Climate Change Management

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Planetary Health and Climate Change: Understanding the Impacts of Climate Change to the Well-Being of Our Planet

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Chapter 19
Past is Present: Climate Adaptation, Resilience, and Malaria in the Holocene

Gwen Robbins Schug

Abstract Planning for global warming requires an understanding of past climate change events, their impacts, and human strategies for resilience. From small-scale societies to urban civilizations, human communities have reorganized in the face of environmental change in a wide variety of typically unappreciated ways, which had diverse consequences for health. This chapter provides case studies of past Rapid Climate Change events, the social factors that shaped risk and responses, and the long-term impact of different choices on human health and well-being. The cases are focused on a One Health—or One Paleopathology—perspective on vector borne infections, particularly malaria. Archaeological data on malaria in the past demonstrate the full range of human diversity, the promise of communication, cooperation, Indigenous leadership, and stewardship in the pursuit of an equitable, sustainable, healthy future.

Keywords Climate adaptation · Equitable sustainability · Environmental health · Bioarchaeology · IPCC · UN sustainable development goals

Introduction: ONE Health, Planetary Health, and Paleopathology

Climate change poses a complex set of hazards for planetary health and security, not just for humans but for all species on Earth (Kemp et al. 2022; Solomon 2007; Woodward et al. 2014). Paradoxically, anthropogenic global warming is exceeding the magnitude and pace of all past Rapid Climate Change (RCC) events, yet the past is the best source of predictive power for understanding the impacts of rapid climate change on humans, animals, and our ecosystems (Burke et al. 2018; Ceballos et al. 2015; Rockman and Hritz 2020; Solomon 2007; Stephens et al. 2019) Accordingly,

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the Intergovernmental Panel on Climate Change (IPCC) has argued that planning for a warmer world requires basic research to model the physical, social, and biological aspects of vulnerability and resilience (Doherty et al. 2009). Anthropology is a particularly important component of this modeling as our discipline integrates humanistic, social science, and scientific perspectives on human evolution that situate our species and our current predicament within a deep time perspective that recognizes the importance of nuanced historical, cultural, and ecological aspects to equitable sustainable development (Larsen 2023; Lewis et al. 2023; Robbins Schug et al. 2023).

ONE Health (OH) is an increasingly prominent global strategy for interdisciplinary research on intersecting aspects of environmental, animal, and human health (Kahn 2022; Kaplan et al. 2022). Initially conceptualized as ONE Medicine (Cassidy 2018), OH has been promoted by the World Health Organization for decades as a critical way to think about zoonotic infection risk (Bidaisee and Macpherson 2014; Bird and Mazet 2018; Cunningham, Daszak, and Wood 2017; Day 2010; Webster et al. 2016). Recently OH has also been applied to thinking about health risks in the face of global climate change—zoonotic disease spillover, food security, and toxic environments (Zinsstag et al. 2018). Paleopathologists and bioarchaeologists have also become interested in applying the OH perspective to past populations and questions about health in deep time (Buikstra 2023; Buikstra et al. 2022a, b; Buikstra et al. 2022a, b; Mitchell 2024; Rayfield et al. 2023), combining it with more established paradigms in anthropology such as biocultural theory (Agarwal and Glencross 2011; Blakey 1998; Blakey and Watkins 2022; Goodman 1999; Zuckerman and Armelagos 2011; Zuckerman and Martin 2016), the concept of epidemiological transition (Barrett et al. 1998; Cohen 1984; Harper and Armelagos 2010; Larsen 2018), and structural violence (Lans 2018a; de la Cova 2008, 2010, 2020, 2022; Lans 2018b, 2021, 2022; Mant et al. 2021; Mant and Holland 2019; Nystrom and Robbins Schug 2020; Watkins 2010; Rachel Watkins 2018; Watkins 2020).

However, in some ways, OH's promise is limited by its strong focus on medical and veterinary science, without much cross-over as of yet (David et al. 2021). Paleopathology too has largely remained deeply focused primarily on human health. While we broadly think about interactions with other species and ecological circumstances, our focus is not on basic research on health in other animals, plants, or environments. Thus, the concept of Planetary Health (PH) is an important framework for directing research in paleopathology as it is focused on combining priorities from OH with climate and environmental justice and informing policy for a more equitable sustainable future. OH has not traditionally included much of a focus on environment or policy (Essack 2018), while PH is unapologetically focused on the human future (Whitmee et al. 2015), particularly in the face of environmental and climate crisis (Horton et al. 2014), and in the hope of avoiding further depletion of Earth's resources and deepening a planetary level emergency (Garcia-Gonzalez et al. 2024). Human health is not distinct from the health of our planet. Bioarchaeology and paleopathology can contribute to PH goals as our research examines moments of crisis and disruption in past populations, characterizes the experience of resilience, and defines what parameters promoted recovery, adaptation, and growth after disruptive shocks in the past (Robbins Schug 2020a, b; Robbins Schug et al. 2019, 2023).

