Pacific Islands Rheumatic Heart Disease Genetics Network

COLLABORATING INSTITUTIONS

University of Oxford, Oxford, UK
Institut National de la Santé et de la Recherche Médicale, Paris, France
University of Melbourne, Melbourne, Australia
Ministry of Health, Suva, Fiji Islands
Colonial War Memorial Hospital, Suva, Fiji
Paris Centre de recherché Cardiovasculaire, Paris France
Centre Hospitalier Territorial Gaston-Bourett, Nouméa, Nouvelle-Calédonie
Institut Pasteur de Nouvelle-Calédonie, Nouméa, New Caledonia

MISSION STATEMENT

The group A streptococcus is a bacterium that causes a diverse range of human diseases all of which occur at higher rates amongst Pacific Islanders than anywhere else in the world. The most significant of these, rheumatic heart disease (RHD), results from an excessive response to group A streptococcus leading to damage to heart valves causing heart failure and an increased risk of stroke. Only a fraction of individuals infected by the causative bacteria go on to develop RHD. While factors such as living conditions are important, looking for discrepancies in the human genome could help to explain this inter-individual variability in susceptibility. Human genetics is a field of research that strives to detect these differences aiming to provide valuable insights into the mechanisms by which disease develops. Such insight is desperately needed for RHD as our current lack of understanding limits design of diagnostic tests, vaccines and treatment.

The **Pacific Islands Rheumatic Heart Disease Genetics Network** aims to establish a network of clinicians and scientists at institutions across Pacific Island Nations working alongside investigators from the UK, France and Australia with the aim of using human genetics research to investigate susceptibility to RHD. In the initial phase beginning the network aims to recruit, gather information from and obtain a blood sample from 1200 patients and 1200 volunteers from Fiji, and 1000 patients and 1000 volunteers from New Caledonia. From each individual we will prepare the blood sample for analysis by extracting DNA and will use technologies that read sequence variation in the genome. Any discrepancies that we detect between patients and volunteers can implicate particular genes in the development of disease, which will inform our understanding of the mechanisms by which disease develops.