymer surfaces
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The oceans play a key role in the regulation of the Earth’s climate. However, much of the oceans' biogeochemical processes remain undersampled, making future predictions on the Earth's climate unreliable. Oceanographic surveys are limited to a relatively small scale due to the high costs of ship based water sampling (~£15k per ship, per day) or the opacity of deep seawater to electromagnetic radiation used for remote sensing. For this reason in situ sensors have been identified as a solution to providing large scale data on biogeochemical processes in the world’s oceans. Sensors that are deployed in the ocean for long periods are prone to biofouling, a process by which microorganisms colonise immersed surfaces, producing a slime or biofilm on the sensor equipment. These biofilms can have a detrimental effect on the functioning of sensors and so need to be limited to ensure accurate, long-term measurements by the sensors.

We are developing methods of biofilm remediation using a combination of biocompatible polymers and controlled release of chemical effectors of cell physiology. One such chemical that has been tested for its efficacy for reducing biofilm formation is nitric oxide, which has been shown to reduce marine biofilm formation by up to 75% on hydrophobic, abiotic surfaces. Further experiments will study the effects of other chemical agents and their effects on biofilm community structure, using DNA based community analysis techniques.

Novel chemical countermeasures against staphylococcal biofilms
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Some natural and synthetic related pyrrolomycins, a family of halogenated pyrrole antibiotics, showed anti-biofilm properties in vitro at low concentration against preformed staphylococcal biofilms. Moreover, considering the human cell toxicity, the selectivity indexes (ratio of cytotoxicity to antibiofilm activity) of some of them was very interesting.

The present study aims to investigate if the pyrrolomycins could also prevent staphylococcal biofilm formation. The evaluation of S.aureus ATCC25923 biofilm formation inhibition was conducted by safranin staining method. At tested concentrations of 0.18, 0.09, 0.045 μg/mL the novel pyrrolomycin derivative IV resulted effective as biofilm inhibitor showing inhibition percentages ranging from 56.5 to 29% against S.aureus ATCC 25923. We are investigating if sortase A which is responsible for the anchoring of surface proteins to Gram positive cell wall, could be the rational target of pyrrolomycins. The surface proteins play pivotal roles in the adhesion to host’s tissues, and the evasion of host-immune responses, moreover they facilitate attachment on biological and abiotic surfaces in the first steps of biofilm formation. It has been observed that inhibition of sortase A by different chemicals resulted in decrease of virulence and staphylococcal biofilm formation.

A molecular modeling study conducted by using a crystal structure of sortase A, recovered from protein data bank, and by studying docking properties of a known sortase A inhibitor and of pyrrolomycins, is in progress. In vitro experiments on sortase inhibition activity are needed to confirm the computational results.