As a discipline within anthropology, paleopathology also deeply accounts for political, economic, and social dimensions of the Anthropocene, enriching the PH paradigm, which has been criticized for ignoring capitalism's role in creating our current crisis and blocking equitable sustainable solutions (Myers 2017). This chapter describes the intersections of PH, climate change, and paleopathology, focusing on malaria as this parasitic infection has been defined as one of our greatest future health challenges (Pruss-Ustun et al. 2006) and it has been a leading cause of childhood mortality for at least 5000 years (Kariuki and Williams 2020). This chapter reviews the current state of knowledge about malaria in human evolution and archaeology, addressing the growing risk of vector borne disease in the face of global warming and providing some examples of biocultural adaptations to the disease in the past and Indigenous and Local Knowledge (ILK) about malaria today. The goal is to introduce Planetary Health to paleopathologists to inspire research that is designed with policy makers in mind and to introduce paleopathology to those in the Planetary Health world, which will benefit from the deep time perspective on ILK and biocultural adaptation to disease in the face of a changing climate.

Malaria: The Natural History of a Growing Public Health Concern

Malaria, along with other vector-borne illnesses, is a major threat to human health and well-being worldwide, with over one billion people affected and one million annual deaths from the disease (WHO 2022). That threat is growing in the context of a changing climate and rising economic inequality. Today, malaria is widespread in Africa and parts of Asia due to socio-economic disparity, lack of access to adequate resources for treatment or even blood smear, antigen, and PCR tests (CDC 2020). However, the threat is rapidly expanding. Historically, the disease was also present in more temperate regions of the planet before 1950, when air conditioning, window screens, insecticides, drainage and public health infrastructure, and insecticides were widely employed to reduce mosquito population density, habitat, and access to humans (CDC 2020). Currently there is widespread concern about a resurgence of malaria with global warming extending warm temperatures across multiple seasons; changing patterns of rainfall, humidity, and frequency of extreme weather events involving drought and flooding; expanding the geographic range of suitable habitats for mosquitos and reducing the time to reproductive maturity for the *Anopheles* mosquito (Colón-González et al. 2021; Samarasekera 2023). Understanding these growing risks requires accounting for the natural history, evolution, and interactions of the pathogen, the host species, and the vectors.

Humans get malaria by infection with parasitic protozoans (*Plasmodia* spp.), which enter the blood stream through mosquito (*Anopheles* spp.) bites. The protozoa that cause malaria spend part of their lifecycle in the body of female mosquitos, who bite—humans and other mammals, birds, reptiles, amphibians, and fish—to get a blood meal, a source of necessary amino acids for producing their eggs (Al-Rashidi et al. 2022). When female mosquitos ingest *Plasmodia* gametocytes in the blood of a human host, it alters their own patterns of behavior according to the sexual cycle of the parasite (Cator et al. 2014). In the mosquito host, the gametocytes mate in the gut of the mosquito, grow and multiply for 10–18 days, and then the sporozoites migrate to the salivary glands and the female mosquito becomes infectious (CDC 2020). During this pre-infectious period, the female mosquitos experience reduced attraction to feeding hosts, are less persistent in attempts to feed, they probe the host less frequently and for less time than during their infectious phase (Cator et al. 2014). Behavioral changes may be related to mortality risks to the mosquitos when feeding leading to parasite-host manipulation that favors feeding during infectious periods.

When a female mosquito does take a blood meal, the plasmodium sporozoites spread to the host. In mammals, they travel to the liver, where they go through the asexual part of their life cycle. At this point, they either become dormant hypnozoites or they mature into schizonts, which then rupture and release merozoites (CDC 2020). Merozoites infect red blood cells (RBCs) and these blood stage parasites are responsible for the symptoms associated with malaria in humans, as the parasite goes through multiple rounds of multiplication, invasion of RBCs, maturation, and infection (Schellenberg et al. 1994). This life cycle is shared among five species of protozoa that can cause malaria in humans (*P. falciparum*, *vivax*, *malariae*, *ovale*, and *knowlesi*). As humans, our risk is compounded by the fact that mosquitos that spread malaria also host a variety of other pathogens, leading to dengue, encephalitis, filariasis, yellow fever, and zika.

