Journal: Texila International Journal of Academic Research
Publisher: Texila International Journal
ISSN: 2520-3088
Volume 13 Issue 2, 2026
DOI: 10.21522/TIJAR.2014.13.02.Art028

Artemisinin Partial Resistance in Sub-Saharan Africa: Epidemiological Patterns, Molecular Markers, and Implications for Malaria Control

Hamad Nnimbo[1*], Amitabye Luximon-Ramma[1,2]
[1]*School of Public Health, Texila American University, Guyana*
[2]*School of Health Sciences, University of Technology, Mauritius, La Tour Koenig, Mauritius*

Abstract

Artemisinin partial resistance (ART-R) represents a growing concern for malaria control in Sub-Saharan Africa. This narrative review synthesizes current evidence on the epidemiology, molecular markers, therapeutic efficacy, transmission dynamics, and surveillance of ART-R. Structured searches of peer-reviewed literature and grey sources published between 2020 and 2025 were conducted, focusing on clinical studies of artemisinin-based combination therapy (ACT) efficacy, PfKelch13 (PfK13) mutations, and surveillance reports. Data were extracted descriptively and synthesized thematically across four domains: emergence patterns, molecular markers and phenotypic expression, treatment efficacy and partner drug susceptibility, and transmission and surveillance capacity. Validated PfK13 mutations associated with ART-R, including R561H, C469Y, A675V, and R622I, have emerged independently across Sub-Saharan African countries. While delayed parasite clearance is observed with these mutations, first-line ACTs continue to show high cure rates in many settings, reflecting the combined activity of artemisinin derivatives and partner drugs. Candidate PfK13 mutations and markers of altered partner drug susceptibility have also been reported, highlighting potential emerging vulnerabilities in the ACT framework. Prolonged parasite clearance may increase the window of transmission, particularly in low to moderate transmission settings. Surveillance capacity is expanding but remains uneven, with gaps in genomic monitoring, timely reporting, and integration into policy processes. Overall, ART-R in Sub-Saharan Africa remains focal and of low prevalence, with limited evidence of widespread clinical impact. Strengthening integrated molecular and therapeutic surveillance, improving data-to-policy translation, and implementing targeted interventions in high-risk areas are critical to prevent wider dissemination and sustain ACT effectiveness, thereby supporting malaria control gains across the region.

Keywords: *ACT Efficacy, Artemisinin Partial Resistance, Malaria, Molecular Surveillance, PfK13 Mutations, Sub-Saharan Africa.*

Introduction

Malaria remains among the most important global public health concerns, with an estimated 282 million cases and over 600,000 deaths annually, primarily occurring in low- and middle-income countries. Sub-Saharan Africa bears the greatest burden, accounting for more than 90% of global malaria cases and deaths [1]. *Plasmodium falciparum* is the predominant species in this region and is responsible for most severe disease outcomes, including hospitalizations and mortality [1]. Malaria transmission across Sub-Saharan Africa is highly heterogeneous, ranging from perennial high-transmission settings to seasonal or low-transmission areas [2]. This variability influences acquired immunity, clinical

Received: 10.02.2026 ***Accepted: 17.03.2026*** ***Published on: 30.04.2026***
****Corresponding Author: nnimbo3@gmail.com***

manifestations, and the effectiveness of control interventions [3]. In addition, socioeconomic conditions, environmental factors, and health system capacity contribute to substantial variation in malaria burden [4]. These differences create diverse epidemiological contexts that shape both transmission dynamics and intervention effectiveness.

In this context, artemisinin-based combination therapies (ACTs) remain the cornerstone of treatment for uncomplicated *P. falciparum* malaria. These therapies combine a fast-acting artemisinin derivative with a longer-acting partner drug, enabling rapid parasite clearance and sustained therapeutic effect [5]. Together with vector control strategies such as insecticide-treated nets and indoor residual spraying, ACTs have contributed to significant reductions in malaria morbidity and mortality across the region [6]. However, the durability of these gains depends on the continued effectiveness of antimalarial drugs. Artemisinin partial resistance, first identified in Southeast Asia, is characterized by delayed parasite clearance and has been linked to mutations in the *Pfkelch13* (PfK13) gene [5]. This form of resistance is not typically characterized by immediate treatment failure, but rather by changes in parasite clearance dynamics, making early detection dependent on clinical and molecular indicators. Although ACTs largely remain effective, the presence of molecular markers associated with reduced artemisinin susceptibility raises concern about potential future declines in treatment efficacy [7].

