



Advances and opportunities in malaria population genomics

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Abstract | Almost 20 years have passed since the first reference genome assemblies were published for *Plasmodium falciparum*, the deadliest malaria parasite, and *Anopheles gambiae*, the most important mosquito vector of malaria in sub-Saharan Africa. Reference genomes now exist for all human malaria parasites and nearly half of the ~40 important vectors around the world. As a foundation for genetic diversity studies, these reference genomes have helped advance our understanding of basic disease biology and drug and insecticide resistance, and have informed vaccine development efforts. Population genomic data are increasingly being used to guide our understanding of malaria epidemiology, for example by assessing connectivity between populations and the efficacy of parasite and vector interventions. The potential value of these applications to malaria control strategies, together with the increasing diversity of genomic data types and contexts in which data are being generated, raise both opportunities and challenges in the field. This Review discusses advances in malaria genomics and explores how population genomic data could be harnessed to further support global disease control efforts.

Malaria is a disease caused by parasitic protozoans in the genus *Plasmodium*, which are transmitted between vertebrate hosts by female mosquitoes in the genus *Anopheles*. The *Plasmodium* life cycle involves haploid asexual stages in vertebrate hosts and, in mosquitoes, a diploid stage with sexual recombination between one or more pairs of identical, inbred or outbred gametes¹. Individual parasite species are usually specialized to infect a narrow range of vertebrate and mosquito hosts. The predominant malaria parasite species that infect humans (*Plasmodium falciparum* and *Plasmodium vivax*) evolved between 10,000 and 60,000 years ago^{2,3}, making malaria one of the very oldest human infectious diseases, in addition to one of the most lethal⁴. In 2019, malaria was responsible for more than 400,000 deaths, mostly of young children in sub-Saharan Africa, with an estimated 3.2 billion people around the world susceptible to infection⁵. Although annual malaria mortality has been more than halved in the past 20 years, drug and insecticide resistance, the lack of a highly efficacious vaccine and disruptions such as the COVID-19 pandemic threaten to halt or reverse these gains⁵.

As an ancient disease that inflicts mortality disproportionately on children, malaria has provided a strong evolutionary pressure on human populations to resist infection and disease⁴. Reciprocally, strong evolutionary pressure has been exerted on parasites by the human immune system and antimalarial drugs. As humans have carried malaria parasites around the world, parasites have evolved to enhance their transmissibility by

local anopheline mosquito vector species in different regions⁶, which have themselves been under intense selective pressure owing to insecticide use over the past century⁷. This complex co-evolutionary history between humans, *Plasmodium* parasites and *Anopheles* mosquitoes is written in the genome of each organism, and genomic tools and data are of key importance for understanding the fundamental genetic underpinning of malaria and developing new strategies to eliminate it. Indeed, every modern malaria intervention, including antiparasitic drugs and insecticides, has been met with an evolutionary response that may be studied through genomic variation. Furthermore, the failure to develop a highly efficacious malaria vaccine is partially attributable to the extreme variability of genes encoding the most immunogenic parasite antigens⁸. Population genomics could therefore be used to help develop effective new interventions, as well as to support the efficient deployment of existing disease control measures through resistance surveillance⁹, tracking the movement of parasites and vectors¹⁰ and measuring changes in transmission intensity using population genomic response indicators¹¹.

In this Review, we provide a brief history of the use of population genomics in malaria research and discuss recent advances, focusing on parasites and vectors. We describe innovations for efficient data generation on a large scale and analyses designed to make use of such data for genomic epidemiology. We identify gaps in the availability of reference genome assemblies for anopheline vectors that impede the understanding of key

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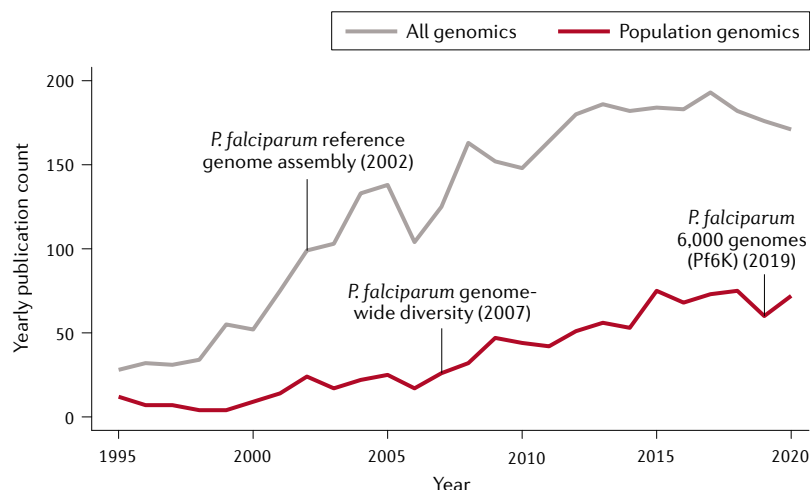
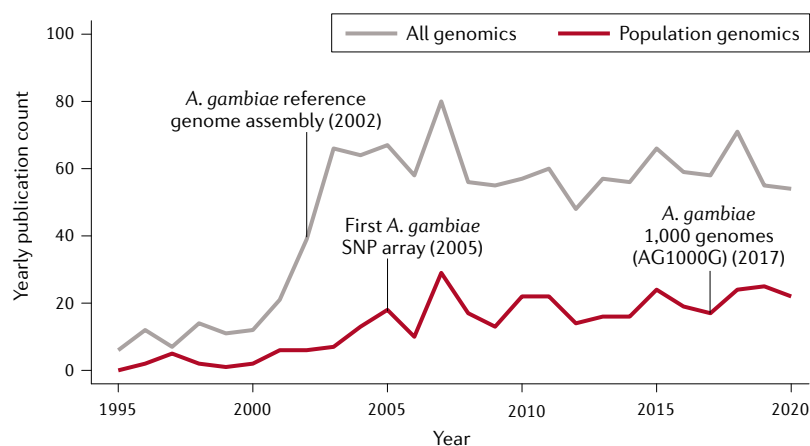
a Plasmodium genomics publications**b Anopheles genomics publications**

Fig. 1 | Malaria population genomics publications 1995–2020. Timelines of *Plasmodium* and *Anopheles* genomics publications and highlighted publications. **a** | *Plasmodium* genomics publications. An increasing fraction of *Plasmodium* genomics papers over time also include terms signifying population diversity in the title and/or abstract. Highlighted milestones include the publication of the first *Plasmodium falciparum* reference genome assembly in 2002 (REF.¹⁵), co-publications reporting the characterization of genome-wide diversity in 2007 (REFS^{17–19}) and the release of the Pf6K data set in 2019 (REF.¹⁷⁰). ‘All genomics’ data represent articles in the NCBI PubMed database published from 1 January 1995 to the present day that include the search terms “*Plasmodium*” and “genom*” in the title or abstract. ‘Population genomics’ data represent ‘all genomics’ articles that also include the search terms “population”, “epidemi*”, “polymorph*” or “diversity” in the title or abstract. **b** | *Anopheles* genomics publications. An increasing fraction of *Anopheles* genomics papers over time also include terms signifying population diversity. Highlighted milestones include the publication of the first *Anopheles gambiae* reference genome assembly in 2002 (REF.²⁵), the first genome-wide single nucleotide polymorphism (SNP) genotyping array for *A. gambiae* in 2005 (REF.¹⁷¹) and the publication of the AG1000G project in 2017 (REF.²⁹). Search queries as above with the replacement of “*Plasmodium*” with “*Anopheles*”.

disease-transmitting members of this ancient and diverse mosquito genus. Finally, we make a case for using epidemiological data analysis techniques that consider variation caused by recombination to enable comparisons of diverse genomic data sets and complement and extend conventional analyses of variation that consider differences in allele frequency. This article does not discuss advances in understanding human or vector genomic

adaptations to malaria, functional genomics, experimental evolution or parasite or vector transcriptomics, which have been addressed by other recent reviews^{12–14}.

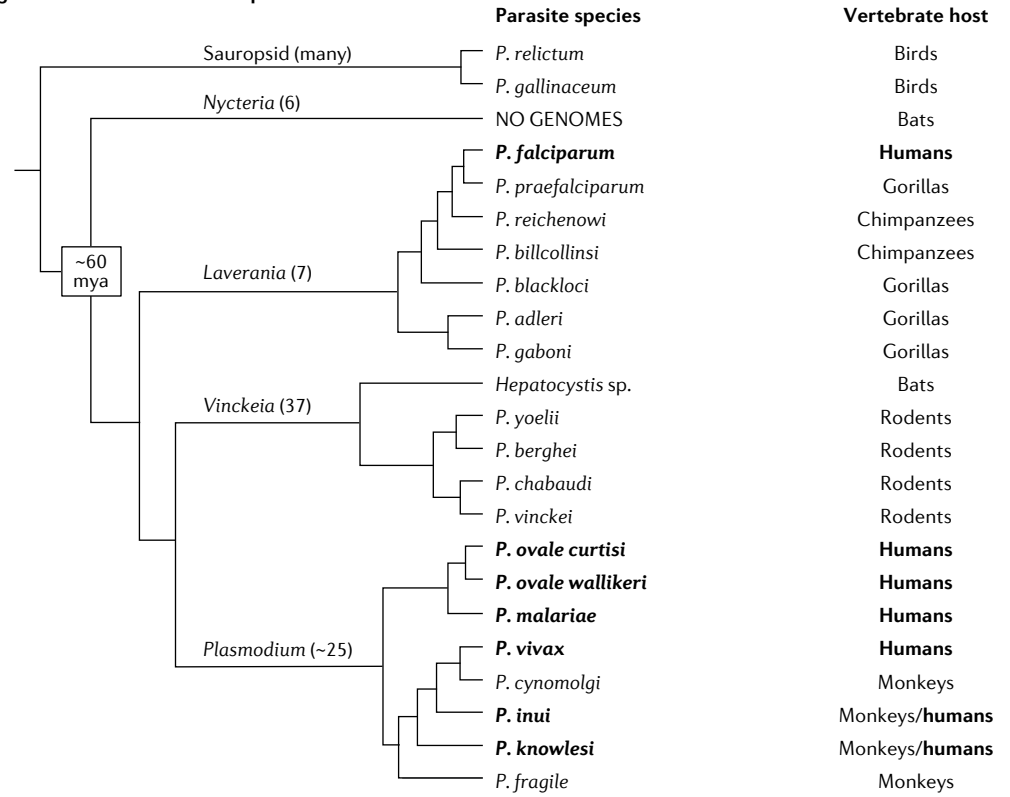
Advent of malaria population genomics

The malaria genomics era began with the sequencing and assembly of the West African 3D7 clone of *P. falciparum*, which was published in 2002 (REF.¹⁵) after nearly a decade of collaborative effort between the Sanger Centre (now the Wellcome Sanger Institute), the Institute for Genomic Research (TIGR), the Stanford Genome Technology Center and the Naval Medical Research Center¹⁶ (FIG. 1). This 23 Mb reference genome revealed that *P. falciparum* harbours almost 5,300 genes, including more than 200 genes associated with immune evasion in the var, rifin and stevor gene families, localized to the subtelomeres. More than 60% of the predicted proteins had no sequence similarity with proteins in other organisms and could not be assigned function¹⁵. Following publication of the *P. falciparum* genome, multiple groups embarked on characterizing genomic variation in this species, together profiling geographically diverse isolates using Sanger sequencing^{17–19} in a template that would later be applied to *P. vivax* and other parasite species^{20,21}. These studies identified enough genetic variants to allow targeted and higher-throughput single nucleotide polymorphism (SNP) genotyping of *P. falciparum* parasites^{22–24} to facilitate deeper analyses of selection and demographic history.