In human hosts, there is a life history component to the epidemiology of malaria that must also be considered. In areas with a high burden of malaria transmission today, breastfeeding infants are protected by maternal antibodies for the first few months of life. In malaria endemic areas, equatorial Africa and South Asia for example, childhood mortality is highest in the 2–5-year age category, after which repeated infections in endemic areas provide semi-protective acquired immunity (CDC 2020). In these areas, infants 6-24 months of age are at greatest risk for infection and typically also suffer from co-morbid anemia. In areas where malaria is not endemic, such as Latin America, epidemic outbreaks can occur because children and adults do not have this acquired immunity status (CDC 2020). Pregnant women are most susceptible to malaria in all regions because their immune systems are depressed. Malaria during pregnancy can lead to premature birth, low birth weight, and high infant mortality.

Vector mosquito species exhibit genetic preferences for feeding on specific animal hosts during the gonotrophic cycle—preferences that may be related to the length of time required to digest blood from different vertebrate hosts, and which affect the length of time for eggs to form, oviposition, the number of eggs, and hatch rates (Al-Rashidi et al. 2022). While mosquitoes express preferences for feeding on certain species, they will regularly bite other animals who then acquire parasitic plasmodia that do not typically infect their taxon. For example, Great African Ape *Plasmodium* species are transmitted by *A. vinckei, moucheti, and marshallii* (Obame-Nkoghe et al. 2023; Prugnolle et al. 2013) and all three of these species will also bite *Homo sapiens*

(Loy et al. 2017). Cross-species transmission of *Plasmodium spp.* has been reported among humans, chimpanzees, and gorillas (Contacos 1970; Loy et al. 2017, 2018; Paupy et al. 2013; Plenderleith et al. 2022; Prugnolle et al. 2013; Rayner et al. 2011). *Plasmodium* infection can lead to fever and anemia in Great African Apes, with the greatest fecal parasite burden occurring in the pregnant females and immature animals, but the parasite often does not cause severe disease and acquired immunity may have facilitated zoonotic reservoir effects in the past (Loy et al. 2018).

In fact, this phenomenon shaped the evolution of *P. falciparum* to become the most highly prevalent malarial pathogen in sub-Saharan Africa and the greatest cause of most human morbidity and mortality related to malaria in that region (Bhatt et al. 2015; WHO, n.d.). This species is presently an obligate parasite of humans but its genome demonstrates this was not always the case. *P. falciparum* is most closely related to *P. reichenowi*, which causes malaria in chimpanzees (Escalante and Ayala 1994; Rich et al. 2009). Previous work suggested *P. falciparum* jumped to humans from infecting members of a different ancestral ape lineage that led to Gorillas anywhere from hundreds of thousands of years ago (Hughes and Verra 1998) to as little as 50,000 years ago from an ancestral lineage (*P. praefalciparum*) (Sundararaman et al. 2013, 2016). Recent evidence contradicts this view, suggesting this parasite jumped to human hosts much more recently, within the past 10,000 years (Liu et al. 2010; Loy et al. 2018). Whenever the leap occurred, it has been highly successful since then, spreading to live in 70 species of *Anopheles* mosquito (Molina-Cruz et al. 2016). The evolution of host preference in *P. falciparum* explains a large part of its historical and modern distribution in human populations (Uhl and Thomas 2022).

Planetary Health: Malaria in the Context of a Changing Climate

The PH framework recognizes that contemporary human demographic and epidemiological patterns depend not only on evolutionary history and biological factors but also on human behavioral and social factors. To address disease risk, we must examine the policies and practices that undermine an equitable sustainable future and which could limit the potential for future generations of human societies to flourish. In other words, topics for OH and PH research overlap but PH seeks to meaningfully address conceptual, informational, and governmental failures that prevent meaningful policy changes to ensure human survival and resilience. PH has a goal of ensuring the "highest attainable standard of health, wellbeing, and equity worldwide through judicious attention to human systems—political, economic, and social—that shape the future of humanity and the Earth's natural systems" (Whitmee et al. 2015). This chapter combines PH with paleopathology to outline the biological and evolutionary factors that promote the spread of disease, its history in human communities over the long term, the biocultural and social factors that promoted spread of malaria in prehistory, and why we need to shift to a framework that empowers local and Indigenous communities to eradicate disease.

A PH and paleopathology approach to malaria is particularly critical in this time of extreme anthropogenic global warming because biologically and socially speaking, pathogens, vectors, and hosts are all deeply impacted by both extreme weather events and longer term trends in average surface temperatures and patterns of rainfall. Although malaria is currently endemic in tropical and sub-tropical regions of the Earth, historically, epidemics of malaria have also impacted temperate and boreal ecozones (Gething et al. 2011). The contemporary distribution of the disease is largely shaped by mosquito-breeding control efforts over the past century, malaria treatment, and eradication programs. When modeling suitable habitats for malarial parasites and their mosquito vectors in the future, we do better to assume that the historical distribution reflects a more accurate representation of suitable habitat given these control measures could be overwhelmed in the future (Ostfeld and Keesing 2020).