In Sub-Saharan Africa, the detection of PfK13 polymorphisms has been increasingly reported, but their epidemiological and clinical significance remains incompletely understood [8, 9]. Current evidence is fragmented across molecular surveillance, therapeutic efficacy studies, and transmission assessments, limiting integrated interpretation. In addition, the presence of both validated and novel PfK13 mutations presents challenges for classification and risk assessment, particularly where phenotypic evidence is limited [10, 11].

Given the heterogeneity of malaria transmission, drug pressure, and health system capacity across Sub-Saharan Africa, a comprehensive understanding of the emergence and spread of artemisinin partial resistance is essential. This review aims to synthesize current evidence on epidemiological patterns, molecular markers, therapeutic efficacy, transmission dynamics, and surveillance capacity to inform timely and adaptive malaria control strategies.

Methods

This is a structured narrative review that synthesizes evidence on the emergence of artemisinin partial resistance (ART-R) in Sub-Saharan Africa from 2020 to 2025. The review was conducted between January and March 2025.

Strategy

Structured searches were performed in PubMed, Google Scholar, and grey literature sources covering the period 2020 - 2025. Keywords and Medical Subject Headings (MeSH) included “artemisinin partial resistance,” “kelch13 mutations,” “PfK13,” “ACT failure,” “therapeutic efficacy,” “malaria treatment,” and “Sub-Saharan Africa,” combined with Boolean operators (“AND” “OR”). Backward citation searching of reference lists from included studies was conducted to identify further eligible publications.

Eligibility Criteria

Included studies comprised original clinical investigations assessing ACT efficacy, parasite clearance dynamics, or therapeutic outcomes in Sub-Saharan African populations; molecular studies reporting PfK13 polymorphisms associated with ART-R; and surveillance or programmatic reports documenting emerging resistance trends. Review articles were included

to provide context and to identify additional primary sources. Only studies conducted in Sub-Saharan Africa reporting data on artemisinin susceptibility were considered. Studies unrelated to artemisinin resistance, PfK13 mutations, or ACT outcomes were excluded unless providing relevant contextual information.

Data Extraction and Synthesis

Data were extracted descriptively, including country, ACT regimens, therapeutic outcomes, parasite clearance patterns, and reported PfK13 mutations (validated or candidate). Relevant surveillance findings and policy updates were also included to contextualize emerging trends. Quantitative synthesis or meta-analysis was not performed due to variability in study designs and outcome definitions. Findings were organized thematically into four key domains: epidemiologic patterns of emergence, molecular markers and phenotypic expression, therapeutic efficacy and partner drug susceptibility, and transmission dynamics with surveillance capacity.

Results

This section synthesizes evidence from 39 sources (2020-2025) on artemisinin partial resistance in sub-Saharan Africa. The included evidence comprised different study designs, including modelling and genomic surveillance approaches, molecular surveillance of PfK13 mutations, therapeutic efficacy studies, systematic reviews, and World Health Organization reports. Findings were organized into key domains including epidemiologic patterns of emergence, molecular markers and phenotypic expression, therapeutic efficacy and partner drug susceptibility, and transmission dynamics with surveillance capacity.

Epidemiologic Patterns of Emergence

The reviewed studies reported increasing detection of PfK13 mutations associated with artemisinin partial resistance across several Sub-Saharan African countries. In Rwanda, nonsynonymous PfK13 mutations increased over successive survey years [12].

In Uganda, PfK13 variants including A675V, C469Y, 469F, and 561H were detected across multiple districts, with frequencies in some locations ranging from approximately 10% to over 50% depending on district and survey period [8]. In Western Kenya, PfK13 mutations associated with artemisinin resistance were detected across serial cross-sectional school-based surveys conducted in 2019, 2022, and 2023, showing temporal variation in detection and prevalence of key variants across study years [13].

Spatial heterogeneity was observed across countries. In Uganda, mutations were unevenly distributed across districts, with higher concentrations in northern regions [8]. In Kenya, mutations were distributed across multiple counties, with variation in detection across survey years (Osoti et al., 2025). In Tanzania, Rwanda, and Uganda, R561H has been reported, while A675V and C469Y were mainly reported in northern Uganda, and R622I in Ethiopia and Eritrea [8, 14–16].

