

Final year projects

Dr SJ Forsythe, Reader in Microbiology. ED179.

Email: Stephen.forsythe@ntu.ac.uk

Homepages: www.theagarplate.com www.food-microbiology.co.uk

Laboratory Practicals:

(1) *Salmonella* recovery media

Salmonella is a major cause of foodborne illness. Since the organism in the food is in a stressed state, the subsequent recovery media must be optimised to enable stressed cells to grow. This project looks at the affect of media age and light exposure on *Salmonella* recovery.

Background to projects 2-5. *Enterobacter sakazakii* is a recently recognised bacterial pathogen that is associated with infant formula meningitis and mortality (~50% rate). The normal route is through contaminated infant formula milk. These series of projects are designed to cover different aspects of the organism, and together would considerably help our understanding of this pathogen.

(2) The presence of *Enterobacter sakazakii* in plant material

(3) Isolation and characterisation of bacteriophages and bacteriocins active against *Enterobacter sakazakii*

(4) Recovery of *Enterobacter sakazakii* during rehydration of infant formula milk.

(5) Capsule and liposaccharide formation in *Enterobacter sakazakii*

Bioinformatics-Genomics Dissertations

(1) DNA Atlases; making sense of bacterial genomes.

These days DNA is sequenced faster than the DNA products can be identified. Therefore techniques for looking at bacterial genomes have been developed to aid the researcher recognise important areas of interest. DNA Atlases are a new means of colour coding bacterial genomes so that the viewer can quickly correlate the DNA sequence of 100s of genes with their probable function. This dissertation will discuss their value as a teaching tool.

(2) Comparative genomic analysis of *Campylobacter jejuni* and *Helicobacter pylori*.

The genome of many bacteria has now been sequenced and can be accessed over the internet. The dissertation will compare the genome of two related organisms to better understand their host range and virulence factors.

(3) Comparative genomic analysis of *Escherichia coli* K12 and *Escherichia coli* O157:H7.

The genome of many bacteria has now been sequenced and can be accessed over the internet. The dissertation will compare the genome of a non-pathogenic strains of *E. coli* with the the enterohaemorrhagic strain *E. coli* O157:H7 in order to recognise important virulence factors.

(4) Comparative genomic analysis of *Bacillus cereus* and *Bacillus anthracis*

The genome of many bacteria has now been sequenced and can be accessed over the internet. The dissertation will compare the genome of a non-pathogenic strains of *Bacillus cereus* with the bioterrorism species *Bacillus anthracis* in order to recognise important virulence factors.