With the present 1.4 degrees Celsius of warming, we are already seeing strong impacts on the epidemiology of malaria (Kulkarni et al. 2022; Samarasekera 2023). Warmer temperatures affect the natural history, reproductive cycles, and behavior of the parasites and the vectors in ways that favor disease transmission (Caminade et al. 2014, 2016, 2019). For example, the worst-case regional scenario (RCP 8.5) in sub-Saharan Africa will put an additional 76 million people at risk of malaria infection by 2080, and that is only considering risks from *P. falciparum* (Ryan et al. 2020, 2023). Warmer temperatures and changing patterns of rainfall will increase transmission of malaria in highland areas of sub-Saharan Africa, Asia, South America, the Pacific and Mediterranean, where the disease is already endemic (Karypidou et al. 2020; Ryan et al. 2020). Mosquito population habitats are already starting to expand into Global North areas not usually affected by malaria—North America, Europe, north Africa, and northern Asia (Fletcher 2022; Kulkarni et al. 2022; van der Watt et al. 2022a, b).

Extreme weather events—flooding and El Niño events in particular—have recently led to malaria epidemics in Pakistan and Mozambique as well as transmission events in the United States, Ethiopia, and Columbia (Samarasekera 2023). These events are predicted to worsen over time as global mean surface temperatures (GMST) climb to levels not seen for millions of years (Steinthorsdottir et al. 2021; Von Der Heydt 2022). Earth's natural cycles have brought global cooling for approximately 65 million years and with that, a commensurate decline in atmospheric CO_2 levels. Our current GMST has already surpassed the warm period in the mid-Holocene (Marcott et al. 2013). Further warming is expected as the present 400 ppm of atmospheric CO_2 has not been seen since the mid-Pliocene period (3 million years ago), when Earth's GMST was 1.8–3.6 °C cooler than pre-industrial temperatures (Burke et al. 2018). Within the next century, if we do not address the causes of global warming, we face a climate more similar to that of the Eocene, 50 million years ago, when atmospheric CO_2 was 1400 ppm, GMSTs were 13 °C warmer than the present, there were no permanent ice sheets, and sea level was 25 m above the present (Burke et al. 2018; Miller et al. 2020).

Even in the near future, with changes of lesser magnitude, climate change may present opportunities for spillover of other mosquito-borne pathogens, like arborviruses that do not currently have significant impacts on human communities (Mordecai et al. 2020). Arborviruses, like dengue and chikungunya are transmitted by *Aedes aegypti* and represent another growing threat to urban communities in sub-Saharan Africa. Some researchers have argued that specific prediction scenarios for climate change there may favor transmission of these pathogens over malaria as the vector's peak transmission rate is at 29 °C compared to 25 °C for malaria transmission by *A. gambiae* (Mordecai et al. 2020). Because many efforts at disease prevention are specifically focused on malarial pathogens, their vectors, and human social conditions that facilitate the spread and severity of this disease, other pathogens may be able to gain ground in establishing themselves and thriving in human populations.

Zoonotic spillover of *Plasmodium spp.* that do not currently infect humans, but which cause disease in our closest living relatives is also a growing threat with deforestation, altered ecosystem dynamics, global warming, and other environmental and climate changes (Cuenca et al. 2021). Currently, we know of 13 *Plasmodium spp.* in Asia, seven in Africa, and two in South America that infect mosquito species that preferentially feed on simians—monkeys and apes—and which are thus candidates for zoonotic spillover (Fig. 19.1). *P. schwetzi* in Africa; *P. cynomolgi, inui*, *knowlesi*, and *eylesi* in Asia; and both *P. Simium* and *P. brasilianum* in South America have been documented to also infect humans in lab or natural environments (Antinori et al. 2021). Climate change, socio-economic factors, and extreme weather events, such as the El-Niño Southern Oscillation (ENSO) events in South America and monsoon in South and East Asia are expected to drive transmission among primates in this areas, leading to greater opportunity for spillover events and pathogen evolution (Abiodun et al. 2020; Alam et al. 2016; Baghbanzadeh et al. 2020; Brugueras et al. 2020; Dhimal, Ahrens, and Kuch 2015; Mabaso and Ndlovu 2012; Yi et al. 2019). Reconstructing the co-evolution of mosquitos, plasmodia, and hominins is a critical part of preparing for greater threats from malaria in a warmer world (Antinori et al. 2021; Cuenca et al. 2021; Faust and Dobson 2015; Fornace et al. 2023; Lempang et al. 2022; Naserrudin et al. 2022; Van De Straat et al. 2022).

