Anopheles sampling collections in the health districts of Korhogo (Côte d'Ivoire) and Diébougou (Burkina Faso) between 2016 and 2018

PAUL TACONET (MIVEGEC, UNIVERSITÉ DE MONTPELLIER, CNRS, IRD, MONTPELLIER, FRANCE), PAUL.TACONET@IRD.FR, ORCID = 0000-0001-7429-7204 (CORRESPONDING AUTHOR)

BARNABAS ZOGO (INSTITUT PIERRE RICHET, BOUAKÉ, CÔTE D'IVOIRE), BARNABASZOGO@GMAIL.COM

DIEUDONNÉ DILOMA SOMA (INSTITUT DE RECHERCHE EN SCIENCES DE LA SANTÉ, BOBO-DIOULASSO, BURKINA FASO), DIEUSOMA@YAHOO.FR, ORCID = 0000-0001-8294-9110

LUDOVIC P AHOUA ALOU (INSTITUT PIERRE RICHET, BOUAKÉ, CÔTE D'IVOIRE), LUDOVICALOU@GMAIL.COM, ORCID = 0000-0003-1444-297X

KARINE MOULINE (MIVEGEC, UNIVERSITÉ DE MONTPELLIER, CNRS, IRD, MONTPELLIER,FRANCE), KARINE.MOULINE@IRD.FR, ORCID = 0000-0001-9523-2506

ROCH KOUNBOBR DABIRÉ (INSTITUT DE RECHERCHE EN SCIENCES DE LA SANTÉ, BOBO-DIOULASSO, BURKINA FASO), DABIREROCH@GMAIL.COM, ORCID = 0000-0002-3471-3506

ALPHONSINE AMANAN KOFFI (INSTITUT PIERRE RICHET, BOUAKÉ, CÔTE D'IVOIRE), KOFFI_ALPHONSINE@YAHOO.FR

CÉDRIC PENNETIER (MIVEGEC, UNIVERSITÉ DE MONTPELLIER, CNRS, IRD, MONTPELLIER, FRANCE ; INSTITUT DE RECHERCHE EN SCIENCES DE LA SANTÉ (IRSS), BOBO-DIOULASSO, BURKINA FASO), CEDRIC.PENNETIER@IRD.FR, ORCID = 0000-0002-3362-6371

NICOLAS MOIROUX (MIVEGEC, UNIVERSITÉ DE MONTPELLIER, CNRS, IRD, MONTPELLIER, FRANCE), NICOLAS.MOIROUX@IRD.FR, ORCID = 0000-0001-6755-6167

Abstract

Characterizing the entomological profile of malaria transmission at fine spatiotemporal scales is essential for developing and implementing effective vector control strategies. Here, we present a fine-grained dataset of Anopheles (Diptera: Culicidae) mosquitoes resulting from a series of collections in 55 villages of the rural districts of Korhogo (Northern Côte d'Ivoire) and Diébougou (South-West Burkina Faso) between 2016 and 2018. In the framework of a randomized controlled trial, Anopheles mosquitoes have been periodically collected by Human Landing Catch inside and outside households, and analyzed individually to identify genus and - for a subsample - species, insecticide resistance genetic mutations, plasmodium falciparum infection using molecular tools, and parity status. Overall, more than 3000 human-nights of collection were performed, representing a total sampling effort of approximately 45000 hours. More than 60000 anopheles were collected (mainly *An. gambiae s.s.*, *An. coluzzii*, and *An. funestus*). The data are published as a Darwin Core archive in the Global Biodiversity Information Facility - France, comprising 4 files (events, occurrences, mosquito characterizations, and environmental data).

Research area

Ecology

Classifications

Biodiversity, Taxonomy

Data Description

Background and context

Malaria is a major vector-borne disease, still affecting more than 200 million people and causing more than 500,000 deaths worldwide annually (WHO 2022). Malaria parasites are transmitted to humans by infected female mosquitoes of the genus *Anopheles*. Although malaria control efforts have led to a sustained decrease of the disease burden between 2000 and 2015 (mainly through the widespread use of long-lasting insecticidal nets (LLIN) (Bhatt et al. 2015)), progress is now stalling (WHO 2022). Vector resistance to insecticides, population growth and environmental changes are involved in such worrying trends. To reinvigorate progress, locally tailored vector control (VC) strategies, built on a thorough knowledge of the local determinants of malaria transmission, are needed (WHO 2017; Wilson et al. 2020). To do so, it is of particular importance to characterize entomological profile of malaria transmission at fine and operational spatiotemporal scales (Wilson et al. 2020; WHO 2017 ; Ferguson et al. 2010).