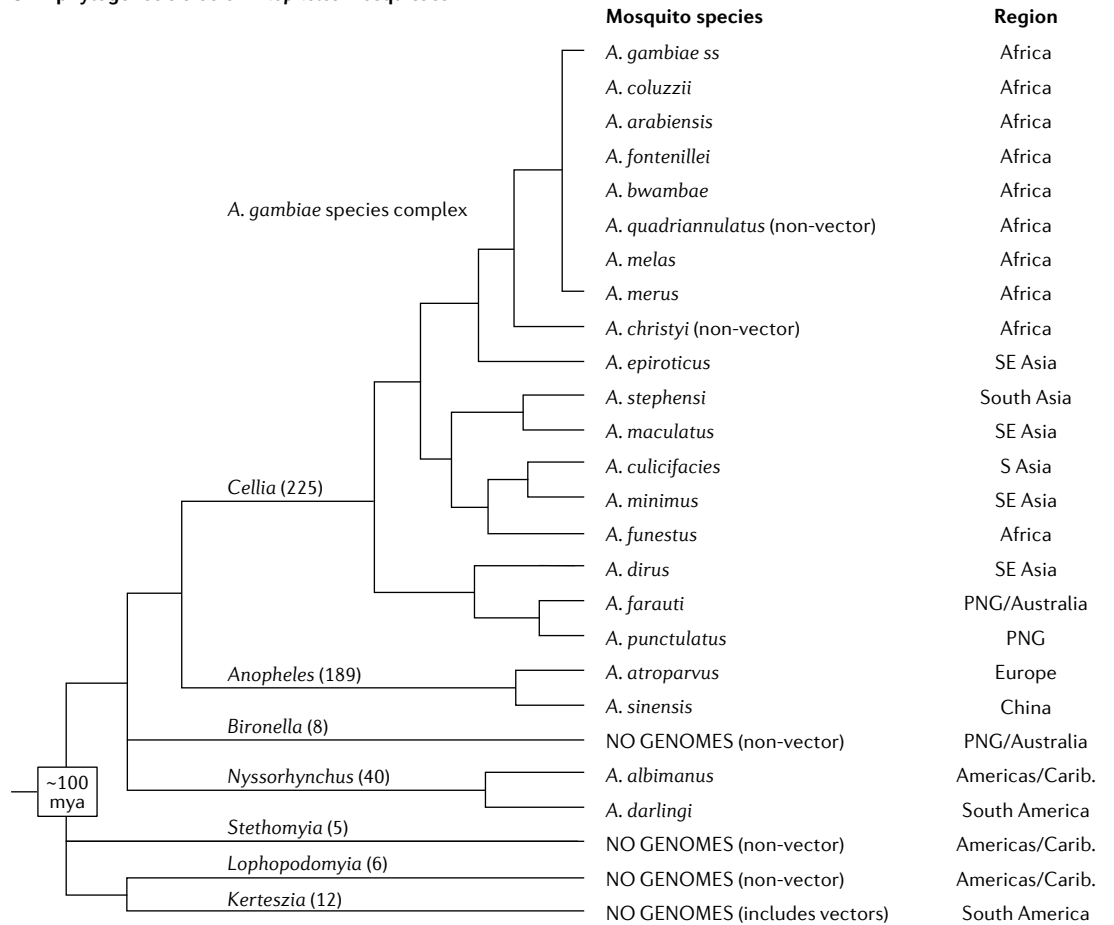
The first reference genome assembly for a mosquito, *Anopheles gambiae*, was published in 2002 (REF.²⁵), the same week as the *P. falciparum* assembly publication and driven by a collaboration between Celera Genomics and investigators at diverse academic institutions. *A. gambiae* is the most important malaria vector in sub-Saharan Africa and likely the most competent malaria vector in the world owing to its anthropophilic feeding preference, preference for biting indoors and susceptibility to *Plasmodium* infection²⁶. The 278 Mb genome of *A. gambiae* was found to contain ~14,000 genes, with many related to immunity, olfaction and other traits contributing to malaria vectorial capacity²⁵. Although genes encoding the targets of major insecticidal classes had been identified before this sequencing project^{27,28}, the *A. gambiae* reference genome assembly provided the first complete catalogue of metabolic genes for any mosquito and would later prove essential in identifying diverse non-target site mechanisms of insecticide resistance in this species^{29,30}.

Efforts to construct the first *A. gambiae* reference genome assembly identified extremely high levels of genetic variation. Nearly half a million SNPs were identified among mosquitoes sequenced from pooled DNA, despite the fact that all mosquitoes were derived from a single captive colony²⁵. This mosquito colony (known as the PEST colony) was founded as a hybrid population of two cytological forms, Mopti and Savanna, which were later distinguished as the sibling species *A. gambiae sensu stricto* and *Anopheles coluzzii*, respectively³¹, which are both part of a species complex that now includes at least eight members³². The admixture of these two highly polymorphic sister species in this initial

a A phylogenetic tree of *Plasmodium* parasites



b A phylogenetic tree of *Anopheles* mosquitoes



◀ **Fig. 2 | Genome assemblies for *Plasmodium* parasites and *Anopheles* mosquitoes.** Malaria is a disease caused by various parasite species hailing from diverse subgenera and groups of the ancient and polyphyletic *Plasmodium* genus (order Haemosporida). *Plasmodium* parasites are transmitted by different anopheline mosquito vectors, which last shared a common ancestor approximately 100 million years ago (mya)⁴⁰. Numbers in parentheses following subgenus or group labels indicate the approximate number of formally described parasite or mosquito species in each lineage. Reference genome assemblies exist for all species except where indicated. **a** | A phylogenetic tree of *Plasmodium* parasites, with topology informed by Galen et al.¹⁷² and Otto et al.³. The common ancestor of mammal-infecting members of *Plasmodium* is estimated to have existed less than 60 mya, as bats are hypothesized to be the ancestral mammalian hosts and this is the estimated date of the Chiroptera radiation¹⁷³. Species that infect humans are in bold. **b** | A phylogenetic tree of *Anopheles* mosquitoes with reference to available genomic resources. Topology informed by Foster et al.¹⁷⁴ and Neafsey et al.⁴². Reference genome assemblies are lacking for *Kerteszia* and other subgenera from the Americas, limiting comparative genomic opportunities to understand vectorial capacity and genomic investigations of insecticide resistance in many vector lineages. PNG, Papua New Guinea; ss, *sensu stricto*.

reference assembly project helped to inspire many subsequent studies to distinguish intra-species diversity¹⁸ from genomic divergence between morphologically identical cryptic species^{32–36}. These studies yielded the first genomic perspective on the tendency of *Anopheles* mosquito species to rapidly radiate into new taxa, which has been of great interest to biologists studying speciation. As the presence of cryptic species has confounded efforts to measure insecticide resistance phenotypically and genotypically for more than half a century^{37–39}, the genomic delineation of morphologically identical species has immense value for disease control.

Reference assemblies for *P. falciparum* and *A. gambiae* were just the first steps towards malaria population genomics. Although malaria is referred to as a single disease, the term encompasses infections caused by a range of parasite species that are transmitted by at least 40 species of *Anopheles* mosquito. Many of these are not closely related sister species within their respective haemosporidian parasite and anopheline mosquito clades (FIG. 2). The diverse evolutionary lineages of the anophelines that transmit malaria diverged approximately 100 million years ago⁴⁰ as the continents were separating from each other; similarly, the *Plasmodium* parasite species that infect humans belong to divergent branches of an ancient and polyphyletic genus that comprises species that infect a broad range of primates, rodents, birds, reptiles and ungulates. The deep divergence of parasite and vector lineages makes it difficult to generalize biological knowledge about many aspects of the disease and necessitates the genomic study of its diverse agents. Reference assemblies for many malaria parasites and anopheline mosquito vectors other than *P. falciparum* and *A. gambiae* have been described since 2002 (REFS^{3,41–45}) (FIG. 2). However, deep explorations of population genomic diversity have not yet been commonly conducted for species other than *P. falciparum*, *P. vivax* and *A. gambiae/A. coluzzii*.

In the past decade, advances in malaria genomics have been driven largely by the advent of high-throughput next generation sequencing (NGS) and the use of the reference genomes described above to analyse short reads produced by this approach. The increase in throughput afforded by NGS has expanded malaria genomics

applications to include large-scale data sets capturing parasite and vector genetic diversity in natural populations around the world^{21,29,46,47}, allowing for new strategies in identifying and tracking drug and insecticide resistance markers^{48,49} and new approaches to improve our understanding of malaria epidemiology.

Challenges in generating genomic data

Several technical challenges must be addressed before large-scale parasite and vector sequencing can realize its full potential⁵⁰. These challenges include procuring high-quality DNA from parasite and mosquito samples, and contending with the high degree of heterozygosity in vector genomes. Finding solutions to these challenges has been a major focus of innovation in the malaria genomics community and some practical solutions have emerged. We detail some of these challenges and innovations below.

Isolation of parasite DNA

The primary obstacle to producing high-quality parasite genomic data at scale has been obtaining sufficient parasite DNA for sequencing, in part owing to host DNA contamination. In a typical blood sample from a malaria-infected individual there is commonly at least 1,000-fold less parasite DNA than human DNA owing to the disparity in genome size between the host and parasite and a typically low level of parasitaemia. The highly A/T-rich (81%) genome of *P. falciparum*¹⁵ further exacerbates sequencing coverage issues in clinical samples for this parasite species, as many sequencing library construction methods are biased against incorporation of highly A/T-rich DNA fragments⁵¹. It is therefore often a costly and inefficient exercise to simply sequence total DNA from infected blood samples to obtain parasite genomic data.

In vitro cultivation of *Plasmodium* species, including *P. falciparum*, can facilitate access to pure parasite DNA⁵². However, in vitro parasite culture is laborious and risks introducing artefacts into the genetic diversity profile from the original natural infection as mutations can be selected for by growth under in vitro culture conditions⁵³. Furthermore, other parasites that infect humans, such as *P. vivax*, *Plasmodium malariae* and *Plasmodium ovale* have proved difficult to adapt to in vitro culture⁵⁴.

The development of methods for obtaining enriched parasite DNA from infected blood samples without the need for in vitro culture has been driven by the increased capacity of NGS for profiling population samples. These methods include column-based host leukocyte depletion prior to DNA extraction⁵⁵, hybrid selection of extracted DNA using oligos complementary to the parasite genome^{56,57} and selective whole-genome amplification (SWGA) of extracted DNA using priming oligos specific to the parasite genome^{58–60}. Practically, hybrid selection and SWGA enable the sequencing of blood spots from finger prick samples and avoid the need for the high-volume venous blood collections required for leukocyte depletion, better facilitating sampling for population genomic studies. SWGA has now been widely implemented, although it does not produce spatially uniform sequencing coverage across parasite genomes or usable depths of sequencing coverage from samples with degraded DNA^{9,61,62}.

Obtaining high-grade vector DNA

Many key vector species lack reference genome assemblies, which is a barrier to the application of population genomic approaches to malaria in many regions of the world. High-quality reference assemblies are needed for many secondary (or locally primary) vector species in Africa, including *Anopheles moucheti* and *Anopheles nili*⁶³. In Latin America, Southeast Asia and the Southwest Pacific, many primary and secondary malaria vectors lack high-quality reference genome assemblies and indeed may not be recognized taxonomically^{64–68}. The key to good mosquito assemblies, whether sequencing data are based on short or long reads, is high molecular weight DNA. The most effective method for preserving mosquitoes in order to keep high molecular weight DNA intact for sequencing involves flash freezing them in liquid nitrogen and shipping them on dry ice if sequencing facilities are not locally available. However, liquid nitrogen is not available in many settings and international dry ice shipments are expensive and logistically complex. Until sequencing capacity becomes further decentralized, simple and cost-effective means to preserve high molecular weight DNA in mosquitoes are needed to facilitate sample collection in regions without access to these specialized resources.

Addressing vector heterozygosity

As mentioned above, producing reference genomes for *Anopheles* mosquitoes has been hampered by the high degree of heterozygosity in *Anopheles* genomes. A recent effort to characterize diversity in 765 wild *A. gambiae sensu stricto* and *A. coluzzii* mosquitoes caught at numerous collection sites in Africa identified more than 52 million SNPs in the 141 Mb region of the genome most accessible to accurate variant calling — a rate of one variant allele every 2.2 nucleotides²⁹. This degree of heterozygosity is striking among eukaryotes and presents a challenge for genome assembly algorithms that are geared towards the much lower levels of heterozygosity typical of humans and other vertebrates. The separate assembly of maternal and paternal haplotypes into distinct haplotigs can occur when divergence between similar assembly fragments is mistakenly inferred to represent paralogy (duplication) rather than heterozygosity and if not recognized can inflate the size of a haploid reference assembly. However, haplotype-aware graph-based assembly algorithms have improved tolerance of heterozygosity and are being applied to new anopheline assembly projects^{69,70}. Further, the DNA input requirements for long-read sequencing have become smaller in recent years, enabling long-read sequencing libraries to be made from a single mosquito instead of a pool of mosquitoes, reducing genetic variation in the sequencing template⁷¹.

Using malaria population genomic data

The creation of reference assemblies and polymorphism data sets for malaria parasites and vectors has improved our understanding of diverse aspects of malaria biology over the past 15 years, and genomic data from

natural populations could inform control and elimination strategies. We feature some uses of such data sets below.

Characterizing genomic diversity

Genomic variation has been characterized in various ways in parasites and vectors. ‘Pre-genomic’ approaches developed before reference genome assemblies were available, such as microsatellites⁷² and allele-specific PCR⁷³ with agarose gel profiling of PCR amplicon size polymorphisms⁷⁴, continue to find use owing to their simplicity and low cost. Post-genomic approaches include small SNP genotyping panels^{75–78}, large SNP genotyping arrays^{23,79}, targeted sequencing of amplicons^{80–84} or molecular inversion probes (MIPs)⁸⁵ and shotgun whole-genome sequencing (WGS). These approaches^{46,86–88} are summarized in BOX 1.

Large-scale resequencing studies identifying SNPs across the genomes of *P. falciparum* and *P. vivax* in blood samples from around the world have shown clear population structure within and between countries and continents^{19,21,46,47,88}. The extent and nature of parasite genomic diversity reflects prehistoric transmission levels, human and parasite movement during the colonial era and population bottlenecks caused by control efforts in the last century^{21,46,47,50,88,89}. Similar efforts characterizing the genetic diversity of malaria vectors across Africa — primarily *A. gambiae* and *A. coluzzii* — revealed incredible population diversity and structure across the continent²⁹. Such resequencing studies provide a framework for the development of geographically targeted genotyping panels where WGS is not feasible. Key applications of these large-scale catalogues of diversity are described below.