Falciparum malaria itself arose as a threat to human communities in the context of a changing climate and new spillover events have been recently documented and spillover is considered a growing threat to previously successful malaria eradication programs in the Global South. The disease was considered eradicated in southern and southeastern Brazil until it was recently recognized in 28 patients who had had contact with howler monkeys in the Atlantic Forest (Brasil et al. 2017). Zoonotic transmission of *P. simium* is not the only recent example; *P. knowlesi* is another species of malarial parasite that usually affects macaques and has now been identified in more than 100 cases of malaria in people belonging to the Iban ethnic group in Kapit, Borneo (Singh et al. 2004). While these two species have been on the public health radar for more than 50 years (Chin et al. 1965; Deane, Deane, and Neto 1966), we are now witnessing autochthonous malaria cases arising more frequently from monkey-mosquito-human transmission of these pathogens on an epidemiologically visible scale.

Fig. 19.1 Global distribution of non-human simian *Plasmodium spp.* that have potential for malaria spillover into human hosts. Adapted from data in Antinori et al. (2021)

Malaria Has Been a Planetary Health Crisis for 10,000 years

Zoonotic spillover is an important force driving risk of malaria but biocultural and social change has been equally impactful in the evolution and natural history of this disease. Climatic stability is the force responsible for the current state of evolution of *Homo sapiens*. We have occupied a stable environment for the past 12,000 years and this stability enabled settled lifestyles, domestication and food production, urbanism, and eventually the conditions for global warming (Larsen 2023). Genetic data suggests malaria has been an influential human disease for most of that time, occurring in association with climatic and socio-cultural shifts at the Holocene epoch's opening (Liu et al. 2010). *P. falciparum* exhibits low levels of genetic diversity compared to *P. gaboni* and *reichenowi* (Bopp et al. 2013; Loaiza et al. 2012; Sundararaman et al. 2016) indicating a recent population bottleneck, approximately 10ky BP (years ago) (Carter and Mendis 2002; Conway et al. 2000; Hedrick 2011; Loy et al. 2018). The parasite may have undergone strong selection just as our species began interacting with landscapes, plants, and other animals in new ways—at the incipient stages of animal domestication, deforestation, agricultural production, and new levels of migration (Hartl et al. 2002).

P. vivax, on the other hand, seems to have had a more convoluted evolutionary history (Ananias A. Escalante et al. 2005; Loy et al. 2018; Neafsey et al. 2012; Tachibana et al. 2012). It is an endemic parasite in African apes and similar genetically to *P. simium;* it has recently been argued it may have jumped to infecting humans from contact with New World Monkeys in Central and South America (Antinori et al. 2021). This transition may have been facilitated by the parasite's natural history—with a long dormant stage in the host liver (Uhl and Thomas 2022). The ability to remain dormant for extended periods of time means these two plasmodia can survive in smaller, more rural populations and can remain infectious to mosquitos even after their human hosts took long journeys to travel to new areas of the world.

Evidence from human skeletal remains demonstrates *P. falciparum* malaria has had substantial health impacts in human communities for at least seven millennia. Genetic data confirms this disease has been the strongest known selective pressure on the human genome, driving the prevalence of genetic anemias in *Homo sapiens* (Lee and Coban 2018; Tishkoff and Williams 2002; WHO, n.d.) since the disease was promoted by anthropogenic climate and environmental changes associated with plant and animal domestication, subsistence transition to agriculture, and most importantly, increasing population density and urbanism in human communities (Bianucci et al. 2008; Grauer 2019; Lalremruata et al. 2013; Larsen 2023; Marciniak 2016; Nerlich 2016; Nerlich et al. 2008; Sallares and Gomzi 2001; Schats 2023; Shin et al. 2018; Smith-Guzmán 2015a; Zink et al. 2002).

The earliest skeletal evidence for *P. vivax* is in the Joseon Dynasty, Korea (1392–1910 CE), where it shows up alongside increased population growth rates and settlement density after the domestication of rice and millet (Shin et al. 2018). *P. falciparum* is in evidence much earlier, in ancient Egypt (2820–2630 BCE) (Bianucci et al. 2008). Malaria thrived in the New Kingdom (1500–500 BCE) because of the high-density urban environments (Nerlich et al. 2008), innovations such as irrigation (Lalremruata et al. 2013), and heightened social inequality. This would have been a devastating disease for the human population. Malaria symptoms include fever, chills, muscle aches, headache, tiredness, nausea, vomiting, diarrhea, and in some cases anemia, jaundice, kidney failure, seizures, confusion, coma, and death (CDC 2020; WHO 2021). Even with modern medical treatment, this disease remains a leading cause of childhood mortality, contributes to syndemics globally, leads to long-term sequelae and health impacts.