In this paper, we present a dataset resulting from a set a mosquito collections carried-out in the frame of a randomized controlled trial (RCT) as part of a project called REACT (*Insecticide resistance management in Burkina Faso and Côte d'Ivoire: research on vector control strategies*). Involving three scientific partners - the Institut de Recherche pour le Développement (IRD, France), the Institut de Recherche en Science de la Santé (IRSS, Burkina Faso), and the Institut Pierre Richet (IPR, Côte d'Ivoire), the REACT project aimed to assess whether addition of complementary VC strategies to LLINs reduces malaria transmission and provides additional protection against malaria, in areas with high proportion of insecticide resistant vectors in rural Burkina Faso (BF) and Côte d'Ivoire (CI). In this frame, periodical entomological surveys aiming at characterizing the anopheles populations were carried out between 2016 and 2018. Data on anopheles species composition, abundance, biting behaviour, insecticide resistance genetic mutations, and infection by malaria parasites were collected. This paper aims to detail these data along with the necessary contextual information to use them properly.

Methods

Study areas, temporal coverage, sampling frequency

The study areas of the REACT project are the rural health districts of Korhogo (Côte d'Ivoire) and Diébougou (Burkina Faso). Each study area covers about 2500 squared km. Both countries are endemic for *Plasmodium falciparum* malaria (WHO 2022). The main Anopheles species in these countries are *An. arabiensis*, *An. gambiae s.s.* and *An. coluzzii* which belong to the *Anopheles gambiae* complex, and *An. funestus* which is a member of the *Funestus* group (Sinka et al. 2010, 2012; Wiebe et al. 2017). In both countries, resistance of Anopheles to insecticides has been reported for several decades (Moyes et al. 2020; Sherrard-Smith et al. 2019).

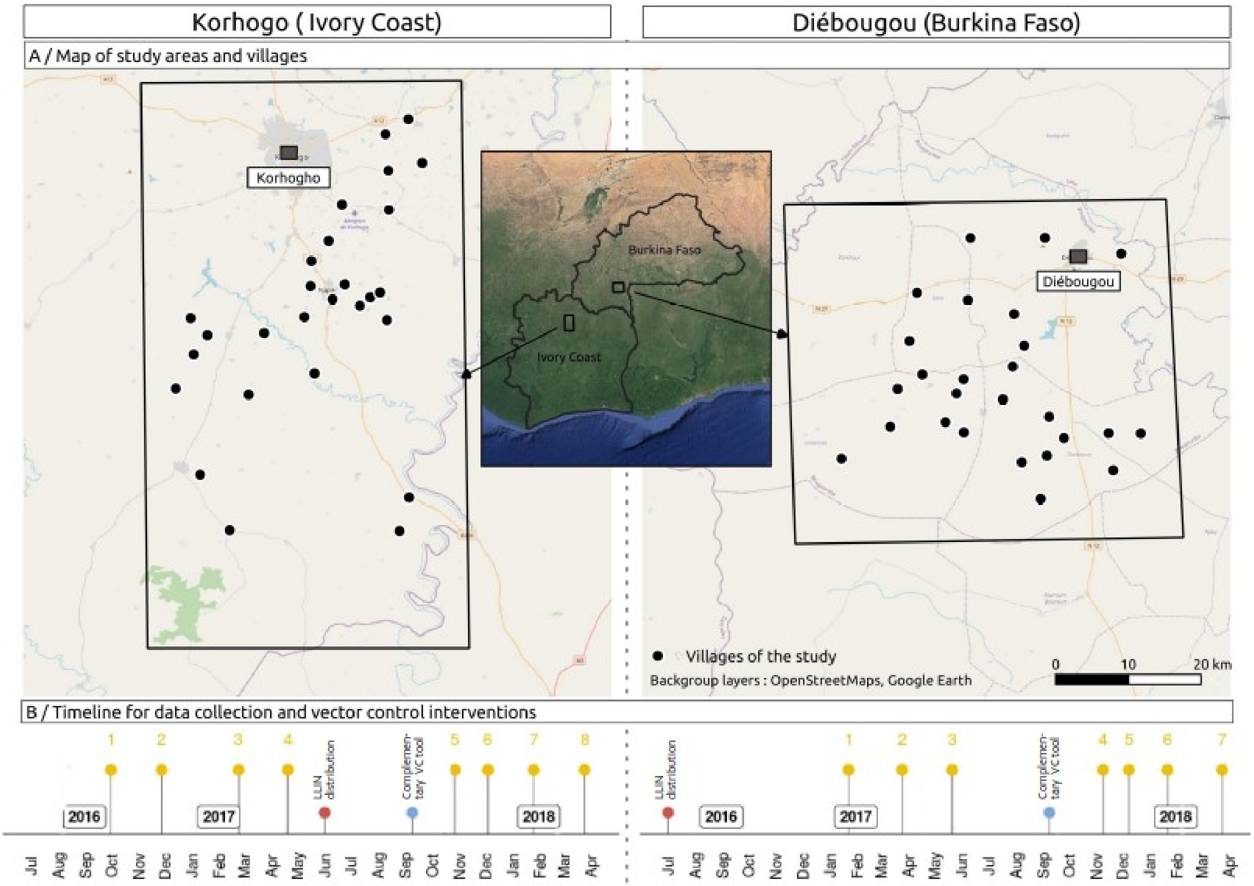
The Diébougou area is located in the southwest of Burkina Faso, in the Sudanian bioclimatic region (CILSS 2016). The climate is characterized by a dry season from October to April (including a 'hot' period from October to November and a 'cold' period from December to February) and a rainy season from May to September. The daily temperatures range from 18-36°C, 25-39°C and 23-33°C in the cold dry, hot dry and rainy seasons respectively. The average annual rainfall is 1200 mm. The natural vegetation is dominated by savannah trees interspersed with riparian forests. The main economic activity is agriculture (cereal cultivation) followed by artisanal gold mining and charcoal and wood production (INSD 2015, 2017). The main vector control tool in the Diébougou region is the LLIN, distributed universally by the government every 3-4 years since 2010 (PNLP 2014a). The last distribution before the REACT project was in July 2016.

