fusion of Zn-Pc-containing liposomes with the cell envelope and studied the effect of photoactivation at 670nm on the viability of sensitised bacteria. Fusion was monitored by quantification of the dye in OM and CM fractions and by determination of mixing of bacterial and liposomal lipid using the self-quenching fluorescent probe octadecyl rhodamine B chloride (R18). Localisation of Zn-Pc within the CM appears to be a prerequisite for efficient killing using low doses of light generated using a diode laser.

**CSC/MI 22 Attachment of Staphylococcus epidermidis RP62A to chemically modified cellulose derivatives**

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5Coagulase negative staphylococci, most notably Staphylococcus epidermidis, have been identified as a predominant cause of cardiovascular implant infection, which begins with the colonization of the device by the bacteria. One possible approach to reduce this event is to understand how the physicochemical properties of bacterial surface influence attachment to biomaterials.

In the present study, the attachment of coagulase negative Staphylococcus epidermidis expressing capsular polysaccharide/adhesin (PS/A), the most common etiological agent of implantable medical devices, was assessed in vitro to cellulose diacetate (CDA), to CDA chemically modified by de-acetylation (CDA-D) and by phosphorylation (CDA-P), as well as to low density Polyethylene (LDPE).

The quantification of S. epidermidis attached to cellulose diacetate (CDA) in phosphate buffer saline (PBS) elicited information regarding the interaction between the bacterial strain and the polymeric biomaterial. There was a significant difference in the adhesion of RP62A to CDA, compared to LDPE. Chemical modifications of CDA by de-acetylation and by phosphorylation were effective in lowering bacterial attachment. These chemical treatments increased the acidic parameter of the surface energy and decreased the acid-base interactions with acidic sites of the capsular PS/A. In other terms, these treatments also promoted a decrease in hydrophobicity that linearly correlates with a decrease in the number of attached cells.

**CSC/MI 23 Biofilm morphogenesis parallel control mechanisms in bacteria and moulds**

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3Cell-cell signalling is increasingly recognised as being critical to morphogenesis in virtually all living systems. N-acyl homoserine lactones have been recognised as general sensors of cell density in Gram-negative bacteria and are implicated in the structural development of bacterial biofilms. Roles for similar lactone-based molecules in the regulation of phenotype in filamentous fungi, whilst long established, have been largely overlooked. We have investigated the possible role of extracellular signal molecules in the morphogenesis and differentiation of a range of filamentous fungi Aspergillus nidulans, Aspergillus niger, Cladosporium cladosporioides and Penicillium chrysogenum. Preliminary data suggested that a water-soluble signal molecule responsible for the induction of conidiation. Each of the organisms was extracted with water and concentrates prepared. These, when placed on developing lawn cultures of the moulds were found to markedly enhance the rate of formation and extent of conidiation, not only in the producer strain but also to a lesser extent in the other fungi. The extracts were fractionated by Gel permeation chromatography and tested for induction potential. Two distinct fractions corresponding to 6500-4500 daltons and 600-250 daltons were detected. The higher molecular weight fractions were protease resistant and heat stable, these fractions were polygalomous in their induction of conidiation in the range of fungi used. The lower molecular weight fractions were protease resistant and heat labile this material was species specific. We suggest that such molecules would diffuse away from a colony formed on an aqueous substrate, yet be concentrated within the more hydrophobic mycelial mat. In such a fashion both the asymmetry and the radial expansion of conidiation in fungal colonies might be explained.

**CSC/MI 24 Effect of environmental conditions on secreted proteins of biofilm-grown Actinobacillus actinomycetemcomitans**

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Little is known concerning the expression of proteins in bacterial biofilms or the effects of environmental variables on such expression. The purpose of this study was to determine the effects of a number of environmental factors on the profile of proteins secreted by Actinobacillus actinomycetemcomitans, an organism which grows as a biofilm on tooth surfaces and which is implicated in the pathogenesis of various forms of periodontitis. Biofilms were grown on agar plates under different conditions (a CO2-enriched aerobic atmosphere, an anaerobic atmosphere, presence of serum or blood, presence of serum, presence of blood) and the secreted proteins extracted and subjected to 2-Dimensional polyacrylamide gel electrophoresis. Differential expression of a number of the secreted proteins was observed under the different growth conditions and some of these were subjected to sequencing by Edman degradation. Homology searches were carried out using the FastA3 algorithm and EMBL database. Three of the proteins (those up-regulated by growth in the presence of blood) were found to have a high degree of sequence homology with proteins produced by the closely-related organism Haemophilus influenzae. These included a triose phosphate isomerase, a thiol peroxidase and a superoxide dismutase. An ability to adapt to prevailing environmental conditions may facilitate the survival of the organism in the changing microenvironment of its habitat and may modulate its pathogenic potential.

**CSC/MI 25 The impact of genetic code ambiguity in the cell wall structure and adhesion of Saccharomyces cerevisiae**

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Genetic code ambiguity in Saccharomyces cerevisiae has a major impact on gene expression, cell size and shape and adaptation to severe stress conditions, namely osmotic, oxidative and drug induced stress. In order to investigate the molecular mechanism of stress resistance and elucidate how genetic code ambiguity alters cell shape and size we carried out a detailed study of the cell wall of S. cerevisiae expressing ambiguity at the leucine-CUG codon. For this, a Candida albicans ser-RNA35 which decodes the leucine CUG codon as serine, was expressed in S. cerevisiae and the cell wall