Genomic analyses indicate that several African PfK13 variants emerged independently within local parasite populations rather than through importation from Southeast Asia [9]. In Western Kenya, serial surveys showed temporal variation in mutation detection, including absence of A675V and R561H in 2019, detection of multiple variants in 2022, and emergence and fluctuation of key mutations in 2023 [13].

In West Africa, studies from Ghana and Nigeria report a high proportion of PfK13 wild-type parasites alongside multiple novel non-synonymous polymorphisms, many of which are geographically or ecologically restricted and not yet classified as validated artemisinin resistance markers [10, 11].In Central Africa, molecular surveillance of Plasmodium falciparum isolates between 2016 and 2021 showed limited PfK13 diversity, with a small

number of nonsynonymous mutations reported and a predominance of wild-type alleles [17].

Molecular Markers and Phenotypic Expression

Mutations in the PfK13 propeller domain are associated with delayed parasite clearance, the clinical phenotype defining artemisinin partial resistance [7]. A total of 13 PfK13 propeller-domain mutations have been recognized as molecular markers associated with artemisinin partial resist A total of 13 PfK13 propeller-domain mutations have been consistently reported as validated molecular markers of artemisinin partial resistance in global surveillance datasets, including: F446I, N458Y, C469Y, M476I, Y493H, R539T, I543T, P553L, R561H, P574L, C580Y, R622I, and A675V. This list is periodically updated based on emerging evidence and WHO-supported global surveillance data [5].

In addition to validated markers, several PfK13 propeller-domain mutations are classified as candidate or associated markers of artemisinin partial resistance. These include P441L, G449A, C469F, A481V, R515K, P527H, N537I/D, G538V, and V568G [5]. These variants have been reported in surveillance studies, and a subset has shown in vitro or field signals of reduced artemisinin susceptibility, although they have not met validation thresholds for confirmed resistance status [7]. Experimental studies report that PfK13 mutations are associated with altered parasite biology, including reduced hemoglobin endocytosis and impaired activation of artemisinin during early ring stages [18].

Higher day 3 parasitemia is reported among infections carrying validated mutations compared with wild-type parasites [19]. Where assessed, parasite clearance half-life was prolonged relative to historical baselines [20]. PfK13 polymorphisms beyond the validated and candidate markers have also been reported in surveillance datasets, although their phenotypic relevance remains unconfirmed due to insufficient clinical and in vivo evidence [21].

Quantitative measures of parasite clearance, including parasite clearance half-life and proportion of patients with detectable parasitemia on day 3, were reported in multiple therapeutic efficacy studies [19, 20]. In several studies, infections carrying validated PfK13 mutations were associated with higher proportions of day 3 positivity compared with infections with wild-type alleles [19]. There is also documented evidence on the presence of multiple PfK13 polymorphisms within single study populations, with varying frequencies across sites [21].

Therapeutic Efficacy and Partner Drug Susceptibility

Across the reviewed studies, PCR-corrected efficacy of first-line artemisinin-based combination therapies (ACTs) remains within policy-recommended thresholds, with most studies reporting day 28 or day 42 cure rates above 90%, while a few studies reported values below lower values [22, 23]. Variation in reported efficacy was observed across transmission settings and follow-up durations, with differences in 28-day and 42-day endpoints across studies [22, 24–26]. Validated PfK13 mutations associated with artemisinin partial resistance were reported, with studies documenting prolonged parasite clearance half-life in infections carrying these mutations [8]. Higher day 3 parasite positivity was also reported in infections with validated PfK13 mutations compared with wild-type infections [19].

Markers associated with reduced susceptibility to ACT partner drugs, including lumefantrine, amodiaquine, and piperaquine, were reported in selected surveillance settings [27]. However, simultaneous high-level resistance to both artemisinin and partner drugs leading to widespread treatment failure was not documented in the reviewed studies [5, 8, 25]. Geographical variation in the frequency of

partner drug resistance markers was observed across both regional and within-country surveillance settings, with heterogeneity reported between ecological zones and transmission sites [27, 28].

Recurrent parasitemia in high-transmission settings was frequently attributed to reinfection rather than recrudescence following PCR genotyping, which distinguishes new infections from true treatment failure in therapeutic efficacy studies [24–26]. Evidence from therapeutic efficacy studies indicates that PCR-corrected analyses reduce estimated treatment failure compared with uncorrected outcomes, particularly in settings with high reinfection pressure [24].