Beyond skeletal evidence for the earliest impacts of this disease, paleopathological analysis of ancient texts from the Bronze Age in China, Egypt, and India provide a sense of prehistoric Indigenous and Local Knowledge (ILK) about recurrent fevers and what might have been malaria (Dagen 2020). The earliest textual references to a disease like malaria are from the Chinese medical treatise, *Nei Cheng* (2700 BCE), which describes paroxysmal fevers combined with splenomegaly; urine color was also used to diagnose the disease by the Tang Dynasty (618–907 CE) (Wu et al. 2013). The *Atharva Veda* describes the disease in South Asia during the second millennium BCE, relating details about the habitat, mouth parts, and behavior of mosquitoes (*Maśaka*); describing the parasite and the fevers (*takman*) it caused (Kaur and Singh 2017). This text also describes control of mosquitos in different life stages and the treatments for malaria using fragrant grasses and herbs. Interestingly, the *Atharva Veda* not only describes grassy, overgrown habitats as a breeding ground for mosquitoes, but the text also attributes malarial habitats to dirty and unsanitary living conditions.

The Eber's Papyrus documents the disease and its impacts on the New Kingdom of Egypt, although, as discussed below, studies of human remains offer more direct evidence for the presence of the disease in ancient Egypt (Miller et al. 1994). Cuneiform tablets demonstrate the disease was recognized as causing deadly fevers in Mesopotamia by the sixth century BCE (Major 1954). There it was attributed to a mosquito-like God of Pestilence (Dagen 2020). Hippocrates also documented recurrent fevers in the late summer, early autumn in the low lying marshes of Greece. The Roman author Varro, writing in the second century BCE, recommended moving homes to more elevated parts of the city to take advantage of breezes that would lessen biting insects and Columella suggested in the 1rst century AD that it was these "stinging creatures" that spread disease in the marshy areas of the settlement. At that time, malaria caused by *P. malariae, vivax, and falciparum* was endemic and the greatest effects were felt by men in the military, slaves, and the poor who occupied the marshy areas of the city (Dagen 2020).

These sources demonstrate social determinants of health played a very influential role in the impact of malarial parasites in the past as they do today. Lifestyle changes related to settled village living and urbanization were also accompanied by social inequality and structural violence. In the present, these are compounded by capitalism and colonialism, which not only create conditions where parasites are more easily transmitted, they also magnify the impacts of sequelae. This is evidenced, for example, by the epidemiological patterns of malaria in the Roman Empire (Beard 2015; Bourbou 2020; Gowland and Western 2011; Llanos-Lizcano et al. 2024; Loufouma Mbouaka et al. 2021; Marciniak 2016; Marciniak et al. 2018; Packard 2021), Late Antique and Medieval Europe (Newfield 2016; Wilson et al. 2023), and in Medieval England (Perry and Gowland 2022; Robb et al. 2021). It is further in evidence in Roman period Egypt (Lalremruata et al. 2013) where malaria was co-morbid with *M. tuberculosis* infection, a pathogen well understood to be most prevalent in disadvantaged segments of society, whose epidemiology is influenced by over-crowded conditions, poor sanitation, and reduced access to resources (Roberts and Buikstra 2003). The combined impact of malaria, comorbid conditions, and social inequality make this the ultimate syndemic disease.

Paleopathological data is important for understanding the types of biocultural and social environments that make malaria more devastating throughout history but it does have limitations. The deep-time history of malaria is difficult to trace. The disease does not directly impact human bone tissue, so paleopathologists have typically studied this disease through lesions related to a sequala of malaria infection, chronic acquired anemia (Brickley 2024). Immunological assays of human skeletal remains (Nerlich 2016) have supported the idea that paleopathologists can diagnose anemia in past populations through the presence of porotic lesions in human skeletons that result from systemic infection, chronic inflammation, and fever. The five skeletal lesions commonly associated with anemia (Smith-Guzmán 2015b) are porotic hyperostosis of the parietal and occipital bones, *cribra orbitalia*, abnormal porosity on the humerus, femur, and vertebral bodies (including the sacrum) (Fig. 19.2). However, these lesions are also associated with numerous other metabolic and infectious diseases.

Recently progress has also been made in detecting malaria in past populations through paleomolecular techniques that have provided direct evidence of *P. falciparum* infection in ancient human skeletal remains (Bianucci et al. 2008; Gelabert et al. 2017; Khairat et al. 2013; Lalremruata et al. 2013; Llanos-Lizcano et al. 2024;