Identification and monitoring of parasite drug resistance loci. Malaria parasites have evolved resistance to all widely deployed antimalarial drugs⁹⁰. In some cases, resistance has spread globally, whereas for other compounds it remains rare and patchily distributed. Retrospective genomic resistance surveillance can inform understanding of how drug resistance emerges, long after the opportunity to directly measure patient phenotypes has passed and with greater resolution than individual locus-based surveys⁹¹. Prospective genomic surveillance can identify signatures of emerging drug resistance in the form of selective sweeps even before specific resistance loci are identified⁹². Parasite resistance to chloroquine helped to undermine the WHO Global Malaria Elimination Campaign of 1955–1969 (REF.⁹³). In 2000, the gene primarily responsible for mediating chloroquine resistance, *pfprt* — which encodes an ATP-binding cassette transporter — was identified in parasites⁹⁴. Subsequent resistance surveillance efforts revealed that resistance to chloroquine spread around the globe after arising de novo in Southeast Asia and South America⁹⁵. Resistance to sulfadoxine/pyrimethamine⁷² — the successor to chloroquine as a first-line therapy — also emerged first in Southeast Asia and South America and was transported to Africa before the genes associated with resistance (dihydrofolate reductase, *pdhfr*, and dihydropteroate synthase, *pfahps*) could be discovered⁹⁶.

Haplotigs

Units of a genome assembly constructed from overlapping sequencing reads but representing separate homologous haplotypes from the same genomic region in a diploid sequencing template.

Population structure

Deviation from a single randomly mating population owing to demographic, geographical and/or evolutionary factors.

Box 1 | Generating population genomic data in *Plasmodium* and *Anopheles*

In addition to whole-genome sequencing, multiple other technologies are used for targeted sequencing or genotyping of parasites and vectors.

***m*sp/*glurp* genotyping**

Nested PCR assays have been used to detect polymorphisms in the genes *m*sp1 and *m*sp2, which encode highly polymorphic *Plasmodium falciparum* merozoite surface proteins 1 and 2 and the gene *glurp* encoding glutamate-rich protein. Common applications include estimation of complexity of infection in population genetic studies and to distinguish recrudescence from new infections in therapeutic efficacy studies^{73,74}. Although these methods are straightforward and inexpensive, they provide lower resolution than sequencing approaches.

Microsatellite genotyping

A staple genotyping approach for diverse organisms, including *Plasmodium* and *Anopheles*, particularly in the pre-genomic era^{143,176}. Amplification and sequencing or gel-based characterization of tandem repeats exhibiting length polymorphism gives a readout of allele length, with a high per-locus count of genetic variants. Imprecision in allele length estimation can complicate interpretation and limits the scalability of microsatellite marker panels. Microsatellites were used to identify the intercontinental spread of *P. falciparum* antimalarial drug resistance alleles from Asia to Africa⁷² and more recently, across the eastern Greater Mekong Subregion^{177,178}.

SNP genotyping

Diverse technologies exist for genotyping single nucleotide polymorphism (SNP) loci previously discovered through whole-genome sequencing. The malaria genomics field has employed approaches including Sequenom/Agema, Taqman and high-resolution melting curves for genotyping single biallelic SNPs in large numbers of parasite or vector samples¹⁷⁹. SNP genotyping is inexpensive at scale but requires specialized instrumentation. SNP genotyping microarrays first gave insight into the chromosomal architecture of speciation between *Anopheles gambiae* and *Anopheles coluzzii*¹⁷¹.

PCR amplicon sequencing

Next-generation sequencing (NGS) of short PCR amplicons (100–300 bp) has been used in the malaria genomics field for multiplexed and multiplexed PCRs to genotype single variants and characterize ‘microhaplotypes’ of multiple linked variants^{82,85}. If amplicons are targeted to short windows exhibiting a high density of SNPs, allelic richness at the haplotype level can be high, even if component SNPs are merely biallelic. Amplicon sequencing of highly haplotypically diverse antigens has provided insight into complex infections⁸² and vaccine efficacy¹²², and has been applied for surveillance of known and novel alleles at drug resistance loci^{180,181}.

Capture/hybridization-based sequencing

Hybrid capture of the whole parasite genome has been used to perform selective sequencing of parasite DNA in clinical samples dominated by host DNA^{56,57} and may be employed for targeted sequencing of informative marker panels within parasite and vector genomes. Molecular inversion probes (MIPs) have been applied to capture, amplify and sequence thousands of short targets (100–150 bp) in parasite genomes. MIP capture and sequencing are well-suited for targeted sequencing of more genomic regions than multiplexed amplicon sequencing, but are less sensitive. MIPs recently provided a detailed profile of drug resistance allele prevalence and *P. falciparum* population connectivity in the Democratic Republic of the Congo¹⁸².

Resistance has recently arisen to artemisinin^{97,98}, the current first-line therapy (in combination with various partner drugs) for *P. falciparum* malaria in much of the world. In vitro resistance selection and WGS of a parasite line showing reduced in vitro susceptibility to artemisinin led to the identification of molecular markers for artemisinin resistance⁹⁹. Mutations in the propeller domain of the Kelch domain-containing protein PfK13 (encoded by a gene on chromosome 13, *pfkelch13*) and especially a C580Y mutation in that domain have been corroborated as agents of reduced susceptibility to artemisinin. Genomic evidence for this association has arisen from allelic replacement studies¹⁰⁰, genome-wide association studies^{48,101}, linkage group selection experiments¹⁰² and selection scans^{92,103,104}. Global genomic

surveillance is ongoing for *pfkelch13* mutations and for epistatic or fitness-compensating mutations at loci elsewhere in the *P. falciparum* genome, including resistance mutations for partner drugs used in combination therapy¹⁰⁵. Although *pfkelch13* mutations have been confirmed to occur de novo in geographical locations outside their first origin in the Greater Mekong Subregion (GMS)^{61,62,106,107}, surveillance has shown that they are still rare in sub-Saharan Africa, South America and New Guinea, raising the hope that retrospective⁹¹ and current genomic surveillance efforts^{85,88,108,109} could limit the global spread of resistance to artemisinin-based combination therapies by guiding locally effective treatment policies informing resistance management efforts. For example, given that population genomics has demonstrated that the emergence of the *pfkelch13*^{C580Y} allele both inside and outside the GMS has been driven by dozens of recurrent de novo mutations^{61,62,91,104,106}, a strategy of resistance containment in the GMS without balanced resistance surveillance efforts elsewhere may not be viable over the long term^{110–112}.

Identification and monitoring of mosquito insecticide resistance loci. Population genomics has the potential to enable evidence-based management of insecticide resistance in mosquito vectors¹¹³. The majority of progress in reducing malaria mortality during the past 20 years is attributable to vector control¹¹⁴, and anopheline mosquitoes have collectively evolved resistance to all four of the chemical classes of insecticide currently used for control at the adult stage, namely pyrethroids, organochlorines, carbamates and organophosphates¹¹³. Mutations in genes encoding the binding targets of insecticides were discovered early on using PCR at loci known to confer resistance in agricultural pests: knockdown of *vgsc*, a gene encoding a voltage-gated sodium channel, conferred resistance to pyrethroids and organochlorine insecticides such as DDT²⁷, whereas knockdown of the acetylcholinesterase gene *ace1* conferred resistance to carbamates and organophosphate compounds^{28,115}.

Whole-genome-based approaches have revealed a fascinating array of resistance mechanisms outside of insecticide binding targets, including metabolic resistance encoded by mutations in or upregulation of cytochrome P450 genes and glutathione *S*-transferase (GST) genes¹¹⁶; barrier resistance through modification of the thickness or properties of the insect cuticle¹¹⁷; behavioural resistance — for example, avoidance of insecticide-treated nets or walls — and other more specific mechanisms, such as the overexpression of a sensory appendage protein (SAP2) that binds with high affinity to pyrethroids¹¹⁸. Population genomic data have revealed how diverse adaptations have been achieved through SNPs and gene duplications and other structural variations³⁰ and how such mutations have introgressed among closely related species in different locales²⁹. For example, copy number variants occur in all five of the major clusters of *A. gambiae* gene families associated with metabolic resistance, with high population frequencies and haplotypic structure suggesting that they have been spread by positive selection³⁰. This observation

refutes the notion that resistance is diagnosable by simple genotyping of SNPs in target genes and suggests that WGS and improved bioinformatic methods for copy number variant detection will be invaluable in tracking insecticide resistance³⁰.

Aiding vaccine development. Population genomic approaches have shown that parasite antigenic diversity plays a role in reducing vaccine efficacy¹¹⁹. Development efforts began for many candidate *P. falciparum* vaccines during the pre-genomic era, when the immunogenicity of parasite targets had been measured but not their diversity. Although *P. falciparum* exhibits moderate genomic diversity overall, many of the genes encoding the antigens that have been the focus of most malaria vaccine development efforts, such as those for circumsporozoite protein (CS), apical membrane antigen 1 (AMA1) and thrombospondin-related adhesion protein (TRAP), exhibit extremely high polymorphism (FIG. 3). Most monovalent peptide vaccines based on these antigens have shown limited-to-moderate efficacy in clinical trials to date, in part because they have targeted a single parasite allele and have elicited imperfect cross-protective immunity to other parasite alleles¹²⁰. In a phase II trial of a monovalent peptide vaccine targeting the AMA1 protein of *P. falciparum*, overall efficacy was observed to be 20%, whereas efficacy against

infections by parasites with an allele matching the vaccine allele was 64%¹²¹. Similarly, in a phase III trial of RTS,S/AS01 — the first and only malaria vaccine to be licensed — vaccine efficacy against infections by parasites with an allele matching the vaccine construct at the *P. falciparum* CS protein was 50%, compared with 33% for infections by parasites with a non-matching allele¹²². It is presumed that this high degree of diversity in these genes has been maintained through parasite population bottlenecks or has been subsequently restored through immune-mediated balancing selection, driven by highly allele-specific immune protection¹²³.

Population genomics will play an important role in future vaccine development efforts by mapping differences in vaccine target polymorphism profiles across populations and identifying immunogenic protein targets that are not highly polymorphic in any geographical region. Interestingly, several targets of so-called transmission-blocking vaccines (P230, P25 and P48/45), which do not aim to protect the recipient but instead to reduce the likelihood of onward transmission¹²⁴, show low levels of diversity relative to most targets of infection-inhibiting vaccines in parasite populations (FIG. 3), perhaps owing to reduced selection by natural immunity. In addition, the *P. falciparum* reticulocyte binding protein homologue 5 (RH5) protein plays an important role in red blood cell invasion, and population

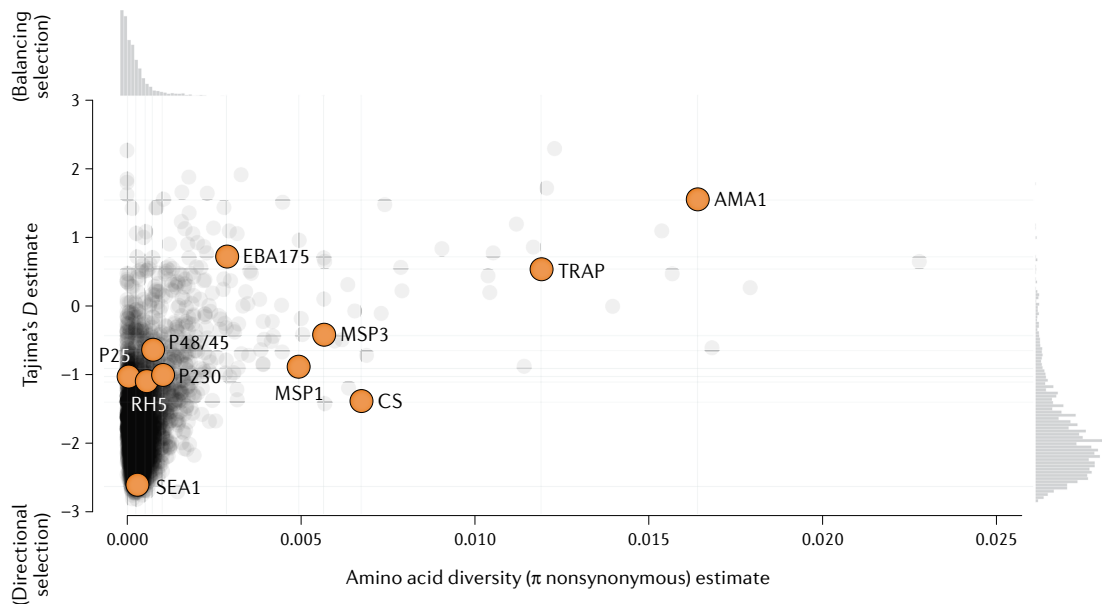


Fig. 3 | Population diversity estimates and evidence of immune-mediated balancing selection in *Plasmodium falciparum* vaccine targets. Many monovalent protein subunit vaccine development efforts began before the extensive diversity of many blood-stage and liver-stage antigens was appreciated. Each dot represents a *P. falciparum* protein; semi-transparent grey dots indicate proteins not targeted by vaccines, opaque orange dots indicate protein targets of vaccines registered for clinical trials at [ClinicalTrials.gov](https://clinicaltrials.gov) since 2000 (REF.¹⁷⁵). The horizontal axis indicates estimates of mean amino acid nonsynonymous pairwise diversity, π . The vertical axis depicts estimates of Tajima's *D*, a neutrality statistic based on the variant site frequency spectrum, where negative values represent an excess of low-frequency variants and positive values represent an excess of high-frequency variants, which can indicate balancing selection. Estimates were computed using a collection of sequenced *P. falciparum* parasites from Malawi in the [Pf3k resource](#). Compared with non-vaccine candidates, vaccine candidates generally exhibit a higher level of diversity (Wilcoxon rank sum test, $W=8322.5$, $P=0.0001$) and show evidence of balancing selection (Wilcoxon rank sum test, $W=8967$, $P=0.0002$). The newer, post-genomic blood-stage vaccine target RH5 exhibits considerably less diversity, as do several targets of transmission-blocking vaccines (P230, P25 and P48/45).

genomic data show that it exhibits low diversity in parasite populations¹²⁵, indicating that a vaccine targeting RH5 may avoid issues with allele-specific protection. Antibodies raised to RH5 have been found to have strong inhibitory activity against *P. falciparum*¹²⁶. Similarly, a monoclonal antibody that binds to an epitope in the *P. falciparum* CS protein that lies near the junction between the N-terminal region of the protein and a repetitive region has been shown to protect against infection¹²⁷. This epitope exhibits very low diversity in parasite populations, which has fuelled efforts to evaluate protection conferred by antibodies targeting this region¹²⁸.