Dynamics and Surveillance Capacity

Delayed parasite clearance associated with validated PfK13 mutations has been reported to prolong the duration of asexual parasitemia, extending the period during which infected individuals may contribute to transmission [29]. Some studies report that artemisinin partial resistance mutations are associated with altered parasite fitness and changes in gametocyte production dynamics, including increased gametocyte carriage during infection [30, 31]. In low-to-moderate transmission settings, prolonged parasite clearance times have been reported to coincide with extended infectious periods [32].

At the population level, reduced ACT efficacy has been associated with sustained parasite circulation in settings approaching elimination, where residual transmission foci may persist despite control efforts [33]. Integration of therapeutic efficacy studies (TES) with molecular surveillance has been reported as a recommended strategy for monitoring artemisinin resistance signals [34].

Genomic sequencing capacity in Africa has expanded in recent years; however, it is concentrated in a limited number of research hubs, with many samples requiring external processing [35]. Dependence on externally funded collaborations and variable reporting timelines have been reported to affect surveillance turnaround times [36]. Linkages between molecular surveillance data, therapeutic efficacy monitoring, and national policy review processes have been reported as inconsistently implemented across settings [37].

Discussion

The evidence synthesized in this review highlights a critical stage in the emergence of artemisinin partial resistance (ART-R) in Sub-Saharan Africa, where molecular signals are evident but widespread clinical failure has not yet materialized in therapeutic efficacy studies [8]. Across settings, PfK13 mutations associated with delayed parasite clearance demonstrate a focal and heterogeneous distribution, supporting the interpretation that selection is occurring locally [9, 14]. These spatial patterns are consistent with the uneven distribution of mutations reported across countries and within surveillance sites in the reviewed studies [8, 14–16, 38].

At the molecular and clinical interface, PfK13 propeller-domain mutations are associated in multiple studies with delayed parasite clearance and increased day 3 parasitemia; however, these associations are not uniform across all settings or study populations [22, 23]. Despite these molecular signals, therapeutic efficacy studies consistently report that first-line artemisinin-based combination therapies (ACTs) largely maintain high PCR-corrected cure rates within recommended thresholds, typically exceeding 90% in most sites, although variation across transmission settings and follow-up durations is evident [22, 23]. This reflects heterogeneity in ACT performance rather than uniform efficacy across all endemic settings.

This divergence between molecular detection of resistance markers and clinical outcomes is partly explained by the continued efficacy of partner drugs and the modifying

effect of host immunity in endemic settings, which together mitigate the clinical impact of delayed parasite clearance phenotypes [27]. In addition, PCR-corrected analyses consistently show lower treatment failure rates compared with uncorrected estimates, as recurrent parasitemia is frequently attributable to reinfection rather than recrudescence in high-transmission environments [24–26]. This distinction is critical for interpreting variability in reported ACT efficacy across studies and transmission settings.

The presence of molecular markers associated with reduced susceptibility to partner drugs, including lumefantrine, amodiaquine, and piperaquine, further suggests emerging pharmacological pressure within ACT combinations [27]. However, available evidence does not demonstrate confirmed widespread dual resistance to both artemisinin and partner drugs, and clinically significant treatment failure attributable to combined resistance remains unreported in the included studies [5, 8, 25]. Notably, substantial geographical variation in the frequency of partner drug resistance markers has been reported across ecological zones and within-country surveillance sites, indicating heterogeneous selection pressures [25, 27].

From a transmission perspective, delayed parasite clearance may extend the duration of asexual parasitemia and, in some cases, increase gametocyte carriage, potentially prolonging infectiousness in treated [30, 31]. These effects are likely more pronounced in low-to-moderate transmission or pre-elimination settings, where residual parasite reservoirs contribute disproportionately to ongoing transmission and may sustain local transmission foci even under high treatment coverage [32]. In such contexts, even modest reductions in drug efficacy may translate into disproportionate epidemiological consequences.

Operationally, surveillance systems across Sub-Saharan Africa demonstrate improving but uneven capacity for detecting and responding to emerging resistance signals. Although molecular surveillance and therapeutic efficacy studies are increasingly integrated in some settings, delays in sequencing, data reporting, and translation into policy continue to limit real-time responsiveness [35, 39]. Furthermore, inconsistent linkage between molecular findings, therapeutic efficacy data, and national treatment guideline review processes represents a persistent structural limitation [37]. These system-level gaps reduce the speed at which emerging resistance signals can inform national policy decisions.