The Korhogo area is located in the north of Côte d'Ivoire, which is also in a Sudanian bioclimatic region (CILSS 2016). The seasonality of the climatology is relatively similar to that of Diébougou. Annual rainfall varies from 1200 to 1400 mm, while the average annual temperature varies from 21°C to 35°C. The natural vegetation is mainly a mixture of savannah and open forest. The region has a high density of hydraulic dams that allow for year-round agriculture. As for the Diébougou region, the main economic activity is agriculture (rice, maï s, cotton). Similarly, the main vector control tool is again the LLIN, distributed universally by the government, as in Burkina Faso, every 3-4 years since 2010 (PNLP 2014b). The last distribution before the REACT project was in 2014. In the frame of the project, LLINs were distributed in the study villages in June 2017.

As mentioned previously, the REACT project consisted in a randomized control trial. Within each area, several villages (27 in the Burkina Faso area, 28 in the Côte d'Ivoire area) were selected at the beginning of the project according to the following criteria :

accessibility during the rainy season, 200 to 500 inhabitants per village, and distance between villages greater than 2 km. In each village, several rounds of mosquito collections (surveys) were carried out using the Human Landing Catch (HLC) sampling method. In the BF area, seven entomological surveys were conducted during 15 months between January 2017 and April 2018. In the CI area, eight entomological surveys were conducted during 18 months between October 2016 and April 2018. As part of the RCT, vector control tools complementary to the LLINs were deployed in selected, randomized, villages in September 2017. The dates of the entomological surveys were chosen to be able to compare the entomological indicators before and after the intervention as part of the RCT, and to span the typical climatic conditions of these tropical areas.

Figure 1 shows the geographic location of the villages, the dates of mosquito samplings, and key dates for VC interventions in the study areas.



Map of the study areas and villages with timeline of mosquito samplings and VC interventions. In the timeline, the entomological surveys are numbered.

Sampling methods

The procedure for conducting HLC was for a person to sit on a stool, and mosquitoes to alight on his exposed legs where they were then collected using a hemolysis tube. Mosquitoes were collected from 17:00 to 09:00 both indoors and outdoors at 4 sites per village. Collectors were organized into two teams of eight persons in each village; the first group collected from 17:00 to 01:00 and the second from 01:00 to 09:00. Collectors were rotated between indoor and outdoor collection sites every hour at each selected house (sites) to reduce potential collector bias. Indoor collection points were rooms that meet the following criteria: being usually inhabited; quiet without excessive movement of peoples; open to the outside through a door or a window. Outdoor collection was conducted in areas usually occupied by people but are sheltered from wind, traffic, fires and are not large meeting areas. The distance between collection sites was at least 50 m. The distance between indoors and outdoors collection points in one site was at least 10 m to minimize competition between mosquito collectors. Mosquitoes collected in individual hemolysis tubes plugged with cotton were stored in hourly bags.

Morphological identification

All captured mosquitoes were morphologically identified in the field to genus and where possible to species levels according to established taxonomic keys (Gillies and B. De Meillon 1968; Gillies and Coetzee 1987).