Understanding infection and transmission

Understanding transmission intensity and dynamics has historically relied on conventional measures such as case incidence and prevalence, and information from patient travel histories. While these data are crucial, genomic data from parasites in natural populations have the potential to improve understanding of malaria transmission and guide strategies to control it^{10,11}, and further research is needed to understand the nature, generalizability and utility of genomic signatures as indicators of transmission intensity.

Although malaria parasites are haploid single-celled organisms — apart from a brief diploid stage in the mosquito — populations of malaria parasites may exhibit considerable genomic heterogeneity within single human and mosquito hosts and this heterogeneity can provide insight into the nature and intensity of disease transmission. Efforts to study parasite genomic variation within mosquitoes at drug resistance markers and other loci of interest are in their early stages^{129,130}; however, the diversity of parasites within human hosts has been well characterized using microsatellite and *msp/giurp* genotyping in the pre-genomic era and, in recent years, using NGS of PCR amplicons and single-cell WGS. Deep sequencing of PCR amplicons using NGS allows sensitive characterization of parasite genetic diversity within the host; this is especially effective when the amplicons target regions with high haplotypic diversity, as it is unlikely that distinct parasites within a host will harbour the same sequence at the target region^{80–83}.

An investigation of declining local transmission in the Thailand–Myanmar border region found that the strongest genetic signal associated with transmission decline was loss of parasite genetic diversity within hosts, as measured by a decline in the proportion of complex infections¹³¹ — suggesting that this measure could be a proxy for local transmission intensity¹³². Complex infections are infections that contain parasites with more than one distinct genomic sequence, where the number of distinct genomic sequences is the complexity of infection (COI). Complex infections may result from separate mosquito bites in a process called superinfection and/or from a single mosquito bite in a process called co-transmission (FIG. 4). Ascertaining levels of transmission intensity from COI estimates requires assumptions about how new complex infections are founded. Genetically distinct parasites may be related (share some recent common ancestry) or unrelated.

As superinfection is expected to be more frequent in high-transmission settings where there is typically a large diversity of parasites, parasites transmitted in different bites are likely to be unrelated. Meanwhile, genetically distinct parasites that are co-transmitted are more likely to be related than unrelated because there are many ways of sampling genetically distinct human-infective sporozoites following recombination between one or more gamete pairs in a single mosquito, yet unrelated sporozoites can be sampled only if two or more unrelated gamete pairs have selfed.

Both co-transmission and superinfection events can be experienced by a single host, thereby giving rise to complex infections with both genetically related and unrelated parasites. Until recently, co-transmission was considered unlikely to account for most complex infections. This is because, with each infectious bite, various bottlenecks reduce the number of surviving parasites and thus the number of distinct genomic sequences among the surviving parasites. For example, mosquitoes typically inject only 10–100 sporozoite-stage parasites per bite¹³³. As few as 20% of these sporozoites may exit the dermal inoculation site¹³⁴ and only a small fraction of these are likely to avoid clearance by the spleen and immune responses to successfully infect the liver and establish a blood-stage infection¹³⁵. However, recent studies using single-cell WGS of parasite-infected host red blood cells suggest that serial co-transmission of parasites may be common^{136–138}. Profiling of parasite genomes from hundreds of single parasite-infected cells identified levels of recent common ancestry and recombination among parasites within hosts that are considered too high to be explained by superinfection alone, indicating multiple rounds of co-transmission of related parasite lineages between hosts^{136–138} and raising questions about whether new infections are typically founded by more sporozoites than previously assumed. Single-cell sequencing studies of parasite genomic diversity at the sporozoite stage within mosquito salivary glands are needed to investigate whether malaria infections are founded by a larger inoculum of parasites than previously thought.

Enabling genomics for malaria control

Several applications for malaria genomic data involve spatially differentiating parasite populations based on their genetic profile¹³⁹. The distinct genomic signatures of parasites allow investigation of the connections between parasite populations to identify previously unappreciated sources and sinks of infections and to assess whether cases in low-transmission areas are caused by local transmission or importation — scenarios that demand distinct intervention strategies and the differentiation of which has implications for achieving or maintaining official malaria elimination status. Meaningful implementation of malaria genomics approaches for public health will require careful consideration of the current operational challenges¹⁴⁰, including sustainable data generation and analysis capacity, harmonization of data and analysis approaches among localities, reagent supply chains, timelines and cost, and the practical value of the information itself.

Complexity of infection (COI). The number of distinct genomic sequences that describe malaria parasites simultaneously infecting a vertebrate host.

Superinfection
The separate transfer of genetically distinct parasites to a vertebrate host over multiple mosquito bites.

Co-transmission
The simultaneous transfer of genetically distinct parasites to a vertebrate host through a single mosquito bite.

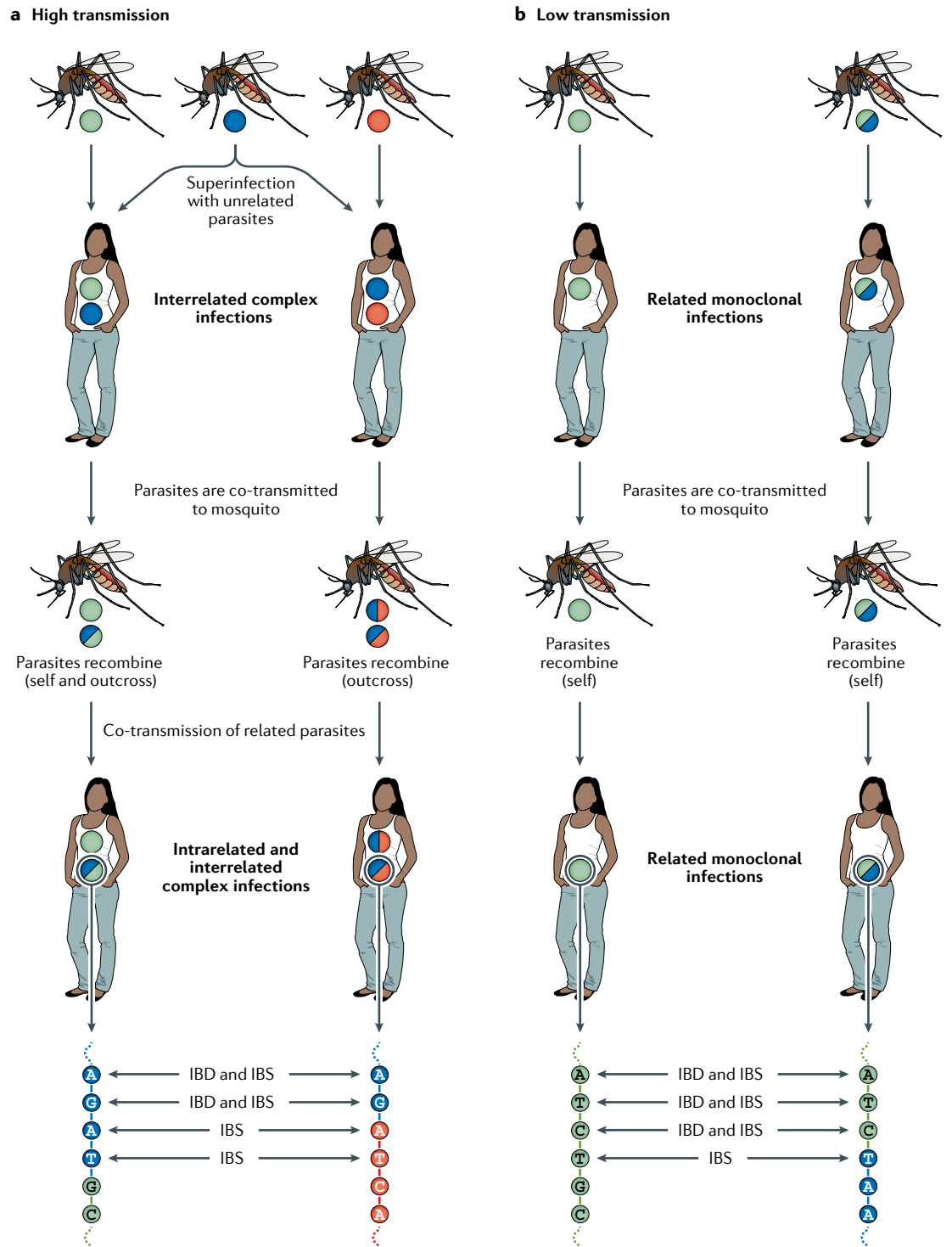


Fig. 4 | **Complex infections, parasite mating and identity by descent.** Complex infections result from multiple mosquito bites (superinfection) and/or from a single mosquito bite (co-transmission). Recombination between genetically distinct malaria parasites can occur after a mosquito feeds on a host with a complex infection; otherwise, reproduction occurs by selfing. Genomic data may be used to observe loci that share the same allele (identical by state (IBS)) and to infer loci that are descended from a recent common ancestor (identical by descent (IBD)). **a** | High transmission, showing three mosquitoes, each infected with parasites from a single lineage, founding interrelated complex infections in two individuals through superinfection. Gametocytes that develop within these complex infections are imbibed by mosquitoes in which they subsequently recombine. Two illustrative scenarios are shown: one in which both selfing and outcrossing occurs, another in which only outcrossing occurs. These mosquitoes founded intra- and interrelated complex infections in two subsequent individuals, this time through co-transmission. **b** | Low transmission, showing the clonal propagation of two distinct but related parasite genomic sequences following selfing in the mosquito. Each circle represents one or more parasites that share the same genomic sequence. Different circles represent distinct genomic sequences; different colours represent different genetic lineages.

π
Describes the mean pairwise genetic difference rate between isolates within a sample; often used as a proxy of effective population size, with larger populations having higher diversity.

Fixation index
(F_{ST}). A commonly used statistic in population genetics, describing genetic differentiation between populations, which may be defined in various ways, including as a function of the variance in allele frequencies between populations.

Identical by descent
(IBD). A descriptor of individuals, chromosomal segments or alleles that are descended from a recent common ancestor; identity by descent is a latent state the probability of which can be inferred under a statistical model or deduced from a pedigree.

Data generation

The capacity to generate and analyse local or regional data will be key to the sustainability of applied malaria genomic epidemiology and to ensure efforts are responsive to local context and needs. Efforts to establish genomic surveillance within malaria-endemic countries are increasing rapidly as data generation technologies advance and sequencing costs have fallen¹⁴¹. There is an emerging consensus that decentralized data generation capacity within malaria-affected countries or in regional hub labs will enable customization of approaches to local questions and capacities, faster turnaround and closer integration with existing malaria control efforts. Several successful demonstrations of the viability of this model exist at individual institutions, and momentum is building through continent-wide endeavours such as the Africa CDC's Pathogen Genomic Intelligence initiative and grassroots collaborative organizations such as the Plasmodium Diversity Network Africa (PDNA)^{50,88}.

Although sequencing costs have fallen markedly over the past two decades, large-scale WGS of parasite and vector samples for surveillance purposes is still impractical in many settings. The additional cost and technical challenge associated with the storage and processing of WGS data relative to targeted genotyping panels are likely to result in a reduced return on investment in a decentralized data generation system^{50,109}. WGS is essential for identifying new genetic variants relevant for surveillance and validating genomic methodological advancements; however, the research community has been actively evaluating the potential role of targeted sequencing and genotyping approaches to recover the most informative genomic regions for malaria genomic epidemiology^{9,140,142}. On the basis of this work, we suggest that for some applications, deep (1,000×) sequencing coverage of small genomic windows — comprising the most informative 20 kb of malaria parasite genomes, such as highly diverse regions and known markers of interest — could be equally or more operationally useful than 100× sequencing coverage of the whole 23–27 Mb parasite genome and require 100-fold lower net data production per sample. Given that the malaria vector genome is tenfold larger than the parasite genome, there is even greater incentive for targeted sequencing for mosquitoes. Evaluation of which approaches are best suited to in-country use must consider the questions being addressed, the cost and maintenance requirements of instruments and reagents, interpretation of the resulting data and the direct value of the resulting data for informing actionable decisions regarding disease control.

Data analysis

The proliferation of sequencing and genotyping approaches and the decentralization of data generation serve the needs of diverse users and applications but complicate the issue of data interoperability between different research and public health efforts. Descriptive statistics that summarize allele frequency variation within populations or across populations vary with data type, as different categories of polymorphism, for example, SNPs and microsatellites, have mutation rates that

vary by 1,000-fold¹⁴³. As such, these widely used statistics, which include π — a measure of intra-population diversity¹⁴⁴ that is often used as a correlate of population size¹⁴⁵ — and the fixation index (F_{ST}) — a measure of inter-population differentiation¹⁴⁶ that is sometimes used as a correlate of gene flow¹⁴⁷ — are inappropriate for studies and meta-analyses that feature different input data types. Some convergence in methodology between data generators is likely, although as technology for generating genomic data for malaria epidemiology advances this could lead to further data interoperability issues over time, potentially impeding a longitudinal perspective on malaria even within geographical regions.