Overall, the findings support a scenario of early-stage ART-R in Africa, where focal emergence of PfK13 mutations and partner drug susceptibility markers occurs alongside sustained ACT efficacy, but with increasing epidemiological complexity requiring intensified and better-integrated surveillance systems. This highlights the need for strengthened molecular–clinical integration to detect early transitions toward clinically significant resistance.

Conclusion

Artemisinin partial resistance in sub-Saharan Africa is currently focal and of low to moderate prevalence, but evidence indicates ongoing emergence and local detection of PfK13 mutations, along with markers of reduced partner drug susceptibility, which may pose a potential threat to the long-term effectiveness of ACTs. While first-line therapies remain largely efficacious, with most therapeutic efficacy studies reporting PCR-corrected cure rates above recommended thresholds, proactive measures are essential. Strengthening integrated surveillance systems, expanding molecular monitoring of PfK13 and partner drug markers, and ensuring timely translation of surveillance findings into adaptive treatment policies are recommended. Targeted interventions in high-transmission and identified hotspot areas, combined with

continued therapeutic efficacy studies, will be important to limit further spread and sustain malaria control gains across the region.

Limitations

This narrative review relied on descriptive synthesis rather than systematic analysis and therefore does not provide quantitative pooled estimates of effect. The included studies varied in methodology, outcome definitions, and reporting standards, which may contribute to heterogeneity in reported findings. Geographic coverage was also incomplete, with some regions underrepresented, potentially limiting the generalizability of the findings. Additionally, the review was based on published articles and grey literature, which may introduce publication and reporting bias and exclude relevant unpublished data.

Author Contributions

HN conceived the study, conducted the literature review, performed data synthesis, and drafted the manuscript. ALR contributed to the review of the manuscript. All authors reviewed and approved the final version.

Conflict of Interest

The authors declare that there are no conflicts of interest.

Ethical Approval

This study is based on a narrative review of published literature and publicly available reports. Ethical approval was not required as it did not involve primary data collection.

Data Availability

All data supporting the findings of this study are derived from published articles and publicly available sources cited within the manuscript. No new datasets were generated or analyzed.

Funding

This study was conducted without dedicated financial support from any public, commercial, or non-profit funding bodies.

Acknowledgement

The authors acknowledge the valuable contributions of researchers whose studies formed the basis of this review.

References

[1]. World Health Organization, 2025, Malaria, Available from: https://www.who.int/news-room/fact-sheets/detail/malaria

[2]. Beke, O. A. H., Assi, S. B., Kokrasset, A. P. H., Dibo, K. J. D., Tanoh, M. A., Danho, M., Remoué, F., Koudou, G. B., Poinsignon, A., 2023, Implication of agricultural practices in the micro-geographic heterogeneity of malaria transmission in Bouna, Côte d'Ivoire, *Malaria Journal*, 22(1), https://doi.org/10.1186/s12936-023-04748-3

[3]. Beloconi, A., Nyawanda, B. O., Bigogo, G., Khagayi, S., Obor, D., Danquah, I., Kariuki, S., Munga, S., Vounatsou, P., 2023, Malaria, climate variability, and interventions: modelling transmission dynamics, *Scientific Reports*, 13(1), https://doi.org/10.1038/s41598-023-33868-8

[4]. Namubiru, C., 2025, Institutional quality, aid flows, and malaria burden: a geospatial analysis of sub-Saharan Africa, *Malaria Journal*, 24(1), https://doi.org/10.1186/s12936-025-05592-3

[5]. World Health Organization, 2025, Malaria: Artemisinin partial resistance, https://www.who.int/news-room/questions-and-answers/item/artemisinin-resistance

[6]. Oxborough, R. M., Chilito, K. L. F., Tokponnon, F., Messenger, L. A., 2024, Malaria vector control in sub-Saharan Africa: complex trade-offs to combat the growing threat of insecticide resistance, *The Lancet Planetary Health*, 8(10), https://doi.org/10.1016/S2542-5196(24)00172-4

[7]. Oyegbade, S. A., Mameh, E. O., Balogun, D. O., Aririguzoh, V. G. O., Akinduti, P. A., 2025, Emerging Plasmodium falciparum K13 gene mutation to artemisinin-based combination therapies and partner drugs among malaria-infected

population in sub-Saharan Africa, *Parasites, Hosts and Diseases*, 63(2), https://doi.org/10.3347/PHD.24053