Molecular analyses

In the BF area, for all the entomological surveys :

- a subsample of 100 non blood-fed *Anopheles spp.* individuals was randomly selected per survey and per village and dissected to identify their parity state (parous or nulliparous) (Detinova, Bertram, and Organization 1962) (parous female are those that have laid eggs at least once);
- all individuals belonging to the *Funestus* group or *Anopheles gambiae* complex were identified to species by PCR;
- DNA extracted from head-thorax of *Anopheles spp.* individuals was used to detect *Plasmodium falciparum* infection using quantitative polymerase chain reaction (qPCR) assay;
- PCR assay were carried out on all mosquitoes belonging to the *An. gambiae* complex to detect the L1014F (*kdr-w*), G119S (*ace-1*), and L1014S (*kdr-e*) mutations (*kdr-w* and *kdr-e* mutations confer insecticide resistance to pyrethroids whereas *ace-1* confers resistance to carbamates and organophosphates).

In the CI area, for the first four entomological surveys : due to the very large numbers of vectors collected, a subsample of *Anopheles spp.* vectors from six villages randomly chosen out of the 28 villages included in the study were further analyzed :

- For all the individuals belonging to the *Anopheles nili* complex or *An. funestus* group collected in these six villages : *Plasmodium falciparum* infection was detected using quantitative polymerase chain reaction (qPCR);
- For one individual of *Anopheles gambiae* complex randomly selected per hour per collection site (indoor/outdoor) during each survey in these six villages : identification of species (PCR), *Plasmodium falciparum* infection (qPCR), L1014F (*kdr-w*) and G119S (*ace-1*) mutations (qPCR).

In the CI area, for the last four entomological surveys :

- For all the individuals belonging to the *Anopheles nili* complex or *An. funestus* group : identification of *Plasmodium falciparum* infection (qPCR);
- For a subsample representing 25% of the total of the *Anopheles gambiae* captured : identification of species (PCR), *Plasmodium falciparum* infection (qPCR), L1014F (*kdr-w*) and G119S (*ace-1*) mutations (qPCR).

References to the methods used for molecular analyses are detailed in Table 1.

Table 1 : Morphological and molecular analyses performed, with references of the methods used.

	Korhogo area (CI)	Diébougou area (BF)
PCR identification of *An. gambiae s.l.* species	Scott, Brogdon, and Collins (1993); Favia et al. (2001)	Santolamazza et al. (2008)
PCR identification of *An. funestus* species	*not performed*	Koekemoer et al. (2002); Cohuet et al. (2002)
(q)PCR *kdr-w*	Bass et al. (2007)	Martinez-Torres et al. (1998)
PCR *kdr-e*	*not performed*	Ranson et al. (2000)
qPCR *ace-1*	Essandoh, Yawson, and Weetman (2013)	Essandoh, Yawson, and Weetman (2013)
qPCR *Plasmodium falciparum*	Boissière et al. (2013)	Boissière et al. (2013)

In addition to the entomological data, a set of environmental data were extracted at the places and times of samplings from Earth-observation satellite products (Wan, Hook, and Hulley 2015a, 2015b; Center 2019). The following information were extracted : % of landscape occupied by each land cover type in a 2-km radius buffer zone around the sampling site, weekly rainfall and weekly land surface temperature in a 2-km radius buffer zone around the sampling site and up to 6 weeks before each sampling event. The methods used to generate this data are detailed in Taconet et al. (2021).

Results

Although not the primary aim of this paper, we provide some key information extracted from the data in Table 2, including some aggregated entomological parameters of malaria transmission. Please note that detailed descriptions of the data - for the pre-intervention phase only - are available in two publications : Soma et al. (2020) ; Zogo et al. (2019).

Data Validation and quality control

Each night of collection, one technician assisted by two local supervisors supervised the mosquito collections in each village to ensure that they were performed properly.

Independent staff supervised rotation of the mosquito collection and regularly checked for the quality of the mosquito collection. The following criteria were checked and reported on an electronic tablet : respected collection location, collector at his post, collector awake, collector in a correct position, collector adequately dressed, correct hourly bags used. If one of the criteria was not respected, required arrangements were immediately made by the supervisor.

All data reported has been curated and the terminology has been homogenized. Data has been validated using the validator available in GBIF.

Re-use potential

These data have been already used in several studies, including (non exhaustively) : description of the entomological profiles of malaria transmission in the study areas during the pre-intervention phase of the RCT (Soma et al. 2020 ; Zogo et al. 2019), modeling of the environmental determinants of malaria vectors biting rates in the BF area (Taconet et al. 2021), modeling of the drivers of physiological and behavioural resistance to insecticides in both study areas (Taconet et al. 2022).

