

Title of PhD project / theme	Understanding how <i>Aedes aegypti</i> and <i>Ae. albopictus</i> mosquitoes have spread across Asia and its consequences for arboviral disease.
Supervisory team	LSHTM: Oliver Brady (lead) NU: Prof. Minakawa (Dr. Sunahara) of the Dept. of Vector Ecology, NEKKEN
Brief description of project / theme	<p>The mosquito species <i>Aedes aegypti</i> and <i>Ae. albopictus</i> are the primary vector species for dengue, Zika, chikungunya and Yellow fever viruses. Their recent rapid global spread outside their native ranges in Africa (<i>Ae. aegypti</i>) and North-East Asia (<i>Ae. albopictus</i>) has been a key driving factor behind the emergence of arboviral diseases as global health problems. Understanding the role environmental changes and increases in trade and travel have played in the expansion of these species is important for targeting vector control efforts to prevent further spread, assess the potential impact of climate change and design mosquito control strategies that are robust to re-importation (1).</p> <p>Key hypotheses of the project include:</p> <ol style="list-style-type: none"> 1. What is the contribution of urbanisation, increases in trade and travel and climate change to spread of <i>Ae. aegypti</i> and <i>Ae. albopictus</i> across Asia? 2. How do patterns of spread in Asia differ between the native <i>Ae. albopictus</i> and newly introduced <i>Ae. aegypti</i> and how are they related to traits of each species (e.g. Cold weather tolerance)? 3. Which area will be most at risk of invasion in the future due to these changing environmental factors? 4. To what extent are current mosquito population genetics shaped by human trade and travel networks? <p>Available datasets:</p> <p>At the continental scale the <i>Aedes</i> mosquito occurrence database (2) is a global database of locations where each species has been reported since 1960 and now consists of over 40,000 records. Data on projected changes in climate, urbanisation and travel have also been recently compiled for a related project on future projection of dengue (3). To investigate mosquito genetic variation, the student will use publicly available genetic data already collated by the VectorBase platform (www.vectorbase.org).</p>

	<p>Key methods to be used:</p> <p>The project will make extensive use of global spatial mapping and modelling techniques within Geographic Information Systems (3) to understand the role of current and future environmental drivers of spread. The project will also involve leading and applying knowledge about entomology, epidemiology and disease surveillance in addition to leaning advanced computer coding skills and working with BigData.</p> <p>Relevant references:</p> <p>(1) Brady, OJ, Hay, SI, The Global Expansion of Dengue: How <i>Aedes aegypti</i> Mosquitoes Enabled the First Pandemic Arbovirus. Ann. Rev. Entomol. 2019. doi.org/10.1146/annurev-ento-011019-024918</p> <p>(2) Kraemer MUG, Sinka ME, Duda KA, Mylne A, Shearer FM, Brady OJ, et al. The global compendium of <i>Aedes aegypti</i> and <i>Ae. albopictus</i> occurrence. Sci Data. 2015;2:150035.</p> <p>(3) Messina JP, Brady O., Golding N, Kraemer MUG, Wint GRW, Ray SE, et al. The current and future global distribution and population at risk of dengue. Nat Microbiol. 2019; 4:1508–1515</p>
<p>The role of LSHTM and NU in this collaborative project</p>	<p>The proposed project combines two highly complementary skillsets with the spatial modelling skills of Dr. Brady (LSHTM) and entomological expertise from one of the many entomological professors working at NU. This collaboration has the potential to build the arboviral research capacities of both institutions in Asia, a region where arboviruses are increasingly becoming the most important infectious disease threats. It is anticipated that the student will be based at LSHTM and spend extended placements at NU and at NU field sites to maximise the opportunities afforded by each institute.</p>
<p>Particular <i>prior</i> educational requirements for a student undertaking this project</p>	<p>The student will require an MSc in epidemiology, Data science or medical statistics. Prior experience with regression modelling, genetic data analysis and entomology is preferred. Technical expertise with at least one computer coding language (ideally R) is also highly desirable.</p>
<p>Skills we expect a student to develop/acquire whilst pursuing this project</p>	<p>Over the course of the project the student is expected to develop advanced skills in mapping/GIS, spatial modelling, Bayesian statistics, machine learning, working with big datasets and entomological expertise.</p>