[8]. Conrad, M. D., Asua, V., Garg, S., Giesbrecht, D., Niaré, K., Smith, S., Namuganga, J. F., Katairo, T., Legac, J., Crudale, R. M., Tumwebaze, P. K., Nsobya, S. L., et al., 2023, Evolution of Partial Resistance to Artemisinins in Malaria Parasites in Uganda, *New England Journal of Medicine*, 389(8), https://doi.org/10.1056/NEJMoa2211803

[9]. Rosenthal, P. J., Asua, V., Bailey, J. A., Conrad, M. D., Ishengoma, D. S., Kamya, M. R., Rasmussen, C., Tadesse, F. G., Uwimana, A., Fidock, D. A., 2024, The emergence of artemisinin partial resistance in Africa: how do we respond?, *The Lancet Infectious Diseases*, 24(9), https://doi.org/10.1016/S1473-3099(24)00141-5

[10]. Ajogbasile, F. V., Oluniyi, P. E., Kayode, A. T., Akano, K. O., Adegboyega, B. B., Philip, C., Ogbulafor, N., et al., 2022, Molecular profiling of the artemisinin resistance Kelch 13 gene in Plasmodium falciparum from Nigeria, *PLOS ONE*, 17(2), https://doi.org/10.1371/journal.pone.0264548

[11]. Matrevi, S. A., Tandoh, K. Z., Bruku, S., Opoku-Agyeman, P., Adams, T., Ennuson, N. A., Asare, B., Hagan, O. C. K., et al., 2022, Novel pfk13 polymorphisms in Plasmodium falciparum population in Ghana, *Scientific Reports*, 12(1), https://doi.org/10.1038/s41598-022-11790-9

[12]. Bergmann, C., Van Loon, W., Habarugira, F., Tacoli, C., Jäger, J. C., Savelsberg, D., Nshimiyimana, F., Rwamugema, E., Mbarushimana, D., et al., 2021, Increase in Kelch 13 Polymorphisms in Plasmodium falciparum, Southern Rwanda, *Emerging Infectious Diseases*, 27(1), https://doi.org/10.3201/eid2701.203527

[13]. Osoti, V., Wamae, K., Musau, M. M., Magudha, J. B., Ndwiga, L., Gichuki, P. M., Okoyo, C., Rosebella, K., et al., 2025, Serial cross-sectional school surveys identifies C469Y, P553L, R561H and A675V kelch 13 mutations associated with artemisinin resistance in Western Kenya, *Scientific Reports*, 15(1), https://doi.org/10.1038/s41598-025-22286-7

[14]. Ishengoma, D. S., Mandara, C. I., Bakari, C., Fola, A. A., Madebe, R. A., Seth, M. D., Francis, F., Buguzi, C. C., Moshi, R., et al., 2024, Evidence of artemisinin partial resistance in northwestern Tanzania: clinical and molecular markers of resistance, *The Lancet Infectious Diseases*, 24(11), https://doi.org/10.1016/S1473-3099(24)00362-1

[15]. Mihreteab, S., Anderson, K., Fuente, I. M. D. L., Sutherland, C. J., Smith, D., Cunningham, J., Beshir, K. B., Cheng, Q., 2025, The spread of molecular markers of artemisinin partial resistance and diagnostic evasion in Eritrea: a retrospective molecular epidemiology study, *The Lancet Microbe*, 6(2), https://doi.org/10.1016/S2666-5247(24)00172-1

[16]. Uwimana, A., Legrand, E., Stokes, B. H., Ndikumana, J. L. M., Warsame, M., Umulisa, N., Ngamije, D., et al., 2020, Emergence and clonal expansion of in vitro artemisinin-resistant Plasmodium falciparum kelch13 R561H mutant parasites in Rwanda, *Nature Medicine*, 26(10), https://doi.org/10.1038/s41591-020-1005-2

[17]. Xu, W., Zhang, X., Chen, H., Zhang, J., Lu, Q., Ruan, W., Wang, X., 2023, Molecular markers associated with drug resistance in Plasmodium falciparum parasites in central Africa between 2016 and 2021, *Frontiers in Public Health*, 11, https://doi.org/10.3389/fpubh.2023.1239274