Examples of potential re-use include :

- comparison of entomological parameters of malaria transmission with other areas (regions, countries, continents);

- intergration in global databases of vectors (e.g. the *VectorBase* database (Amos et al. 2022) or the Malaria Atlas Project (Hay and Snow 2006)) for larger scale studies of mosquito seasonal dynamics;
- species distribution modeling at larger spatial scale using the environmental data.

Data Availability

The data supporting this article are published through the IPT of GBIF France and are available under a CC0 waiver. The DOI of the data is https://doi.org/10.15468/v8fvyn.

The published data include 4 datasets :

- *Event* : The dates and geographic coordinates of the sampling (i.e. mosquito collection) events ;
- *Occurrence* : The collected anopheles along with genus or species identification (1 row = 1 collected mosquito. We choose such a granularity to enable to link the occurrence data with the results of the molecular analysis performed at the individual mosquito scale. Users are free to summarize the data, e.g. by EventID);

- *Extended measurement or fact* : The results of the molecular analysis for the subsample of the collected anopheles. Also includes the place of collection of each mosquito (i.e. indoors or outdoors);
- *Measurement or fact* : The environmental data (meteorological and landscape conditions) at the sampling Event timepoints.

We kindly ask users to give appropriate credit and attribution when using this data.

List of abbreviations

BF: Burkina Faso; CI: Côte d'Ivoire; GBIF: Global Biodiversity Information Facility; HLC: Human Landing Catch; IPR: Institut Pierre Richet; IPT: Integrated Publishing Toolkit ; IRD: Institut de Recherche pour le Développement; IRSS: Institut de Recherche en Science de la Santé; LLIN: Long-Lasting Insecticidal Nets; PCR: Polymerase Chain Reaction; qPCR: quantitative Polymerase Chain Reaction; RCT: Randomized Controlled Trial; REACT: Insecticide resistance management in Burkina Faso and Côte d'Ivoire: research on vector control strategies; VC: Vector Control; WHO: World Health Organisation

Ethical approval

Ethical clearance for the study was granted by the National ethics committee (No. 063/ MSHP/CNER-kp) in Côte d'Ivoire and by the Institutional Ethics Committee of the Institut de Recherche en Sciences de la Santé (No. A06/2016/CEIRES) in Bukina Faso. We received community agreement before the beginning of the study, and we obtained written informed consent from all the mosquito collectors and supervisors. Yellow fever vaccines were administered to all the field staff. Collectors were treated free of charge when they were diagnosed with malaria during the study period according to WHO recommendations. They were also free to withdraw from the study at any time without any consequences.

Consent for publication

Not applicable.

Competing Interests

The authors declare that they have no competing interests.

Funding

This work was part of the REACT project, funded by the French Initiative 5% – Expertise France (No. 15SANIN213)

Authors' contributions

PT: Software, Data curation, Visualization, Writing – original draft; BZ: Supervision, Investigation, Data curation, Conceptualization, Methodology, Writing – review & editing; DDS: Supervision, Investigation, Data curation, Conceptualization, Methodology, Writing – review & editing; LPAA: Supervision, Investigation, Conceptualization, Methodology, Writing – review & editing; KM: Supervision, Conceptualization, Methodology, Funding acquisition, Writing – review & editing; RKD: Supervision, Resources, Conceptualization, Methodology, Funding acquisition, Project administration, Writing – review & editing; AAK: Supervision, Resources, Conceptualization, Methodology, Funding acquisition, Writing – review & editing; CP: Supervision, Resources, Investigation, Conceptualization, Methodology, Funding acquisition, Project administration, Writing – review & editing; NM: Supervision, Resources, Investigation, Data curation, Conceptualization, Methodology, Funding acquisition, Project administration, Writing – review & editing

Acknowledgements

We thank all participants of the study, especially technicians at the IRSS and IPR for their technical assistance. We thank all the mosquito collectors and supervisors for their commitment in the field. We are also grateful to the villagers of all sites for their kind collaboration and hospitality. We thank Sophie Pamerlon (GBIF France) for her help with the use of IPT.

References

Amos, Beatrice, Cristina Aurrecoechea, Matthieu Barba, Ana Barreto, Evelina Y Basenko, Wojciech Bażant, Robert Belnap, et al. 2022. "VEuPathDB: The Eukaryotic Pathogen, Vector and Host Bioinformatics Resource Center." *Nucleic Acids Research* 50 (D1): D898–911. https://doi.org/10.1093/nar/gkab929.