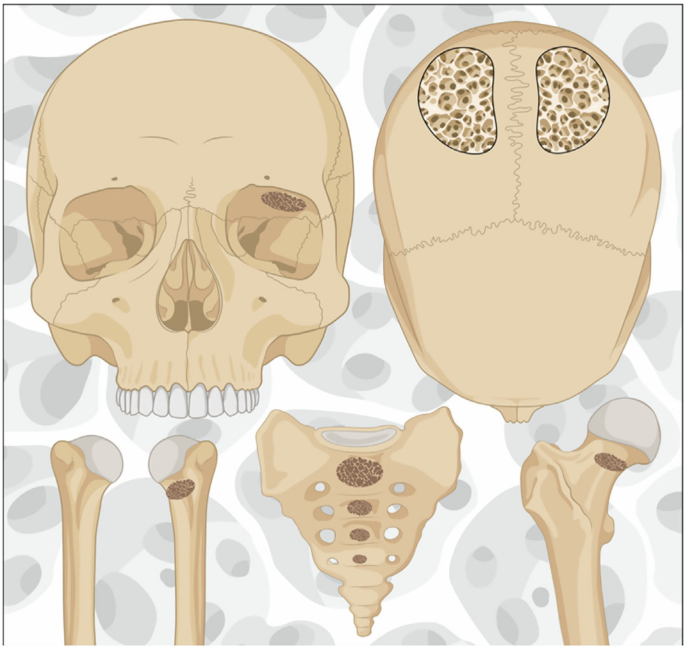

Fig. 19.2 Diagrammatic representation of porous lesions associated with anemia and used with contextual data on paleoenvironments to infer malaria in paleopathology. Shown here are *cribra orbitalia* affecting the orbit, porotic hyperostosis affecting the parietals, humeral and femoral *cribra*, and spinal porosity on the sacrum

Loufouma Mbouaka et al. 2021; Marciniak et al. 2018; Nerlich et al. 2008; Sallares and Gomzi 2001; Timmann and Meyer 2010). The *Plasmodia* can only be detected in cases of well-preserved bone tissue that is carrying a large parasite burden that will yield a large amount of DNA. Paleogenetic techniques have led to diagnoses of malaria in historical, modern skeletal tissue, Roman skeletons, ancient Egyptian and Nubian skeletal and mummified people; and potentially, in Bronze Age tombs in the Mediterranean (Setzer 2010). It is unfortunate that molecular techniques have been inconsistently successful but with additional research on museum collections, there is hope for technical advances that will make this more practical in the future (Brickley 2024).

Malaria's prehistoric distribution and endemicity can also be inferred in archaeological human remains due to the presence of genetic anemias that result from co-evolutionary processes facilitated by anthropogenic environmental and landscape changes first visible on Earth with the advent of widespread reliance on agricultural production (Larsen 2018, 2023). Land clearance favors mosquito reproduction as it is often associated with stagnant water and it often leads to reductions in mosquito diversity, favoring species that transmit disease (https://e360.yale.edu/features/how_forest_loss_is_leading_ to_a_rise_in_human_disease_malaria_zika_climate_change). Phenotypic variation in human red blood cell (RBC) structure and function influences the risk of developing symptoms of severe disease (Haldane 1949; Kariuki and Williams 2020). The evolution of genes responsible for this variation, sickle cell anemia, thalassemia, G6PD (glucose-6-phosphatase) deficiency, and variants in receptor proteins and blood group membrane proteins are all attributed to malaria's spread and endemicity in parts of Afro-Eurasia (Kariuki and Williams 2020).

The analysis of the epidemiology of genetic anemias also confirms that agricultural production is a prime driver of this disease, but agriculture is not the only malarial environment for humans. Based on evidence for skeletal changes—anthroposcopic and histological—associated with alpha and beta thalassemia for example, there is evidence that malaria may have been a significant health problem in northern Vietnam 7000 years ago due to population growth, reduced residential mobility, land clearance, irrigation, and other anthropogenic changes associated with horticulture, not agriculture (Vlok et al. 2021). Thalassemia is a genetic anemia that exists in high prevalence in this region today, with as much as 80% of the human population carrying genes associated with this condition in parts of South and Southeast Asia, in areas where malaria is endemic (Hockham et al. 2019). Even small landscape modifications can increase the risk of mosquito-borne pathogens.

In the past 7000 years, human populations and our domesticates have also increasingly been on the move, with trade contacts and migration bringing new opportunities for disease spillover and epidemics (Robbins Schug and Halcrow 2022) as well as bringing genetic anemia variants related to malaria to new areas. Recently four whole genomes from Arabia were sequenced from skeletal tissue from Dilmun, or ancient Bahrain (600–325 BCE), that demonstrate a deep history for disorders related to G6PD deficiency (Martiniano et al. 2024). Three of the four individuals studied provided evidence consistent with the hypothesis that the mutation was introduced to the Bronze Age Arabian population at Dilmun through population mobility, specifically trade contacts with Bronze Age Mesopotamia, Iran, and/or South Asian groups (Possehl 2007). These results support prior suggestions that malaria was already endemic in South Asia in the Bronze Age (Lovell 1997, 1998, 2016). These data are also supported by skeletal evidence for porotic hyperostosis and cribra orbitalia in infants and young children's skeletal remains at Bronze Age Dilmun and Harappa (Littleton 2011; Robbins Schug and Blevins 2016).

