enzyme activity, oligomerisation state, interaction with other proteins, sub-cellular localization or half-life. Signal transduction through reversible protein phosphorylation is a key regulatory mechanism of both prokaryotes and eukaryotes. Phosphorylation frequently occurs in response to environmental signals and is mediated by specific protein kinases.

Recent studies reported that the eukaryotic-type serine/threonine kinase PkkC from Bacillus subtilis is also involved in bacterial exit from dormancy [1]. Under conditions of nutritional limitation, B. subtilis produces dormant spores, which are resistant to harsh environmental conditions and can survive in a dormant state for years [1].

Generally, growing bacteria release muropeptides in the surrounding environment, due to cell wall peptidoglycan remodelling associated to cell growth and division [1-7]. Therefore, the presence of muropeptides in the close environment of dormant bacteria is a clear signal that conditions are optimal for growth. The process of bacterial cell growth and resuscitation regulation in pathogenic bacteria will be discussed.


Keywords: bacterial, pathogen, protein structure.

MS36.P28

Crystalization of MID962-1200: A trimeric autotransporter from M. catarrhalis

Morphological and pathogenic characteristics of Moraxella catarrhalis are a newly emerging pathogenic bacterium that is involved in otitis media and sinusitis in children as well as lower respiratory tract infections in adults with chronic obstructive pulmonary disease (COPD). Over the last 20 to 30 years, the bacterium has emerged as a genuine pathogen. In immuno compromised hosts, the bacterium can cause a variety of severe infections including pneumonia, endocarditis, septicemia, and meningitis [1]. Today more than 90% of all clinical isolates are β-lactam resistant [2]. One of the most important virulence factors for M. catarrhalis is a 200 kDa outer membrane protein, which is responsible for the IgD binding, namely the Moraxella IgD-binding (MID) protein [3]. MID belongs to the trimeric autotransporter protein family and has N-terminal signal peptide, internal passenger domain and C-terminal translocator domain.

Having an elongated shape the trimeric MID962-1200 shows misleading results in size exclusion chromatography and behaves

Keywords: β-lactamase, carbapenem resistance, X-ray analysis

MS36.P30

Crystalization of MID962-1200: A trimeric autotransporter from M. catarrhalis

Morphological and pathogenic characteristics of Moraxella catarrhalis are a newly emerging pathogenic bacterium that is involved in otitis media and sinusitis in children as well as lower respiratory tract infections in adults with chronic obstructive pulmonary disease (COPD). Over the last 20 to 30 years, the bacterium has emerged as a genuine pathogen. In immuno compromised hosts, the bacterium can cause a variety of severe infections including pneumonia, endocarditis, septicemia, and meningitis [1]. Today more than 90% of all clinical isolates are β-lactam resistant [2]. One of the most important virulence factors for M. catarrhalis is a 200 kDa outer membrane protein, which is responsible for the IgD binding, namely the Moraxella IgD-binding (MID) protein [3]. MID belongs to the trimeric autotransporter protein family and has N-terminal signal peptide, internal passenger domain and C-terminal translocator domain.

Having an elongated shape the trimeric MID962-1200 shows misleading results in size exclusion chromatography and behaves