Bass, Chris, Dimitra Nikou, Martin J Donnelly, Martin S Williamson, Hilary Ranson, Amanda Ball, John Vontas, and Linda M Field. 2007. "Detection of Knockdown Resistance (Kdr) Mutations in Anopheles Gambiae: A Comparison of Two New High-Throughput Assays with Existing Methods." *Malaria Journal* 6 (1): 111. https://doi.org/10.1186/1475-2875-6-111.

Bhatt, S., D. J. Weiss, E. Cameron, D. Bisanzio, B. Mappin, U. Dalrymple, K. E. Battle, et al. 2015. "The Effect of Malaria Control on Plasmodium Falciparum in Africa Between 2000 and 2015." *Nature* 526 (7572): 207–11. https://doi.org/10.1038/nature15535.

Boissière, Anne, Geoffrey Gimonneau, Majoline T. Tchioffo, Luc Abate, Albert Bayibeki, Parfait H. Awono-Ambéné, Sandrine E. Nsango, and Isabelle Morlais. 2013. "Application of a qPCR Assay in the Investigation of Susceptibility to Malaria Infection of the M and S Molecular Forms of An. Gambiae s.s. In Cameroon." *PLOS ONE* 8 (1): 1–10. https://doi.org/10.1371/journal.pone.0054820.

Center, NASA Goddard Earth Sciences Data And Information Services. 2019. "GPM IMERG Final Precipitation L3 1 Day 0.1 Degree x 0.1 Degree V06." NASA Goddard

Earth Sciences Data; Information Services Center. https://doi.org/10.5067/GPM/IMERGDF/DAY/06.

CILSS, 2016. 2016. “Landscapes of West Africa—A Window on a Changing World: Ouagadougou, Burkina Faso, CILSS, 219 p. (Comité Permanent Inter-États de Lutte Contre La Sécheresse Dans Le Sahel) [Also Available at Https://Eros.usgs.gov/Westafrica].” In. https://doi.org/http://dx.doi.org/10.5066/F7N014QZ.

Cohuet, Anna, Frédéric Simard, A. Berthomieu, M. Raymond, Didier Fontenille, and M. Weill. 2002. “Isolation and Characterization of Microsatellite DNA Markers in the Malaria Vector Anopheles Funestus.” *Molecular Ecology Notes* 2 (4): 498–500.

Detinova, Tatiana Sergeevna, D. S Bertram, and World Health Organization. 1962. “Age-Grouping Methods in Diptera of Medical Importance, with Special Reference to Some Vectors of Malaria / t. S. Detinova ; [with] an Annex on the Ovary and Ovarioles of Mosquitos (with Glossary) by d. S. Bertram.” World Health Organization Monograph Series ; No. 47. World Health Organization.

Essandoh, John, Alexander E Yawson, and David Weetman. 2013. “Acetylcholinesterase (Ace-1) Target Site Mutation 119s Is Strongly Diagnostic of Carbamate and Organophosphate Resistance in Anopheles Gambiae s.s. And Anopheles Coluzzii Across Southern Ghana.” *Malaria Journal* 12 (1): 404. https://doi.org/10.1186/1475-2875-12-404.

Favia, G., A. Lanfrancotti, L. Spanos, I. Sidén-Kiamos, and C. Louis. 2001. “Molecular Characterization of Ribosomal DNA Polymorphisms Discriminating Among Chromosomal Forms of Anopheles Gambiae s.s.: An. Gambiae s.s. rDNA Polymorphisms.” *Insect Molecular Biology* 10 (1): 19–23. https://doi.org/10.1046/j.1365-2583.2001.00236.x.

Ferguson, Heather M., Anna Dornhaus, Arlyne Beeche, Christian Borgemeister, Michael Gottlieb, Mir S. Mulla, John E. Gimnig, Durland Fish, and Gerry F. Killeen. 2010. “Ecology: A Prerequisite for Malaria Elimination and Eradication.” *PLoS Medicine* 7 (8): e1000303. https://doi.org/10.1371/journal.pmed.1000303.

Gillies, M. T., and B. De Meillon. 1968. “The Anophelinae of Africa South of the Sahara (Ethiopian Zoogeographical Region).” *Publications of the South African Institute for Medical Research* 54.

Gillies, M. T., and Maureen Coetzee. 1987. “A Supplement to the Anophelinae of Africa South of the Sahara.” *Publ S Afr Inst Med Res* 55: 1–143.

Hay, Simon I, and Robert W Snow. 2006. “The Malaria Atlas Project: Developing Global Maps of Malaria Risk.” *PLoS Medicine* 3 (12): e473. https://doi.org/10.1371/journal.pmed.0030473.