[18]. Hanscheid, T., Mahomed, S. M., Rebelo, M., Henriques, S. O., Grobusch, M. P., 2024, Inaccurate communication in health sciences: The case of 'partial artemisinin resistance' for the treatment of malaria, *New Microbes and New Infections*, 62, https://doi.org/10.1016/j.nmni.2024.101544

[19]. Angwe, M. K., Mwebaza, N., Nsobya, S. L., Vudriko, P., Dralabu, S., Omali, D., Tumwebaze, M. A., Ocan, M., 2024, Day 3 parasitemia and Plasmodium falciparum Kelch 13 mutations among uncomplicated malaria patients treated with artemether-lumefantrine in Adjumani district, Uganda, *PLOS ONE*, 19(6), https://doi.org/10.1371/journal.pone.0305064

[20]. Balikagala, B., Fukuda, N., Ikeda, M., Katuro, O. T., Tachibana, S.-I., Yamauchi, M., Opio, W., Emoto, S., 2021, Evidence of Artemisinin-Resistant Malaria in Africa, *New England Journal of*

Medicine, 385(13), https://doi.org/10.1056/NEJMoa2101746

[21]. Milong Melong, C. S., Peloewetse, E., Russo, G., Tamgue, O., Tchoumbougnang, F., Paganotti, G. M., 2024, An overview of artemisinin-resistant malaria and associated Pfk13 gene mutations in Central Africa, Parasitology Research, 123(7), https://doi.org/10.1007/s00436-024-08301-2

[22]. Bohissou, F. E. T., Nassa, G. J. W., Sondo, P., Rouamba, T., Inoue, J., Kaboré, B., Asua, V., Held, J., Tinto, H., 2025, Spatio-temporal trends of artemisinin-based combination therapy efficacy from 2010 to 2024 in sub-Saharan Africa: a systematic review and meta-analysis, *BMC infectious diseases*, 25(1), https://doi.org/10.1186/s12879-025-12130-8

[23]. Shibeshi, W., Alemkere, G., Mulu, A., Engidawork, E., 2021, Efficacy and safety of artemisinin-based combination therapies for the treatment of uncomplicated malaria in pediatrics: a systematic review and meta-analysis, *BMC Infectious Diseases*, 21(1), https://doi.org/10.1186/s12879-021-06018-6

[24]. Ebong, C., Sserwanga, A., Namuganga, J. F., Kapisi, J., Mpimbaza, A., Gonahasa, S., Asua, V., Gudoi, S., et al., 2021, Efficacy and safety of artemether-lumefantrine and dihydroartemisinin-piperaquine for the treatment of uncomplicated Plasmodium falciparum malaria and prevalence of molecular markers associated with artemisinin and partner drug resistance in Uganda, *Malaria Journal*, 20(1), https://doi.org/10.1186/s12936-021-04021-5

[25]. Issa, M. S., Warsame, M., Mahamat, M. H. T., Saleh, I. D. M., Boulotigam, K., Djimrassengar, H., Issa, A. H., et al., 2023, Therapeutic efficacy of artesunate-amodiaquine and artemether-lumefantrine for the treatment of uncomplicated falciparum malaria in Chad: clinical and genetic surveillance, *Malaria Journal*, 22(1), https://doi.org/10.1186/s12936-023-04644-w

[26]. Ngasala, B. E., Chiduo, M. G., Mmbando, B. P., Francis, F. T., Bushukatale, S., Makene, T., Mandara, C. I., et al., 2024, Efficacy and safety of artemether-lumefantrine for the treatment of uncomplicated falciparum malaria in mainland Tanzania, 2019, *Malaria Journal*, 23(1), https://doi.org/10.1186/s12936-024-04931-0

[27]. Ehrlich, H. Y., Bei, A. K., Weinberger, D. M., Warren, J. L., Parikh, S., 2021, Mapping partner drug resistance to guide antimalarial combination therapy policies in sub-Saharan Africa, *Proceedings of the National Academy of Sciences*, 118(29), https://doi.org/10.1073/pnas.2100685118

[28]. Tumwebaze, P. K., Conrad, M. D., Okitwi, M., Orena, S., Byaruhanga, O., Katairo, T., Legac, J., Garg, S., Giesbrecht, D., et al., 2022, Decreased susceptibility of Plasmodium falciparum to both dihydroartemisinin and lumefantrine in northern Uganda, *Nature Communications*, 13(1), https://doi.org/10.1038/s41467-022-33873-x