Relatedness-based analysis to bridge genomic data types.

Relatedness is a recombination-based measure of recent shared ancestry between two individuals¹⁴⁸. It is an example of a measure that can be compared across different categories of genotypic polymorphism. Although it is not possible to estimate relatedness between samples of different data types, it might be possible to leverage the transitive nature of relatedness and/or the nested nature of some data types, such as SNP barcodes within WGS data, to compare some samples across disparate data sets — an opportunity for future research.

Relatedness is a useful measure for malaria genomic epidemiology because it is recombination based. Unlike π and F_{ST} , which reflect variability in allele frequencies, relatedness is broken down by outcrossing recombination, ranging from one for identical clones to zero for completely unrelated organisms. For a pair of haploid malaria parasites, relatedness is defined as the probability that, at any given locus on the genome, the two alleles are identical by descent (IBD)¹⁴⁹. For diploid mosquito vectors, there are numerous relatedness measures depending on the pattern of IBD among the four alleles at any locus¹⁵⁰. Alleles are IBD if descended from a recent common ancestor in some ancestral population; identity by descent can also be defined in terms of chromosomal segments, descended intact, unbroken by recombination, from a recent common ancestor¹⁵¹. IBD segments can be used to detect regions of the genome under selection by drugs or other unknown agents^{88,89,91,152}. Based on their length, they can also be used for telling closely related and outbred pairs apart from more distantly related but inbred pairs with the same relatedness, although there is a wide distribution of lengths among recent generations¹⁵³. However, IBD segment inference does not solve the issue of achieving commensurate inferences between data types as segment inference specifically requires WGS data¹⁴⁹, whereas relatedness may be inferred under a statistical model using more modest data^{152,154} (FIG. 5).

Relatedness estimates based on different data types are comparable to each other and can facilitate direct comparisons of distinct studies, provided that measurements of uncertainty are used to account for variations in informativeness across different data types. Observations of high relatedness should be interpreted differently for populations with different rates of inbreeding and selfing, however, as high relatedness is intuitively less likely to imply recent shared ancestry

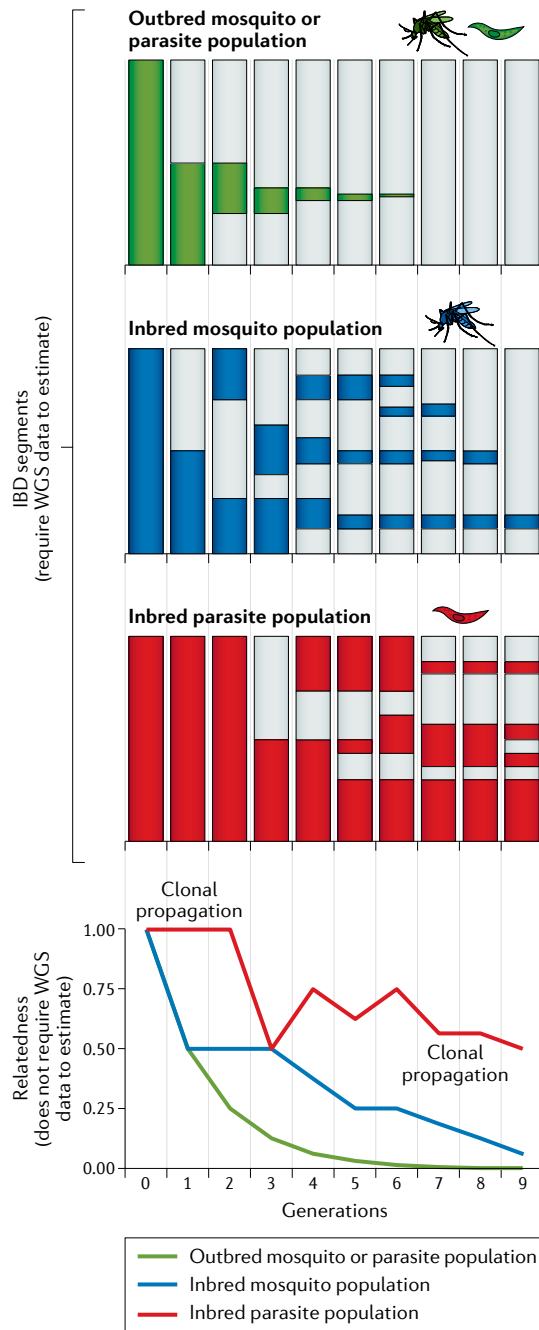


Fig. 5 | The decline of identity by descent over time in outbred and inbred populations. An illustrative example of how recombination over successive generations breaks down chromosomal segments of identity by descent (IBD segments) and decreases relatedness (probability of IBD). IBD segments, used in various applications including selection detection, require whole-genome sequencing (WGS) data to estimate, whereas relatedness values, used in applications including population connectivity characterization, do not require WGS data to estimate. The top three panels show the breakdown of IBD segments over generations when a mosquito or parasite from one population migrates into mosquitoes or parasites from another population. Vertical bars represent chromosomal genomic sequence of an individual (mosquito or parasite) sampled in the receiving population. IBD between the original migrant and the sampled individual is represented by coloured fill. Light grey represents sequence that is not IBD. Generation zero represents a comparison between the original migrant and itself. Thereafter, we show IBD between the migrant and its closest relative. Segments of IBD break down over successive generations; breakdown depends on the opportunity for outcrossing, which is limited in inbred populations, especially parasite populations, because parasites intermittently self. For each of the situations described in the top three panels, the bottom panel shows the corresponding decrease in relatedness.

Where the outcrossing recombination rate is sufficiently high, IBD breaks down more rapidly than allele frequency variation accumulates and thus measures based on IBD, including relatedness, can be used to characterize changes in parasite or vector population demography more rapidly and at a higher spatial resolution than measures based on allele frequency variation such as π or F_{ST} (FIG. 6). In genomic epidemiology, the fast mutation rates of RNA viruses and other measurably evolving pathogens, which generally do not sexually recombine, are used in phylogenetic inference to study pathogen transmission¹⁵⁶. *Plasmodium* parasites exhibit SNP mutation rates typical of eukaryotes, on the order of 10^{-9} (REF.¹⁵⁷) to 10^{-10} (REF.¹⁵⁸) substitutions per site per generation. It is possible to infer malaria transmission networks over short timescales using sensitive sequencing and analysis techniques to capture rare de novo variants¹⁵⁹. However, this is not as practical for malaria as it is for viruses and bacteria¹⁵⁶ because of the slow mutation rate of *Plasmodium* parasites compared with these pathogens, because *Plasmodium* parasites sexually recombine — complicating phylogenetic inference — and because of insufficiently dense sampling of transmission chains in higher burden settings. As for allele frequency variations above, mutations do not occur quickly enough to allow differentiation of malaria parasite movements between populations separated by distance scales of tens of kilometres or timescales of months to years, whereas detection of relatedness between samples can allow population connectivity measurement at these spatiotemporal scales^{10,160} to delineate unconnected population units and rapidly inform disease elimination interventions.

Evidence of IBD between parasite samples has been observed to positively correlate with reductions in parasite transmission^{11,101}, and bottlenecks in vector

in inbred populations. High relatedness thresholds have been used to make informative contrasts between relatedness estimates within studies, and early efforts towards threshold-free approaches may help to make these summaries more commensurate across studies¹⁵⁵. It is important to note that, between two individuals, the fraction of markers that are identical by state (IBS) — those that share the same sequence — is a correlate of relatedness; however, IBS-based measures of relatedness do not account for differences in allele frequencies and thus are not commensurate across data types¹⁴⁹.

Applications of relatedness for malaria. Estimation and interpretation of relatedness between pairs of samples can be applied to multiple epidemiological use cases.

Identical by state (IBS). A descriptor of individuals, chromosomal segments or alleles that share the same genetic sequence; identity by state is a state that can be observed in genetic data.

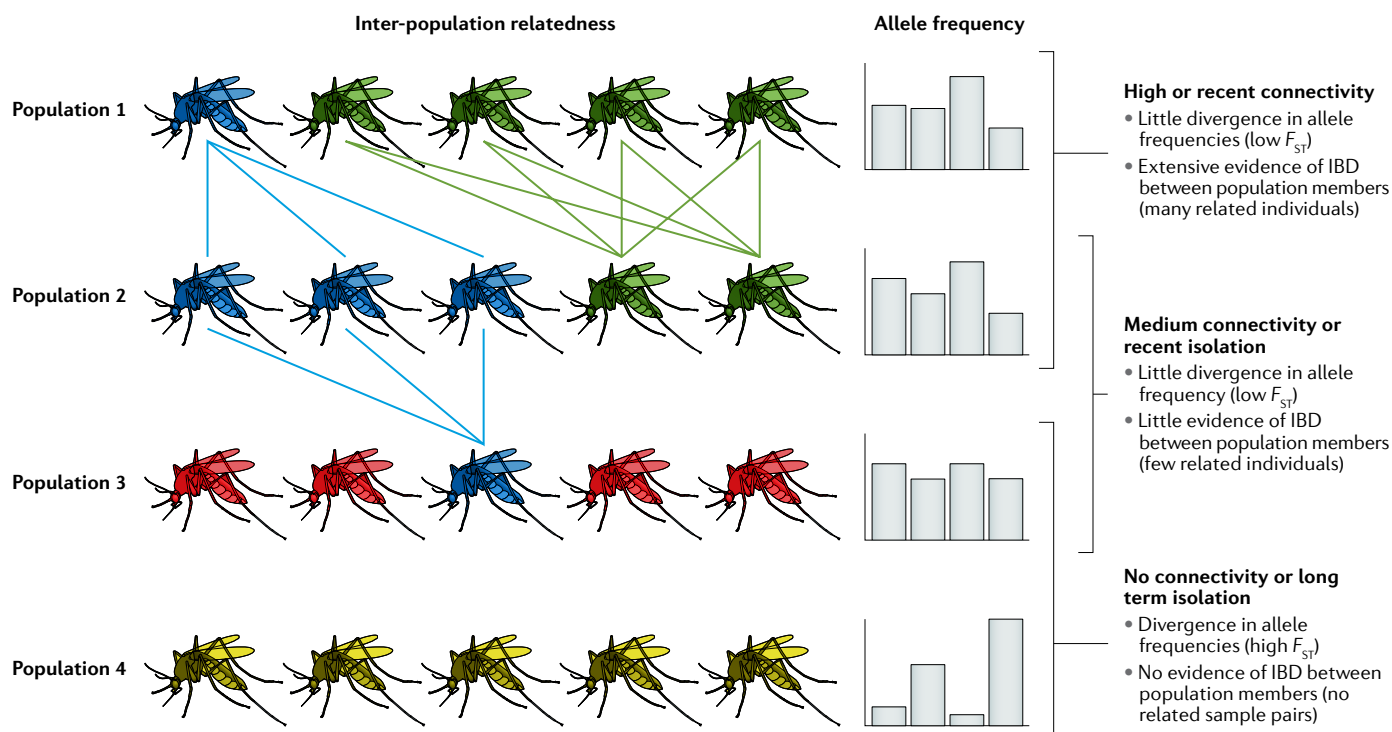


Fig. 6 | Measuring population connectivity using relatedness versus allele frequency variation. An illustrative example of how relatedness, a measure of the probability of identical by descent (IBD), may reveal connectivity between populations of mosquitoes on a timescale more relevant for epidemiological applications than allele frequency variation, using genetic differentiation, the fixation index (F_{ST}), as an example measure of allele frequency variation. Rows represent distinct mosquito populations. Mosquitoes represent individuals sampled, coloured by their dominant lineage, and edge connections indicate high relatedness and therefore high probability of IBD between pairs of mosquitoes across populations. Populations with a higher degree of connectivity are liable to share more

highly related edges. Variability in relatedness between populations may occur with or without appreciable inter-population variation in the allele frequency of genotyped markers. Allele frequencies are indicated by histograms, with vertical axes depicting allele frequencies and horizontal axes depicting markers. F_{ST} describes variation in allele frequency between populations, with poorly connected populations expected to exhibit more vicariant allele frequencies. Genetic drift, migration and/or selection generally take much more time to shift minor allele frequencies among isolated populations relative to recombination, which is expected to rapidly deplete relatedness providing that the rate of outcrossing is sufficiently high.

population size similarly induce inbreeding²⁹, indicating the utility of this feature as a metric for assessing changes in transmission intensity and vector population size. In the fields of fisheries and conservation biology, relatedness prevalence has long been used as a tool for estimating the abundance of a given species, for example, through the technique of close kin mark recapture^{161,162}. Although the life cycles of malaria parasites and anopheline mosquitoes differ in ways that require distinct interpretations of relatedness, the fundamental premise that related individuals are more likely to be co-sampled in smaller populations than larger ones makes this technique equally apt for both parasites and vectors. Relatedness inference has other applications that are beginning to be explored in the malaria context. For example, evidence of 100% relatedness associated with clones has been used to classify *P. falciparum* recurrences as either newly acquired or a product of treatment failure¹⁶³, and evidence of 50% relatedness associated with outcrossed siblings has been used to help classify *P. vivax* recurrences as liver-stage relapses¹⁶⁴. Finally, relatedness estimates can be subjected to downstream analyses, including various clustering algorithms and statistical models that can explicitly articulate hypotheses about malaria epidemiology¹⁶⁵.

