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| Project Reference | T3/73 |
| Project Title | **Implementation of long-read technologies to detect genetic determinants of phenotypic variation in disease and carriage isolate of a bacterial pathogen** |
| Theme(s) | Theme 3: Genetically informed causal inference and risk prediction |
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| Department | Genetics and Genome Biology |
| Project Summary | *Neisseria meningitidis* is the major cause of bacterial meningitis but is also widespread as an asymptomatic coloniser of human oropharyngeal tissues. Invasive meningococcal disease is caused by both hypervirulent and endemic strains that encompass genetically-distinct lineages. Critically, meningococci are highly adaptable with multiple mechanisms for generating genomic variation in DNA sequences encoding key meningococcal virulence traits. This project aims to improve our understanding of the genomic basis for meningococcal virulence by utilising novel combinatorial sequencing technologies (e.g. Illumina and Oxford Nanopore) to analyse the bacterial genomes. This genomic information will be utilised in genomewide association studies with pre-existing phenotypic data to link specific bacterial sequences to variation in virulence-related traits. A major potential outcome of the project will be an ability to predict invasive disease potential during routine surveillance of meningococcal disease cases. |