[29]. Bwire, G. M., Ngasala, B., Mikomangwa, W. P., Kilonzi, M., Kamuhabwa, A. A. R., 2020, Detection of mutations associated with artemisinin resistance at k13-propeller gene and a near complete return of chloroquine susceptible falciparum malaria in Southeast of Tanzania, *Scientific Reports*, 10(1), https://doi.org/10.1038/s41598-020-60549-7

[30]. Mlugu, E. M., Dondorp, A. M., Barnes, K. I., 2024, Resistant malaria parasites gaining momentum in Africa, *The Lancet Infectious Diseases*, 24(11), https://doi.org/10.1016/S1473-3099(24)00413-4

[31]. Proellochs, N. I., Andolina, C., Ramjith, J., Stoter, R., Van Gemert, G.-J., Graumans, W., Campino, S., Vanheer, L. N., Okitwi, M., Tumwebaze, P. K., Conrad, M. D., Clark, T. G., Fidock, D. A., Ménard, D., Mok, S., Bousema, T., 2025, Gametocyte production and transmission fitness of African and Asian Plasmodium falciparum isolates with differential susceptibility to artemisinins, Antimicrobial Agents and Chemotherapy, 69(6), https://doi.org/10.1128/aac.01930-24

[32]. Masserey, T., Lee, T., Golumbeanu, M., Shattock, A. J., Kelly, S. L., Hastings, I. M., Penny, M. A., 2022, The influence of biological, epidemiological, and treatment factors on the establishment and spread of drug-resistant Plasmodium falciparum, *eLife*, 11, https://doi.org/10.7554/eLife.77634

[33]. Abdul-Ghani, R., Mahdy, M. A. K., Beier, J. C., Basco, L. K., 2017, Hidden reservoir of resistant parasites: the missing link in the elimination of falciparum malaria, *Infectious Diseases of Poverty*, 6(1), https://doi.org/10.1186/s40249-016-0227-5

[34]. Liu, Y., Liang, X., Li, J., Chen, J., Huang, H., Zheng, Y., He, J., Ehapo, C. S., Eyi, U. M., Yang, P., Lin, L., et al., 2022, Molecular Surveillance of Artemisinin-Based Combination Therapies Resistance in Plasmodium falciparum Parasites from Bioko Island, Equatorial Guinea, *Microbiology Spectrum*, 10(3), https://doi.org/10.1128/spectrum.00413-22

[35]. Agboli, E., Bitew, M., Malaka, C. N., Kallon, T. M. P. S., Jalloh, A. M. S., Yankonde, B., Shempela, D. M., et al., 2025, Building Pathogen Genomic Sequencing Capacity in Africa: Centre for Epidemic Response and Innovation Fellowship, *Tropical Medicine and Infectious Disease*, 10(4), https://doi.org/10.3390/tropicalmed10040090

[36]. Kaburi, B. B., Harries, M., Hauri, A. M., Kenu, E., Wyss, K., Silenou, B. C., Klett-Tammen, C. J., Ressing, C., Awolin, J., Lange, B., Krause, G., 2024, Availability of published evidence on coverage, cost components, and funding support for digitalisation of infectious disease surveillance in Africa, 2003–2022: a systematic review, *BMC Public Health*, 24(1), https://doi.org/10.1186/s12889-024-19205-2

[37]. Tindana, P., Sekwo, D. E., Baatiema, L., Djimde, A., the Pathogen Genomics Diversity Network, Africa (PDNA), 2024, Researchers' perspectives on the integration of molecular and genomic data into malaria elimination programmes in Africa: a qualitative study, *Malaria Journal*, 23(1), https://doi.org/10.1186/s12936-024-05205-5

[38]. Alemayehu, A. A., Castañeda Mogollón, D., Belay, S. G., Tesfa, H., Mohon, A. N., Balasingam, N., Bayih, A. G., Ashraf, S., Pillai, D. R., 2025, Expansion of the Plasmodium falciparum Kelch13 R622I Mutation in Northwest Ethiopia, *Open Forum Infectious Diseases*, 12(6), https://doi.org/10.1093/ofid/ofaf279

[39]. Ochola, R., 2025, The Case for Genomic Surveillance in Africa, *Tropical Medicine and Infectious Disease*, 10(5), https://doi.org/10.3390/tropicalmed10050129