Conclusions and perspectives

The malaria community is fortunate to have amassed a wealth of genomic data resources and analytical methods to support applications, from fundamental malaria biology to applied malaria control strategies. Many studies have shown the value of these resources for identifying markers and mechanisms of drug and insecticide resistance and for complementing traditional epidemiological disease indicators such as case counts, incidence and travel history with genomic data, in order to inform relative rates of local transmission against case importation, connectivity between populations and efficacy of parasite and vector interventions.

As the research community will undoubtedly continue to make genomic data more practical to generate and use in the fight against malaria, the next problem to solve will be how to manage all of the distributed data generation resulting from enhanced parasite and vector surveillance efforts taking place in disease-endemic countries. Three key gaps remain in realizing the potential of genomic epidemiology for real-world malaria control and elimination strategy: first, local experts should be able to carry out data generation, analysis and interpretation without extensive support from highly specialized and well-resourced institutions; second, to be of

practical value genomic information must be produced on operationally relevant timescales; and third, analysis across genomic data sets and integration with epidemiological metrics must be facilitated, by both encouraging interoperability between data sets and establishing networks between stakeholders.

Given current capacities for data generation and limitations in data computing, we anticipate that information from targeted approaches, such as PCR amplicon-based or MIP-based sequencing and SNP-based genotyping, will foreseeably form the basis of most data generation efforts within malaria-endemic countries as they remain viable to implement at scale in lower resource settings than WGS. Collaborating institutions can generate these data types to support countries and research partners and for research discovery purposes. In parallel, we anticipate that WGS data will continue to inform the understanding of global genetic diversity and dynamics on a genome-wide scale, and continuously improve the design strategy and data interpretation framework for targeted sequencing and genotyping approaches.

The potential value of using variation caused by recombination as a framework for interpreting malaria genomic data and informing disease intervention strategies, as opposed to using variation caused by mutation (as in the genomic epidemiology of measurably evolving pathogens) or variation in allele frequencies (as captured by π and F_{ST}), has already influenced the development of targeted sequencing approaches optimized for relatedness inference. For example, targeted resequencing efforts have begun to focus on closely clustered SNP variants that give rise to many diverse haplotypes¹⁴², so as to better inform relatedness inference¹⁴⁹. Additional

investment will be necessary at the level of analysis and visualization to further identify and exploit signals in malaria genomic data that are relevant to decisions in public health. Key to this effort will be methods to store, house and share data and to support analysis workflows across studies and surveillance efforts that generate epidemiological data^{10,166,167}. In addition to the NCBI Sequence Read Archive and the European Nucleotide Archive, the malaria field has long benefited from genomic data repositories for parasites (PlasmoDB)¹⁶⁸ and vectors (VectorBase)¹⁶⁹, which have recently merged into a common platform called **VEuPathDB**. These databases have provided invaluable curation of reference genome assemblies and annotations, integrated with functional and transcriptomic data to provide insight into the roles of genes. However, their primary audience has been researchers; the operationalization of genomic surveillance methods may require a distinct approach to the management, analysis and sharing of genomic data to serve stakeholders in the public health community.

Although there are many technical considerations to be addressed, perhaps the single biggest issue is data sharing. As a community we must aspire to a future of open data sharing for the benefit of global health while being sensitive to the complexities that prevent data from being shared and released. We must also support countries as they work to understand the risks and benefits of sharing genomic data, set policy for the future and be pragmatic about serving current needs in the meantime. With this in place, genomic variation data at the population level will be empowered to drive transformative impacts in global public health.

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- Baton, L. A. & Ranford-Cartwright, L. C. Spreading the seeds of million-murdering death: metamorphoses of malaria in the mosquito. *Trends Parasitol.* **21**, 573–580 (2005).
- Loy, D. E. et al. Out of Africa: origins and evolution of the human malaria parasites *Plasmodium falciparum* and *Plasmodium vivax*. *Int. J. Parasitol.* **47**, 87–97 (2017).
- Otto, T. D. et al. Genomes of all known members of a *Plasmodium* subgenus reveal paths to virulent human malaria. *Nat. Microbiol.* **3**, 687–697 (2018).
- Kwiatkowski, D. P. How malaria has affected the human genome and what human genetics can teach us about malaria. *Am. J. Hum. Genet.* **77**, 171–192 (2005).
- World Health Organization. World Malaria Report 2020 (WHO, 2020).
- Molina-Cruz, A., Zilversmit, M. M., Neafsey, D. E., Hartl, D. L. & Barillas-Mury, C. Mosquito vectors and the globalization of *Plasmodium falciparum* malaria. *Annu. Rev. Genet.* **50**, 447–465 (2016).
- Ranson, H. & Lissenden, N. Insecticide resistance in African anopheles mosquitoes: a worsening situation that needs urgent action to maintain malaria control. *Trends Parasitol.* **32**, 187–196 (2016).
- Ouattara, A. et al. Molecular basis of allele-specific efficacy of a blood-stage malaria vaccine: vaccine development implications. *J. Infect. Dis.* **207**, 511–519 (2013).
- Jacob, C. G. et al. Genetic surveillance in the Greater Mekong Subregion and South Asia to support malaria control and elimination. Preprint at *medRxiv* <https://doi.org/10.1101/2020.07.23.20159624> (2020).
- Wesolowski, A. et al. Mapping malaria by combining parasite genomic and epidemiologic data. *BMC Med.* **16**, 190 (2018).
- Daniels, R. F. et al. Modeling malaria genomics reveals transmission decline and rebound in Senegal. *Proc. Natl Acad. Sci. USA* **112**, 7067–7072 (2015).
- Lee, H. J. et al. Transcriptomic studies of malaria: a paradigm for investigation of systemic host-pathogen interactions. *Microbiol. Mol. Biol. Rev.* **82**, e00071-17 (2018).
- Lee, M. C. S., Lindner, S. E., Lopez-Rubio, J.-J. & Llinás, M. Cutting back malaria: CRISPR/Cas9 genome editing of *Plasmodium*. *Brief. Funct. Genomics* **18**, 281–289 (2019).
- Kariuki, S. N. & Williams, T. N. Human genetics and malaria resistance. *Hum. Genet.* **139**, 801–811 (2020).
- Gardner, M. J. et al. Genome sequence of the human malaria parasite *Plasmodium falciparum*. *Nature* **419**, 498–511 (2002).
This paper describes the first reference genome sequence assembly for *P. falciparum*.
- Dame, J. B. et al. Current status of the *Plasmodium falciparum* genome project. *Mol. Biochem. Parasitol.* **79**, 1–12 (1996).
- Jeffares, D. C. et al. Genome variation and evolution of the malaria parasite *Plasmodium falciparum*. *Nat. Genet.* **39**, 120–125 (2007).
- Mu, J. et al. Genome-wide variation and identification of vaccine targets in the *Plasmodium falciparum* genome. *Nat. Genet.* **39**, 126–130 (2007).
- Volkman, S. K. et al. A genome-wide map of diversity in *Plasmodium falciparum*. *Nat. Genet.* **39**, 113–119 (2007).
Along with Jeffares et al. and Mu et al., these three co-published papers describe the first efforts to characterize genome-wide variation in *P. falciparum*, using Sanger di-deoxy shotgun and PCR-based sequencing. They describe fundamental population genomic features of the parasite, including variation in population diversity, global population structure and patterns of linkage disequilibrium.
- Neafsey, D. E. et al. The malaria parasite *Plasmodium vivax* exhibits greater genetic diversity than *Plasmodium falciparum*. *Nat. Genet.* **44**, 1046–1050 (2012).
- Hupalo, D. N. et al. Population genomics studies identify signatures of global dispersal and drug resistance in *Plasmodium vivax*. *Nat. Genet.* **48**, 953–958 (2016).
- Neafsey, D. E. et al. Genome-wide SNP genotyping highlights the role of natural selection in *Plasmodium falciparum* population divergence. *Genome Biol.* **9**, R171 (2008).
- Van Tyne, D. et al. Identification and functional validation of the novel antimalarial resistance locus PF10_0355 in *Plasmodium falciparum*. *PLoS Genet.* **7**, e1001383 (2011).
- Kidgell, C. et al. A systematic map of genetic variation in *Plasmodium falciparum*. *PLoS Pathog.* **2**, e57 (2006).
- Holt, R. A. et al. The genome sequence of the malaria mosquito *Anopheles gambiae*. *Science* **298**, 129–149 (2002).
This paper describes the first reference genome assembly for *A. gambiae*, produced from the PEST colony that represented an admixture of *A. gambiae sensu stricto* and *A. coluzzii*.
- Sinka, M. E. et al. The dominant anopheles vectors of human malaria in Africa, Europe and the Middle East: occurrence data, distribution maps and bionomic précis. *Parasit. Vectors* **3**, 117 (2010).
- Martinez-Torres, D. et al. Molecular characterization of pyrethroid knockdown resistance (*kdr*) in the major malaria vector *Anopheles gambiae* s.s. *Insect Mol. Biol.* **7**, 179–184 (1998).
- Weill, M. et al. A novel acetylcholinesterase gene in mosquitoes codes for the insecticide target and is non-homologous to the *ace* gene in Drosophila. *Proc. Biol. Sci.* **269**, 2007–2016 (2002).

