

Title of PhD project / theme	The malaria parasites of Bornean primates; prevalence, evolution, phylogenetic relationships & host specificity investigated through whole genome sequencing.
Supervisory team	<ol style="list-style-type: none"> 1. Richard Culleton – Nagasaki University 2. Chris Drakeley– LSHTM 3. Kamruddin Ahmed – Universiti Malaysia Sabah
Brief description of project / theme	<p>The island of Borneo is home to four major primate groups; gibbons, orang-utans, macaques and humans, each with their own malaria parasite species. The relationship between these parasites, their phylogenies and evolutionary history, and their capacity to jump from host species to host species are little understood. This is because previous studies have worked with limited samples, and have used only small fragments of DNA in molecular studies.</p> <p>Given the remarkable advances in the field of whole genome sequencing from limited amounts of DNA that has taken place in the last five years, it is now time to revisit the phylogenetics of the malaria parasites of primates in Borneo.</p> <p>Previous studies have shown that the gibbons of Borneo are infected with three malaria parasite species, <i>Plasmodium hylobati</i>, <i>P. eylesi</i> and <i>P. youngi</i>, although the phylogenetic relationship of these parasites with other primate malaria parasites remains unresolved. Similarly, orang-utans appear to be host to at least two distinct species, <i>P. pitheci</i> and <i>P. sylvaticum</i>.</p> <p>There is now the need to revisit the molecular phylogenetics of Bornean primate malaria parasites using cutting edge whole genome sequencing analyses for the following reasons:</p> <ol style="list-style-type: none"> <i>i) To resolve the evolutionary histories and phylogenetics of the primate malaria parasites of gibbons, orangutans, monkeys and humans in Borneo</i> <i>ii) To assess the capacity of the parasites to switch between host species</i> <i>iii) To assess the potential of any of these parasites to cause zoonotic disease in humans</i> <i>iv) To investigate how malaria parasites adapt to hosts at the genetic level</i> <p>The primate malaria parasites of Borneo offer a unique opportunity to study host-parasite interactions in multiple groups of primates.</p>

	Extensive sampling will be undertaken through invasive and non-invasive means, parasite DNA extracted, subjected to whole genome sequencing and analysed using the appropriate bioinformatics tools to answer the above questions.
The role of LSHTM and NU in this collaborative project	The LSHTM and NU teams have extensive experience of working with zoonotic malaria in Malaysian Borneo. LSHTM will provide supervisory support on epidemiology, vector biology, and primatology. The NU team will supervise the genomic analysis of samples, and the downstream phylogenetic and genetic analyses.
Particular <i>prior</i> educational requirements for a student undertaking this project	Prior experience of parasite genetics would be beneficial. Some background in bioinformatics would also be preferable. A significant portion of this project will involve field work in Malaysian Borneo, and applicants should be prepared for this.
Skills we expect a student to develop/acquire whilst pursuing this project	Genetics, genomics, bioinformatics and molecular biology techniques, primatology.