



Mardi 29 avril 2025, 11:00

Grande salle + visio.

**(PAN-)GENOMIC VARIATION IN THE *ANOPHELES GAMBIAE*
MOSQUITO SPECIES COMPLEX, AND GENOMIC INSIGHTS
INTO THE EVOLUTION OF EXTREME SPECIALISATION IN ONE
OF ITS MEMBER, *AN. BWAMBAE*.**

par

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👤 Structural variations (SVs) play pivotal roles genome architecture, potentially involved in adaptation and speciation, yet they are often overlooked. In the first part of this seminar, I will delve into the genomic landscape of SVs within *Anopheles gambiae* and *Anopheles coluzzii*, principal African malaria vectors. We used a "map-then-assemble" pangenomic strategy with short-read sequencing data, validated with samples for which short- and long-read data were available. Then we assessed pangenomic diversity and divergence in the two sister species by screening 200 samples across Africa from the *An. gambiae* 1000 genome project consortium. The use of five distinct reference genomes in the literature revealed significant disparities in read mapping efficiency, highlighting the importance of a pangenomic approach in this system. We will dig deeper into the contrasted pan-genomic dynamics between the two species, examining their genomic landscape, composition, and ancestry. We will also explore the significance of these SVs for local adaptation and speciation.

👤 In the second part of this seminar, I will focus on the evolution of extreme specialisation in another member of *Anopheles gambiae* complex (AGC), *An. bwambae*. Aside from *An. gambiae* and *An. coluzzii*, little is known about minor vectors like *An. bwambae*. This species is highly specialized to the thermal springs in Bwambae County (Uganda), in close vicinity with other major vectors (e.g., *An. gambiae* and *An. arabiensis*). Previously reported mtDNA introgression between them raised questions about how this species remain adapted despite the homogenising effects of gene flow. Here we investigated the genomic diversity and evolutionary history of *An. bwambae*, together with its extreme adaptations to thermal springs. We first de novo assembled the reference genome for this species and compared it to those from other species of the AGC. Then, using whole genome sequencing, bioinformatics, population genomics, and phylogenomics approaches, we investigated the genetic diversity, evolutionary history, and adaptation of *An. bwambae* (n=42) compared to *An. gambiae* (n=25). Analyses of 13.5 million SNPs across the genomes of the two species revealed major genomic heterogeneity including a new inversion system on the X chromosome of *An. bwambae*. Genetic structure confirmed that the two species are well distinct, with no evidence of recent gene flow. Nevertheless, historical introgression was detected not only with *An. gambiae*, but also with other species of the AGC. In contrast to *An. gambiae*, *An. bwambae* displayed low diversity, strong inbreeding, and autozygosity, indicative of a very small population. Meanwhile, while genome scans revealed strong positive selection signals on known insecticide resistance loci in *An. gambiae*, none was identified in *An. bwambae*. Genome scans revealed a few genomic regions potentially undergoing introgression, while the majority did not. How *An. bwambae* persisted and adapted despite its small population size and strong inbreeding remains a paradox warranting further investigation.