29. Anopheles gambiae 1000 Genomes Consortium. Genetic diversity of the African malaria vector *Anopheles gambiae*. *Nature* **552**, 96–100 (2017). **This work describes the first large-scale population genomic study of *A. gambiae sensu stricto* and *A. coluzzii* performed on WGS data, documenting signals of selection associated with insecticide resistance and examples of resistance alleles that crossed species boundaries through hybridization and introgression.**
30. Lucas, E. R. et al. Whole-genome sequencing reveals high complexity of copy number variation at insecticide resistance loci in malaria mosquitoes. *Genome Res.* **29**, 1250–1261 (2019).
31. Coetzee, M. et al. *Anopheles coluzzii* and *Anopheles amharicus*, new members of the *Anopheles gambiae* complex. *Zootaxa* **3619**, 246–274 (2013).
32. Barrón, M. G. et al. A new species in the major malaria vector complex sheds light on reticulated species evolution. *Sci. Rep.* **9**, 14753 (2019).
33. Fontaine, M. C. et al. Mosquito genomics. Extensive introgression in a malaria vector species complex revealed by phylogenomics. *Science* **347**, 1258524 (2015).
34. Crawford, J. E. et al. Reticulate speciation and barriers to introgression in the *Anopheles gambiae* species complex. *Genome Biol. Evol.* **7**, 3116–3131 (2015).
35. Crawford, J. E. et al. Evolution of GOUNDRY, a cryptic subgroup of *Anopheles gambiae* s.l., and its impact on susceptibility to *Plasmodium* infection. *Mol. Ecol.* **25**, 1494–1510 (2016).
36. Riehle, M. M. et al. A cryptic subgroup of *Anopheles gambiae* is highly susceptible to human malaria parasites. *Science* **331**, 596–598 (2011).
37. Davidson, G. Insecticide resistance in *Anopheles gambiae* Giles. *Nature* **178**, 705–706 (1956).
38. Davidson, G. Insecticide resistance in *Anopheles gambiae* Giles: a case of simple Mendelian inheritance. *Nature* **178**, 863–864 (1956).
39. Davidson, G. & Jackson, C. E. Incipient speciation in *Anopheles gambiae* Giles. *Bull. World Health Organ.* **27**, 303–305 (1962).
40. Moreno, M. et al. Complete mtDNA genomes of *Anopheles darlingi* and an approach to anopheline divergence time. *Malar. J.* **9**, 127 (2010).
41. Carlton, J. M. et al. Comparative genomics of the neglected human malaria parasite *Plasmodium vivax*. *Nature* **455**, 757–763 (2008). **This paper describes the first reference genome assembly for *P. vivax*, which exhibits a less extreme level of A/T nucleotide composition bias than *P. falciparum*.**
42. Neafsey, D. E. et al. Mosquito genomics. Highly evolvable malaria vectors: the genomes of 16 *Anopheles* mosquitoes. *Science* **347**, 1258522 (2015).
43. Ghurye, J. et al. A chromosome-scale assembly of the major African malaria vector *Anopheles funestus*. *GigaScience* **8**, giz063 (2019).
44. Marinotti, O. et al. The genome of *Anopheles darlingi*, the main neotropical malaria vector. *Nucleic Acids Res.* **41**, 7387–7400 (2013).
45. Carlton, J. M. et al. Genome sequence and comparative analysis of the model rodent malaria parasite *Plasmodium yoelii yoelii*. *Nature* **419**, 512–519 (2002).
46. Manske, M. et al. Analysis of *Plasmodium falciparum* diversity in natural infections by deep sequencing. *Nature* **487**, 375–379 (2012). **The first paper to describe the population genomics of a worldwide collection of *P. falciparum* isolates. It demonstrates the power of WGS data for identifying signals of natural selection and fine-scale population structure in parasite populations.**
47. Pearson, R. D. et al. Genomic analysis of local variation and recent evolution in *Plasmodium vivax*. *Nat. Genet.* **48**, 959–964 (2016).
48. Miotto, O. et al. Genetic architecture of artemisinin-resistant *Plasmodium falciparum*. *Nat. Genet.* **47**, 226–234 (2015).
49. Clarkson, C. S., Temple, H. J. & Miles, A. The genomics of insecticide resistance: insights from recent studies in African malaria vectors. *Curr. Opin. Insect Sci.* **27**, 111–115 (2018).
50. Ghansah, A. et al. Monitoring parasite diversity for malaria elimination in sub-Saharan Africa. *Science* **345**, 1297–1298 (2014).
51. Lan, J. H. et al. Impact of three Illumina library construction methods on GC bias and HLA genotype calling. *Hum. Immunol.* **76**, 166–175 (2015).
52. Trager, W. & Jensen, J. B. Human malaria parasites in continuous culture. *Science* **193**, 673–675 (1976).
53. Claessens, A., Affara, M., Assefa, S. A., Kwiatkowski, D. P. & Conway, D. J. Culture adaptation of malaria parasites selects for convergent loss-of-function mutants. *Sci. Rep.* **7**, 41303 (2017).
54. Gunalan, K., Rowley, E. H. & Miller, L. H. A way forward for culturing *Plasmodium vivax*. *Trends Parasitol.* **36**, 512–519 (2020).
55. Venkatesan, M. et al. Using CF11 cellulose columns to inexpensively and effectively remove human DNA from *Plasmodium falciparum*-infected whole blood samples. *Malar. J.* **11**, 41 (2012).
56. Melnikov, A. et al. Hybrid selection for sequencing pathogen genomes from clinical samples. *Genome Biol.* **12**, R73 (2011).
57. Bright, A. T. et al. Whole genome sequencing analysis of *Plasmodium vivax* using whole genome capture. *BMC Genomics* **13**, 262 (2012).
58. Leichty, A. R. & Brisson, D. Selective whole genome amplification for resequencing target microbial species from complex natural samples. *Genetics* **198**, 473–481 (2014).
59. Oyola, S. O. et al. Whole genome sequencing of *Plasmodium falciparum* from dried blood spots using selective whole genome amplification. *Malar. J.* **15**, 597 (2016).
60. Cowell, A. N. et al. Selective whole-genome amplification is a robust method that enables scalable whole-genome sequencing of *Plasmodium vivax* from unprocessed clinical samples. *mBio* **8**, e02257 (2017).
61. Miotto, O. et al. Emergence of artemisinin-resistant *Plasmodium falciparum* with kelch I3 C580Y mutations on the island of New Guinea. *PLoS Pathog.* **16**, e1009133 (2020).
62. Mathieu, L. C. et al. Local emergence in Amazonia of *Plasmodium falciparum* k13 C580Y mutants associated with in vitro artemisinin resistance. *eLife* **9**, e51015 (2020).
63. Antonio-Nkondjio, C. & Simard, F. in *Anopheles Mosquitoes: New Insights Into Malaria Vectors* (ed. Manguin, S.) (Intech, 2013).
64. St Laurent, B. et al. Behaviour and molecular identification of *Anopheles* malaria vectors in Jayapura district, Papua province, Indonesia. *Malar. J.* **15**, 192 (2016).
65. St Laurent, B. et al. Molecular characterization reveals diverse and unknown malaria vectors in the Western Kenyan Highlands. *Am. J. Trop. Med. Hyg.* **94**, 327–335 (2016).
66. Ruiz-Lopez, F. et al. DNA barcoding reveals both known and novel taxa in the *albitarsis* group (*Anopheles*: *Nyssorhynchus*) of neotropical malaria vectors. *Parasit. Vectors* **5**, 44 (2012).
67. Ahumada, M. L. et al. Spatial distributions of *Anopheles* species in relation to malaria incidence at 70 localities in the highly endemic Northwest and South Pacific coast regions of Colombia. *Malar. J.* **15**, 407 (2016).
68. Beebe, N. W., Russell, T., Burkot, T. R. & Cooper, R. D. *Anopheles punctulatus* group: evolution, distribution, and control. *Annu. Rev. Entomol.* **60**, 335–350 (2015).
69. Garg, S. et al. A haplotype-aware de novo assembly of related individuals using pedigree sequence graph. *Bioinformatics* **36**, 2385–2392 (2020).
70. Korlach, J. et al. De novo PacBio long-read and phased avian genome assemblies correct and add to reference genes generated with intermediate and short reads. *GigaScience* **6**, 1–16 (2017).
71. Kingan, S. B. et al. A high-quality de novo genome assembly from a single mosquito using PacBio sequencing. *Genes* **10**, 62 (2019).
72. Roper, C. et al. Intercontinental spread of pyrimethamine-resistant malaria. *Science* **305**, 1124 (2004).
73. Reeder, J. C. & Marshall, V. M. A simple method for typing *Plasmodium falciparum* merozoite surface antigens 1 and 2 (MSA-1 and MSA-2) using a dimorphic-form specific polymerase chain reaction. *Mol. Biochem. Parasitol.* **68**, 329–332 (1994).
74. Snounou, G. Genotyping of *Plasmodium* spp. Nested PCR. *Methods Mol. Med.* **72**, 103–116 (2002).
75. Daniels, R. et al. A general SNP-based molecular barcode for *Plasmodium falciparum* identification and tracking. *Malar. J.* **7**, 223 (2008). **The first paper to describe a ‘molecular barcoding’ approach to genotyping parasites, in this case 24 biallelic SNPs selected on the basis of high minor allele frequency in Senegal and Thai**
- P. falciparum* populations. It demonstrates the utility of inexpensive genotyping data for diverse applications.**
76. Baniecki, M. L. et al. Development of a single nucleotide polymorphism barcode to genotype *Plasmodium vivax* infections. *PLoS Negl. Trop. Dis.* **9**, e0003539 (2015).
77. Campino, S. et al. Population genetic analysis of *Plasmodium falciparum* parasites using a customized Illumina GoldenGate genotyping assay. *PLoS ONE* **6**, e20251 (2011).
78. Lee, Y., Marsden, C. D., Nieman, C. & Lanzaro, G. C. A new multiplex SNP genotyping assay for detecting hybridization and introgression between the M and S molecular forms of *Anopheles gambiae*. *Mol. Ecol. Resour.* **14**, 297–305 (2014).
79. Neafsey, D. E. et al. SNP genotyping defines complex gene-flow boundaries among African malaria vector mosquitoes. *Science* **330**, 514–517 (2010).
80. Bailey, J. A. et al. Use of massively parallel pyrosequencing to evaluate the diversity of and selection on *Plasmodium falciparum* csp T-cell epitopes in Lilongwe, Malawi. *J. Infect. Dis.* **206**, 580–587 (2012).
81. Aragam, N. R. et al. Diversity of T cell epitopes in *Plasmodium falciparum* circumsporozoite protein likely due to protein-protein interactions. *PLoS ONE* **8**, e62427 (2013).
82. Juliano, J. J. et al. Exposing malaria in-host diversity and estimating population diversity by capture-recapture using massively parallel pyrosequencing. *Proc. Natl Acad. Sci. USA* **107**, 20138–20143 (2010).
83. Gandhi, K. et al. Variation in the circumsporozoite protein of *Plasmodium falciparum*: vaccine development implications. *PLoS ONE* **9**, e101783 (2014).
84. Early, A. M. et al. Host-mediated selection impacts the diversity of *Plasmodium falciparum* antigens within infections. *Nat. Commun.* **9**, 1381 (2018).
85. Aydemir, O. et al. Drug-resistance and population structure of *Plasmodium falciparum* across the Democratic Republic of Congo using high-throughput molecular inversion probes. *J. Infect. Dis.* **218**, 946–955 (2018).
86. Shetty, A. C. et al. Genomic structure and diversity of *Plasmodium falciparum* in Southeast Asia reveal recent parasite migration patterns. *Nat. Commun.* **10**, 2665 (2019).
87. Auburn, S. et al. Genomic analysis of *Plasmodium vivax* in Southern Ethiopia reveals selective pressures in multiple parasite mechanisms. *J. Infect. Dis.* **220**, 1738–1749 (2019).
88. Amambua-Ngwa, A. et al. Major subpopulations of *Plasmodium falciparum* in sub-Saharan Africa. *Science* **365**, 813–816 (2019). **This paper describes efforts by the PDNA to characterize African *P. falciparum* genomic diversity using WGS data. The authors describe signals of natural selection and population structure within the diverse parasite population on this continent.**
89. Miotto, O. et al. Multiple populations of artemisinin-resistant *Plasmodium falciparum* in Cambodia. *Nat. Genet.* **45**, 648–655 (2013).
90. Haldar, K., Bhattacharjee, S. & Safeukui, I. Drug resistance in *Plasmodium*. *Nat. Rev. Microbiol.* **16**, 156–170 (2018).
91. Amato, R. et al. Origins of the current outbreak of multidrug-resistant malaria in southeast Asia: a retrospective genetic study. *Lancet Infect. Dis.* **18**, 337–345 (2018). **A detailed genomic portrait of the emergence and spread of mutations associated with resistance to artemisinin and co-administered partner drugs in the GMS. It demonstrates the rich value of geographically comprehensive parasite genomic data collected longitudinally, for example, in providing the insight that *pfkelch13* artemisinin resistance mutations arise at least 30 times independently.**
92. Cheeseman, I. H. et al. A major genome region underlying artemisinin resistance in malaria. *Science* **336**, 79–82 (2012).
93. World Health Organization. A framework for malaria elimination (WHO, 2017).
94. Fidock, D. A. et al. Mutations in the *P. falciparum* digestive vacuole transmembrane protein PfCRT and evidence for their role in chloroquine resistance. *Mol. Cell* **6**, 861–871 (2000).
95. Welles, T. E. Transporter of a malaria catastrophe. *Nat. Med.* **10**, 1169–1171 (2004).