INSD. 2015. “Tableau de Bord Économique Et Social 2014 de La Région Du Sud Ouest.”

———. 2017. “Enquête Nationale Sur Le Secteur de l’orpaillage (ENSO).”

Koekemoer, L. L., Luna Kamau, R. H. Hunt, and Maureen Coetzee. 2002. “A Cocktail Polymerase Chain Reaction Assay to Identify Members of the Anopheles Funestus (Diptera: Culicidae) Group.” *The American Journal of Tropical Medicine and Hygiene* 66 (6): 804–11.

Martinez-Torres, D., F. Chandre, M. S. Williamson, F. Darriet, J. B. Berge, A. L. Devonshire, P. Guillet, N. Pasteur, and D. Pauron. 1998. “Molecular Characterization of Pyrethroid Knockdown Resistance (Kdr) in the Major Malaria Vector Anopheles Gambiae s.s.” *Insect Molecular Biology* 7 (2): 179–84. https://doi.org/10.1046/j.1365-2583.1998.72062.x.

Moyes, Catherine L., Duncan K. Athinya, Tara Seethaler, Katherine E. Battle, Marianne Sinka, Melinda P. Hadi, Janet Hemingway, Michael Coleman, and Penelope A. Hancock. 2020. “Evaluating Insecticide Resistance Across African Districts to Aid Malaria Control Decisions.” *Proceedings of the National Academy of Sciences* 117 (36): 22042–50. https://doi.org/10.1073/pnas.2006781117.

PNLP. 2014a. “Directives Nationales Pour La Prise En Charge Du Paludisme Dans Les Formations Sanitaires Du Burkina Faso. Ministère de La Santé/Burkina Faso.”

———. 2014b. “Programme National de Lutte Contre Le Paludisme En Côte d’ivoire. 2014. Plan Stratégique National de Lutte Contre Le Paludisme 2012–2015 (Période Replanifiée 2014–2017). Approche Stratifiée de Mise à l’échelle Des Interventions de Lutte Contre Le Paludisme En Côte d’ivoire Et Consolidation Des Acquis. Abidjan: Ministère de La Santé Et l’hygiène Publique. 149 p.”

Ranson, H., B. Jensen, J. M. Vulule, X. Wang, J. Hemingway, and F. H. Collins. 2000. “Identification of a Point Mutation in the Voltage-Gated Sodium Channel Gene of

Kenyan Anopheles Gambiae Associated with Resistance to DDT and Pyrethroids." *Insect Molecular Biology* 9 (5): 491–97. https://doi.org/10.1046/j.1365-2583.2000.00209.x.

Santolamazza, Federica, Emiliano Mancini, Frédéric Simard, Yumin Qi, Zhijian Tu, and Alessandra della Torre. 2008. "Insertion Polymorphisms of Sine200 Retrotransposons Within Speciation Islands of Anopheles Gambiae Molecular Forms." *Malaria Journal* 7 (1): 1–10.

Scott, Julie A., William G. Brogdon, and Frank H. Collins. 1993. "Identification of Single Specimens of the Anopheles Gambiae Complex by the Polymerase Chain Reaction." *The American Journal of Tropical Medicine and Hygiene* 49 (4): 520–29.

Sherrard-Smith, Ellie, Janetta E. Skarp, Andrew D. Beale, Christen Fornadel, Laura C. Norris, Sarah J. Moore, Selam Mihreteab, et al. 2019. "Mosquito Feeding Behavior and How It Influences Residual Malaria Transmission Across Africa." *Proceedings of the National Academy of Sciences* 116 (30): 15086–95. https://doi.org/10.1073/pnas.1820646116.

Sinka, Marianne E, Michael J Bangs, Sylvie Manguin, Maureen Coetzee, Charles M Mbogo, Janet Hemingway, Anand P Patil, et al. 2010. "The Dominant Anopheles Vectors of Human Malaria in Africa, Europe and the Middle East: Occurrence Data, Distribution Maps and Bionomic Précis." *Parasites & Vectors* 3 (1). https://doi.org/10.1186/1756-3305-3-117.

Sinka, Marianne E, Michael J Bangs, Sylvie Manguin, Yasmin Rubio-Palis, Theeraphap Chareonviriyaphap, Maureen Coetzee, Charles M Mbogo, et al. 2012. "A Global Map of Dominant Malaria Vectors." *Parasites & Vectors* 5 (1). https://doi.org/10.1186/1756-3305-5-69.

