

Project proposal

Project title	Mechanisms of sequence inversions in the Neisseria	
First Supervisor	Dr <input type="text" value="v"/>	Lori Snyder
Second Supervisor	tbc	
School	Life Sciences <input type="text" value="v"/>	
Other member of supervisory team (no more than three KU supervisors in total)	<input type="text"/>	
Specific requirements beyond 2:1 degree	<input type="text"/>	

Project summary (max 4,000 characters)

MSc by Research

This M.Sc. project will expand upon previous investigations into sequence inversions in the Neisseria spp, to include Neisseria meningitidis, Neisseria gonorrhoeae, and commensal species such as Neisseria lactamica. Inversions of large sections of the genomes have been observed when comparing different strains of the same bacterial species. Smaller inversions have also been observed. The mechanisms of sequence inversion in the Neisseria spp. have not previously been extensively investigated.

Building on previous work, the student will research the sequences involved in large and small scale inversions in the Neisseria spp., drawing on previous work in my laboratory on N. gonorrhoeae. Investigation of genome sequence read level data will be conducted to identify inversions that have happened during laboratory culturing, to determine whether inversion is occurring currently or whether inversions are rare evolutionary events. Those that are occurring currently will be investigated in light of their potential to represent a novel mechanism of gene regulation. Potential proteins involved in the process of generating the inversions will be explored using knock-out and over-expression mutants of the relevant genes.

A passionate interest in microbiology, genomics, and molecular genetics is required. Student will be expected to produce written pieces of work of publication quality.

Relevant references:

Sequence features contributing to chromosomal rearrangements in Neisseria gonorrhoeae. R Spencer-Smith, EM Varkey, MD Fielder & LAS Snyder – in press for PLoS ONE.

Comparative analysis of two Neisseria gonorrhoeae genome sequences reveals evidence of mobilization of Correa Repeat Enclosed Elements and their role in regulation. LAS Snyder, JACole & MJPallen. BMC Genomics 10: article 70, (2009).

Comparative overview of the genomic and genetic differences between the pathogenic Neisseria strains and species. LAS Snyder, JK Davies CS Ryan & NJ Saunders. Plasmid 54: 191-219, (2005).