96. Peterson, D. S., Walliker, D. & Wellem, T. E. Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase confers resistance to pyrimethamine in falciparum malaria. *Proc. Natl Acad. Sci. USA* **85**, 9114–9118 (1988).
97. Noeld, H. et al. Evidence of artemisinin-resistant malaria in western Cambodia. *N. Engl. J. Med.* **359**, 2619–2620 (2008).
98. Dondorp, A. M. et al. Artemisinin resistance in *Plasmodium falciparum* malaria. *N. Engl. J. Med.* **361**, 455–467 (2009).
99. Ariey, F. et al. A molecular marker of artemisinin-resistant *Plasmodium falciparum* malaria. *Nature* **505**, 50–55 (2014).
100. Straimer, J. et al. Drug resistance. K13-propeller mutations confer artemisinin resistance in *Plasmodium falciparum* clinical isolates. *Science* **347**, 428–431 (2015).
101. Cerqueira, G. C. et al. Longitudinal genomic surveillance of *Plasmodium falciparum* malaria parasites reveals complex genomic architecture of emerging artemisinin resistance. *Genome Biol.* **18**, 78 (2017).
102. Li, X. et al. Genetic mapping of fitness determinants across the malaria parasite *Plasmodium falciparum* life cycle. *PLoS Genet.* **15**, e1008453 (2019).
103. Takala-Harrison, S. et al. Independent emergence of artemisinin resistance mutations among *Plasmodium falciparum* in Southeast Asia. *J. Infect. Dis.* **211**, 670–679 (2015).
104. Anderson, T. J. C. et al. Population parameters underlying an ongoing soft sweep in southeast Asian malaria parasites. *Mol. Biol. Evol.* **34**, 131–144 (2017).
105. Ansbros, M. R. et al. Development of copy number assays for detection and surveillance of piperazine resistance associated plasmepsin 2/3 copy number variation in *Plasmodium falciparum*. *Malar. J.* **19**, 181 (2020).
106. Chenet, S. M. et al. Independent emergence of the *Plasmodium falciparum* kelch propeller domain mutant allele C580Y in Guyana. *J. Infect. Dis.* **213**, 1472–1475 (2016).
107. Uwimana, A. et al. Emergence and clonal expansion of in vitro artemisinin-resistant *Plasmodium falciparum* kelch13 R561H mutant parasites in Rwanda. *Nat. Med.* **26**, 1602–1608 (2020).
108. Taylor, S. M. et al. Absence of putative artemisinin resistance mutations among *Plasmodium falciparum* in sub-Saharan Africa: a molecular epidemiologic study. *J. Infect. Dis.* **211**, 680–688 (2015).
109. Tessema, S. K. et al. Applying next-generation sequencing to track falciparum malaria in sub-Saharan Africa. *Malar. J.* **18**, 268 (2019).
110. Meshnick, S. Artemisinin resistance in Southeast Asia. *Clin. Infect. Dis.* **63**, 1527 (2016).
111. Hastings, I. M., Kay, K. & Hodel, E. M. The importance of scientific debate in the identification, containment, and control of artemisinin resistance. *Clin. Infect. Dis.* **63**, 1527–1528 (2016).
112. Phyto, A. P. et al. Reply to Meshnick and Hastings et al. *Clin. Infect. Dis.* **63**, 1528–1529 (2016).
113. Ranson, H. Current and future prospects for preventing malaria transmission via the use of insecticides. *Cold Spring Harb. Perspect. Med.* **7**, a026823 (2017).
114. Bhatt, S. et al. The effect of malaria control on *Plasmodium falciparum* in Africa between 2000 and 2015. *Nature* **526**, 207–211 (2015).
115. Weill, M. et al. The unique mutation in ace-1 giving high insecticide resistance is easily detectable in mosquito vectors. *Insect Mol. Biol.* **13**, 1–7 (2004).
116. Ranson, H. et al. Identification of a novel class of insect glutathione S-transferases involved in resistance to DDT in the malaria vector *Anopheles gambiae*. *Biochem. J.* **359**, 295–304 (2001).
117. Jones, C. M. et al. The dynamics of pyrethroid resistance in *Anopheles arabiensis* from Zanzibar and an assessment of the underlying genetic basis. *Parasit. Vectors* **6**, 343 (2013).
118. Ingham, V. A. et al. A sensory appendage protein protects malaria vectors from pyrethroids. *Nature* **577**, 376–380 (2020).
119. Bailey, J. A. et al. Microarray analyses reveal strain-specific antibody responses to *Plasmodium falciparum* apical membrane antigen 1 variants following natural infection and vaccination. *Sci. Rep.* **10**, 3952 (2020).
120. Ouattara, A. et al. Designing malaria vaccines to circumvent antigen variability. *Vaccine* **33**, 7506–7512 (2015).
121. Thera, M. A. et al. A field trial to assess a blood-stage malaria vaccine. *N. Engl. J. Med.* **365**, 1004–1013 (2011).
122. Neafsey, D. E. et al. Genetic diversity and protective efficacy of the RTS,S/AS01 malaria vaccine. *N. Engl. J. Med.* **373**, 2025–2037 (2015).
123. Amambua-Ngwa, A. et al. Population genomic scan for candidate signatures of balancing selection to guide antigen characterization in malaria parasites. *PLoS Genet.* **8**, e1002992 (2012).
124. Sauerwein, R. W. & Bousema, T. Transmission blocking malaria vaccines: assays and candidates in clinical development. *Vaccine* **33**, 7476–7482 (2015).
125. Bustamante, L. Y. et al. A full-length recombinant *Plasmodium falciparum* PFRH5 protein induces inhibitory antibodies that are effective across common PFRH5 genetic variants. *Vaccine* **31**, 373–379 (2013).
126. Douglas, A. D. et al. The blood-stage malaria antigen PFRH5 is susceptible to vaccine-inducible cross-strain neutralizing antibody. *Nat. Commun.* **2**, 601 (2011).
127. Tan, J. et al. A public antibody lineage that potently inhibits malaria infection through dual binding to the circumsporozoite protein. *Nat. Med.* **24**, 401–407 (2018).
128. Kisalu, N. K. et al. A human monoclonal antibody prevents malaria infection by targeting a new site of vulnerability on the parasite. *Nat. Med.* **24**, 408–416 (2018).
129. Smith-Aguasca, R. et al. Mosquitoes as a feasible sentinel group for anti-malarial resistance surveillance by next generation sequencing of *Plasmodium falciparum*. *Malar. J.* **18**, 351 (2019).
130. Sumner, K. M. et al. Genotyping cognate *Plasmodium falciparum* in humans and mosquitoes to estimate onward transmission of asymptomatic infections. *Nat. Commun.* **12**, 909 (2021).
131. Nkhoma, S. et al. Population genetic correlates of declining transmission in a human pathogen. *Mol. Ecol.* **22**, 273–285 (2013).
This manuscript performs a rigorous evaluation of multiple population genetic signatures of declining transmission along the Thailand–Myanmar border, finding that the proportion of complex infections provides the strongest signal.
132. Galinsky, K. et al. COIL: a methodology for evaluating malarial complexity of infection using likelihood from single nucleotide polymorphism data. *Malar. J.* **14**, 4 (2015).
133. Medica, D. L. & Sinnis, P. Quantitative dynamics of *Plasmodium yoelii* sporozoite transmission by infected anopheline mosquitoes. *Infect. Immun.* **73**, 4363–4369 (2005).
134. Amino, R. et al. Quantitative imaging of *Plasmodium* transmission from mosquito to mammal. *Nat. Med.* **12**, 220–224 (2006).
135. Wong, W., Wenger, E. A., Hartl, D. L. & Wirth, D. F. Modeling the genetic relatedness of *Plasmodium falciparum* parasites following meiotic recombination and cotransmission. *PLoS Comput. Biol.* **14**, e1005923 (2018).
136. Nkhoma, S. C. et al. Close kinship within multiple-genotype malaria parasite infections. *Proc. Biol. Sci.* **279**, 2589–2598 (2012).
137. Nair, S. et al. Single-cell genomics for dissection of complex malaria infections. *Genome Res.* **24**, 1028–1038 (2014).
138. Nkhoma, S. C. et al. Co-transmission of related malaria parasite lineages shapes within-host parasite diversity. *Cell Host Microbe* **27**, 93–103.e4 (2020).
This study employs single-cell WGS data of 485 parasites from 15 clinical infection samples to demonstrate strong evidence for serial co-transmission of genetically distinct malaria parasites in Malawi, a high-transmission setting. Prior to this work, complex infections in such a setting were assumed to be generated primarily through superinfection rather than co-transmission.
139. Dalmat, R., Naughton, B., Kwan-Gett, T. S., Slyker, J. & Stuckey, E. M. Use cases for genetic epidemiology in malaria elimination. *Malar. J.* **18**, 163 (2019).
140. Noviyanti, R. et al. Implementing parasite genotyping into national surveillance frameworks: feedback from control programmes and researchers in the Asia-Pacific region. *Malar. J.* **19**, 271 (2020).
141. Apinijoh, T. O., Ouattara, A., Titanji, V. P. K., Djimde, A. & Amambua-Ngwa, A. Genetic diversity and drug resistance surveillance of *Plasmodium falciparum* for malaria elimination: is there an ideal tool for resource-limited sub-Saharan Africa? *Malar. J.* **18**, 217 (2019).
142. Tessema, S. K. et al. Sensitive, highly multiplexed sequencing of microhaplotypes from the *Plasmodium falciparum* heterozygome. *J. Infect. Dis.* <https://doi.org/10.1093/infdis/jjaa527> (2020).
In this paper, the authors describe an amplicon sequencing panel for *P. falciparum* designed with the express purpose of profiling highly heterozygous microhaplotypes for the purpose of IBD inference.
143. McDew-White, M. et al. Mode and tempo of microsatellite length change in a malaria parasite mutation accumulation experiment. *Genome Biol. Evol.* **11**, 1971–1985 (2019).
144. Nei, M. & Li, W. H. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proc. Natl Acad. Sci. USA* **76**, 5269–5273 (1979).
145. Nei, M. *Molecular Evolutionary Genetics* (Columbia Univ. Press, 1987).
146. Balding, D. J. Likelihood-based inference for genetic correlation coefficients. *Theor. Popul. Biol.* **63**, 221–230 (2003).
147. Rousset, F. Genetic differentiation and estimation of gene flow from F-statistics under isolation by distance. *Genetics* **145**, 1219–1228 (1997).
148. Wright, S. Coefficients of inbreeding and relationship. *Am. Nat.* **56**, 330–338 (1922).
149. Taylor, A. R., Jacob, P. E., Neafsey, D. E. & Buckee, C. O. Estimating relatedness between malaria parasites. *Genetics* **212**, 1337–1351 (2019).
150. Weir, B. S., Anderson, A. D. & Hepler, A. B. Genetic relatedness analysis: modern data and new challenges. *Nat. Rev. Genet.* **7**, 771–780 (2006).
151. Thompson, E. A. Identity by descent: variation in meiosis, across genomes, and in populations. *Genetics* **194**, 301–326 (2013).
152. Henden, L., Lee, S., Mueller, I., Barry, A. & Bahlo, M. Identity-by-descent analyses for measuring population dynamics and selection in recombining pathogens. *PLoS Genet.* **14**, e1007279 (2018).
153. Speed, D. & Balding, D. J. Relatedness in the post-genomic era: is it still useful? *Nat. Rev. Genet.* **16**, 33–44 (2015).
154. Schaffner, S. F., Taylor, A. R., Wong, W., Wirth, D. F. & Neafsey, D. E. hmmlBD: software to infer pairwise identity by descent between haploid genotypes. *Malar. J.* **17**, 196 (2018).
155. Taylor, A. R., Echeverry, D. F., Anderson, T. J. C., Neafsey, D. E. & Buckee, C. O. Identity-by-descent with uncertainty characterises connectivity of *Plasmodium falciparum* populations on the Colombian-Pacific coast. *PLoS Genet.* **16**, e1009101 (2020).
156. Biek, R., Pybus, O. G., Lloyd-Smith, J. O. & Didelot, X. Measurably evolving pathogens in the genomic era. *Trends Ecol. Evol.* **30**, 306–313 (2015).
157. Lemieux, J. *Genomic Analysis of Evolution in Plasmodium falciparum and Babesia microti*. Thesis, Harvard Medical School (2015).
158. Hamilton, W. L. et al. Extreme mutation bias and high AT content in *Plasmodium falciparum*. *Nucleic Acids Res.* **45**, 1889–1901 (2017).
159. Redmond, S. N. et al. De novo mutations resolve disease transmission pathways in clonal malaria. *Mol. Biol. Evol.* **35**, 1678–1689 (2018).
160. Taylor, A. R. et al. Quantifying connectivity between local *Plasmodium falciparum* malaria parasite populations using identity by descent. *PLoS Genet.* **13**, e1007065 (2017).
This manuscript, which analyses *P. falciparum* 93-SNP barcode and WGS data from the Thailand–Myanmar border, is the first to demonstrate that IBD-based relatedness estimates can be a useful tool for resolving parasite population connectivity over a geographic scale of less than 100 km and that they can be computed using SNP barcode as well as WGS data.
161. Skaug, H. J. Allele-sharing methods for estimation of population size. *Biometrics* **57**, 750–756 (2001).
162. Bravington, M., Skaug, H. & Anderson, E. Close-kin mark-recapture. *Stat. Sci.* **31**, 259–274 (2016).
163. Plucinski, M. M., Morton, L., Bushman, M., Dimbu, P. R. & Udhayakumar, V. Robust algorithm for systematic classification of malaria late treatment failures as recrudescence or reinfection using microsatellite genotyping. *Antimicrob. Agents Chemother.* **59**, 6096–6100 (2015).
164. Taylor, A. R. et al. Resolving the cause of recurrent *Plasmodium vivax* malaria probabilistically. *Nat. Commun.* **10**, 5595 (2019).

165. Watson, J. A. et al. A cautionary note on the use of unsupervised machine learning algorithms to characterise malaria parasite population structure from genetic distance matrices. *PLoS Genet.* **16**, e1009037 (2020).
166. Tessema, S. et al. Using parasite genetic and human mobility data to infer local and cross-border malaria connectivity in Southern Africa. *eLife* **8**, e43510 (2019).
167. Chang, H.-H. et al. Mapping imported malaria in Bangladesh using parasite genetic and human mobility data. *eLife* **8**, e43481 (2019).
168. Bahl, A. et al. PlasmoDB: the *Plasmodium* genome resource. A database integrating experimental and computational data. *Nucleic Acids Res.* **31**, 212–215 (2003).
169. Lawson, D. et al. VectorBase: a home for invertebrate vectors of human pathogens. *Nucleic Acids Res.* **35**, D503–D505 (2007).
170. Pearson, R. D., Amato, R., Kwiatkowski, D. P. & MalariaGEN *Plasmodium falciparum* Community Project. An open dataset of *Plasmodium falciparum* genome variation in 7,000 worldwide samples. Preprint at *bioRxiv* <https://doi.org/10.1101/824730> (2019).
171. Turner, T. L., Hahn, M. W. & Nuzhdin, S. V. Genomic islands of speciation in *Anopheles gambiae*. *PLoS Biol.* **3**, e285 (2005).
172. Galen, S. C. et al. The polyphyly of *Plasmodium*: comprehensive phylogenetic analyses of the malaria parasites (order Haemosporida) reveal widespread taxonomic conflict. *R. Soc. Open Sci.* **5**, 171780 (2018).
173. Eick, G. N., Jacobs, D. S. & Matthee, C. A. A nuclear DNA phylogenetic perspective on the evolution of echolocation and historical biogeography of extant bats (chiroptera). *Mol. Biol. Evol.* **22**, 1869–1886 (2005).
174. Foster, P. G. et al. Phylogeny of Anophelinae using mitochondrial protein coding genes. *R. Soc. Open Sci.* **4**, 170758 (2017).
175. Duffy, P. E. & Patrick Gorres, J. Malaria vaccines since 2000: progress, priorities, products. *NPJ Vaccines* **5**, 1–9 (2020).
176. Richard, G.-F., Kerrest, A. & Dujon, B. Comparative genomics and molecular dynamics of DNA repeats in eukaryotes. *Microbiol. Mol. Biol. Rev.* **72**, 686–727 (2008).
177. Imwong, M. et al. The spread of artemisinin-resistant *Plasmodium falciparum* in the Greater Mekong subregion: a molecular epidemiology observational study. *Lancet Infect. Dis.* **17**, 491–497 (2017).
178. Imwong, M., Hien, T. T., Thuy-Nhien, N. T., Dondorp, A. M. & White, N. J. Spread of a single multidrug resistant malaria parasite lineage (PfPailin) to Vietnam. *Lancet Infect. Dis.* **17**, 1022–1023 (2017).
179. Volkman, S. K., Neafsey, D. E., Schaffner, S. F., Park, D. J. & Wirth, D. F. Harnessing genomics and genome biology to understand malaria biology. *Nat. Rev. Genet.* **13**, 315–328 (2012).
180. Rao, P. N. et al. A method for amplicon deep sequencing of drug resistance genes in *Plasmodium falciparum* clinical isolates from India. *J. Clin. Microbiol.* **54**, 1500–1511 (2016).
181. Ngondi, J. M. et al. Surveillance for sulfadoxine-pyrimethamine resistant malaria parasites in the Lake and Southern Zones, Tanzania, using pooling and next-generation sequencing. *Malar. J.* **16**, 236 (2017).
182. Verity, R. et al. The impact of antimalarial resistance on the genetic structure of *Plasmodium falciparum* in the DRC. *Nat. Commun.* **11**, 2107 (2020).

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Author contributions

D.N. and B.M. wrote the first draft of the manuscript. D.N. and A.T. designed the figures. All authors edited and reviewed the manuscript.

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