Soma, Barnabas Mahugnon Zogo, Anthony Somé, Bertin N'Cho Tchiekoi, Domonbabele François de Sales Hien, Hermann Sié Pooda, Sanata Coulibaly, et al. 2020. "Anopheles Bionomics, Insecticide Resistance and Malaria Transmission in Southwest Burkina Faso: A Pre-Intervention Study." *PLOS ONE* 15 (8): e0236920. https://doi.org/10.1371/journal.pone.0236920.

Taconet, Paul, Angélique Porciani, Dieudonné Diloma Soma, Karine Mouline, Frédéric Simard, Alphonsine Amanan Koffi, Cedric Pennetier, Roch Kounbobr Dabiré, Morgan Mangeas, and Nicolas Moiroux. 2021. "Data-Driven and Interpretable Machine-Learning Modeling to Explore the Fine-Scale Environmental Determinants of Malaria

Vectors Biting Rates in Rural Burkina Faso." *Parasites & Vectors* 14 (1). https://doi.org/10.1186/s13071-021-04851-x.

Taconet, Paul, Diloma Dieudonné SOMA, Barnabas Zogo, Karine Mouline, Frédéric Simard, Alphonsine Amanan Koffi, Roch Kounbobr Dabiré, Cédric Pennetier, and Nicolas Moiroux. 2022. "Insecticide Resistance and Biting Behaviour of Malaria Vectors in Rural West-Africa : A Data Mining Study to Adress Their Fine-Scale Spatiotemporal Heterogeneity, Drivers, and Predictability." *bioRxiv*. https://doi.org/10.1101/2022.08.20.504631.

Wan, Zhengming, Simon Hook, and Glynn Hulley. 2015a. "Mod11a1 MODIS/Terra Land Surface Temperature/Emissivity Daily L3 Global 1km SIN Grid V006." NASA EOSDIS Land Processes DAAC. https://doi.org/10.5067/MODIS/MOD11A1.006.

———. 2015b. "Myd11a1 MODIS/Aqua Land Surface Temperature/Emissivity Daily L3 Global 1km SIN Grid V006." NASA EOSDIS Land Processes DAAC. https://doi.org/10.5067/MODIS/MYD11A1.006.

WHO. 2017. "WHO Global Vector Control Response 2017–2030." *WHO*. http://www.who.int/vector-control/publications/global-control-response/en/.

———. 2022. "World Malaria Report 2022. Geneva: World Health Organization; 2022." Licence: CC BY-NC-SA 3.0 IGO. https://www.who.int/publications/i/item/9789240064898.

Wiebe, Antoinette, Joshua Longbottom, Katherine Gleave, Freya M. Shearer, Marianne E. Sinka, N. Claire Massey, Ewan Cameron, et al. 2017. "Geographical Distributions of African Malaria Vector Sibling Species and Evidence for Insecticide Resistance." *Malaria Journal* 16 (1): 85. https://doi.org/10.1186/s12936-017-1734-y.

Wilson, Anne L., Orin Courtenay, Louise A. Kelly-Hope, Thomas W. Scott, Willem Takken, Steve J. Torr, and Steve W. Lindsay. 2020. "The Importance of Vector Control for the Control and Elimination of Vector-Borne Diseases." *PLOS Neglected Tropical Diseases* 14 (1): e0007831. https://doi.org/10.1371/journal.pntd.0007831.

Zogo, Barnabas, Dieudonné Diloma Soma, Bertin N'Cho Tchiekoi, Anthony Somé, Ludovic P. Ahoua Alou, Alphonsine A. Koffi, Florence Fournet, et al. 2019. "*Anopheles* Bionomics, Insecticide Resistance Mechanisms, and Malaria Transmission in the Korhogo Area, Northern Côte d'Ivoire: A Pre-Intervention Study." *Parasite* 26: 40. https://doi.org/10.1051/parasite/2019040.

	Korhogo area (CI)	**Diébougou area (BF)**
N° of human-nights of collections	1854	1512
N° of anopheles captured	57716	2989
Mean human biting rate*	31.13 bites/human/night	1.98 bites/human/night
N° anopheles species captured	6 different species	10 different species
% An. gambiae s.s.	97 %	20 %
% An. coluzzii	< 1 %	44 %
% An. funestus	1 %	24 %
% other species	< 1 %	12 %
% bites outdoors	56 %	42 %
Allelic frequency of the kdr-w mutation	89.29 %	66.83 %
Allelic frequency of the kdr-e mutation	NA	13.5 %
Allelic frequency of the ace-1 mutation	31.13 %	7.72 %
Mean sporozoite infection rate	2.5 %	10.9 %
Mean entomological inoculation rate	0.77 infected bites per human per night	0.21 infected bites per human per night