ACRONYM: **Restrict-Pneumo-AMR**

Title: **Prevention and Restriction of Antimicrobial Resistance in Pneumococci by Multi-Level Modelling**

Keywords: pneumococci, clinical cohorts, functional genetics, environmental drivers, fitness of traits, multi-level modelling

Consortium composition:

Type	Name	Institute	Country
C	Bentley, Stephen	Wellcome Trust Sanger Institute / Wellcome Trust Genome Campus, Hinxton	United Kingdom
P	Fittipaldi, Nahuel	University of Toronto / Public Health Ontario Laboratories	Canada
P	Kellner, James	University of Calgary / Dept. Of Pediatrics & Alberta Health Services / Calgary Zone	Canada
P	Schmeck, Bernd	Philipps-University Marburg / Institute for Lung Research	Germany
P	Turner, Paul	University of Oxford / Centre for Tropical Medicine and Global Health, Nuffield Dept. of Medicine	United Kingdom
P	van der Poll, Tom	University of Amsterdam / Academic Medical Center, Center of Experimental & Molecular Medicine	Netherlands

Abstract:

Streptococcus pneumoniae is a major health threat in industrialized and developing countries. The pathogen affects both young and old people, immune-competent as well as immunocompromised individuals. By genetic recombination within diverse populations, individual strains are not only able to evade vaccination but also able to acquire antimicrobial resistance (AMR), which can then be transmitted onwards.

This proposal aims to understand the mechanisms and distribution of this pneumococcal AMR repertoire at the genetic, bacterial, host and population levels to layout new strategies for risk assessment, prevention and reduction of AMR. In particular, the environmental, immunological and pharmacological drivers of resistance emergence and selection, the genetic population dynamics, as well as the fitness of the new traits in different host conditions will be analysed and modelled.

To this end, a multinational consortium of researchers with complementary expertise has been formed. Available to the consortium are clinically important and newly emerged pneumococcal AMR strains, together with related patient metadata (clinical, genetic and transcriptomic) from clinical cohorts as well as highly detailed carriage sampling from a Thai cohort. Consortium members have proven expertise in microbiology, bacterial genetics, bioinformatics, in vivo/in vitro models while others are clinicians expert in the treatment of pneumococcal infections in both paediatric and adult patients.

In a concerted effort, this consortium will develop countermeasures against antimicrobial resistance in a major health threat by multi-level modelling of its resistance emergence, selection, and transmission in diverse environments.