Spatiotemporal Genomics in Anopheles mosquitoes
Caroline Colijn, Dominic Kwiatkowski, and Mara Lawniczak

Over the next five years, will generate whole genome sequence data on 50,000 mosquitoes from the species that account for most malaria transmission in Africa. These specimens will be collected in systematic spatiotemporal sampling frameworks to study evolutionary responses to malaria control. Additionally, for some sites and species (subject to museum collections) we will sequence genomes from historic specimens collected over the past century to understand longer term evolutionary changes, including when the first molecular signatures of insecticide resistance arose in different locations and longer term evaluation of population structure stability. We are looking for a postdoc interested in examining demographic and evolutionary patterns across the entire genome, although insecticide resistance will be a major focus of our analysis both for its practical importance and because it provides a remarkable opportunity to study the evolution of an animal species under intense selective pressure and in near real time. A suite of new vector control tools will be deployed over the next decade including next generation bednets, novel insecticide formulations for indoor residual spraying, attractive toxic sugar baits to combat outdoor-biting mosquitoes, and possibly field testing of gene drive. We seek a postdoc interested in developing mathematical and statistical approaches to detect early warning signs of emerging resistance. Advances we make in this area will allow vector control programmes to take action, e.g. by rotating to a different insecticide formulation, while allowing us to gain unprecedented insights into the evolutionary process.

Furthermore, the spatial and temporal dimensions of this dataset will make it particularly valuable for analysis of vector population size, dispersal and long-range migration, which are of central importance for planning gene drive strategies and for monitoring vector control interventions in general. Depending on interests, the successful applicant can also lead or contribute to efforts to use haplotype sharing methods to estimate recent migration and population size (Al-Asadi *et al.,* 2019) and to construct genome wide genealogies to estimate longer term fluctuations in population size, population structure and rates of gene flow between species (Speidel *et al.,* 2019, Kelleher *et al.,* 2019). We are also keen to develop new tree based methods for identifying non neutral processes and this might also be an area a successful applicant is interested in pursuing. There is growing recognition that the process of speciation is far more reticulate than previously thought, i.e. the Tree of Life has many intertwining branches. These longitudinal *Anopheles* data will be an excellent system to investigate the evolutionary process because of the porous species boundaries and the extremely strong selective pressure that is exerted by insecticides on the whole genus.