Biocultural Adaptations to Malaria in the Past and Present

The evolutionary and paleopathological data presented here demonstrates that social determinants and biocultural environments have always been influential in the spread of malaria. Anthropological research in living global communities indicates some variables that increase susceptibility relate to individual choices—consistent use of mosquito netting, insecticides, environmental control measures, and health care-seeking behavior (Monroe et al. 2021). However, individual choices do not exit in a social vaccuum. There is an influential aspect of social pressure in malaria control, particularly dealing with mothers' perceptions, attitudes, and behaviors related to disease control (Cardona-Arias 2022). Importantly, effective prevention and treatment also requires consideration of economic conditions and resources; structure, function, and access to healthcare systems; capitalistic control over anti-malarial drugs; and other socio-cultural and geographical factors that promote inequitable access (Cardona-Arias 2022; Kienberger and Hagenlocher 2014; Onyango et al. 2016; Ricci 2012). For this reason, to understand societal adaptive response capacity in the present and to drive effective policy change in the future requires an understanding of local power and money dynamics as influential actors as well as the power exerted by global experts and development organizations, which can change local dynamics considerably, often without accountability (Parkhurst et al. 2021).

This recognition has created growing interest in combining scientific and other Western ways of knowing with ILK about weather and ecosystems, traditional adaptations to climate and environmental change, and strategies for resilience (Leal Filho et al. 2022). Globally, Indigenous people (5% of the global population) are actively working to conserve forests and protect biodiversity on around 25% of the world's land mass (Garnett et al. 2018). Overall, these lands protected by Indigenous stewards are in better health than surrounding areas (Dawson et al. 2021; Heller et al. 2023) yet the customary rights of Indigenous peoples to the land they protect are rarely respected or codified and, in some cases, traditional livelihoods are criminalized, and Indigenous people are displaced or forced into meager subsistence (Bijoy et al. 2022). In some ways, a focus on ILK could shift power dynamics to exert authority in prediction scenarios for the global North. It is critical that scientists who want to participate in these alternative systems are not simply extracting information for their own purposes but also work to ensure Indigenous peoples rights, roles, and contributions are recognized (Bijoy et al. 2022).

There has been a strong research focus on ILK about ethnopharmacology for a relatively long time. Quinine was a treatment for malaria in the early nineteenth century but its origins trace back to Indigenous Peruvians, who were using cinchona bark to treat fevers when the Spanish arrived in the sixteenth century (Crawford 2016). Artemisinin is an anti-malarial medication isolated in the late twentieth century but Chinese physicians have used *Artemesia annua* for malaria treatment going back to the second century BCE (Tu 2017). Artemisinin-based treatments are still the first line of treatment in Western medicine today. ILK retains promise for new treatments. Among the Baniwa, Baré, Desan, Piratapuia, Tariana, Tukano, Tuyuca, and Yanomami peoples of the Brazilian Amazon Forest, there are at least 55 plants known to prevent or treat malaria and fevers associated with malaria (Frausin et al. 2015). Taxa used for prophylaxis and antimalarial remedies are grown in a variety of circumstances; 62% are domesticated and cultivated in small family and community gardens, or open and cleared areas. Some of these species have been studied scientifically, the majority have yet to be investigated. Sadly, those species that grow wild in the forest or in areas difficult to access are negatively impacted by deforestation and mining so collaboration with Indigenous people to understand the activity of these plants is an urgent priority in the face of climate and environmental change.

However, there is another important aspect that requires additional attention and that is ILK about traditional medicine and why it is sometimes preferred over Western medicine and pharmaceutical derivatives. Despite Universal Health Care being available in Uganda for example, traditional medicine is perceived as less expensive, more easily accessible, and culturally accepted as safe and effective in the treatment of malaria (Tabuti et al. 2023). The transmission and symptoms of this disease are well understood among Indigenous people in Tororo District, where malaria is endemic and more than 45 locally available plants can remedy the symptoms of the disease. In this case as well as the Brazilian case above, fewer than half of these plants have been scientifically investigated. Local and Indigenous perceptions and beliefs about the natural versus supernatural aspects of the disease also determine the type of medicine that will be sought. When malaria is believed to have natural and supernatural parts to its etiology, local traditional healers and remedies are more likely to be prioritized (Al-Adhroey et al. 2010; Joshi and Banjara 2008).

Recently, there has also been critically important research attention on assessing ILK of zoonotic transmission and how animal species may also be useful for therapeutics (see discussion above of Friant et al. 2022; Munajat et al. 2021; Naserrudinet al. 2022). For example, when hunter-gatherers in Orang Asli, Peninsular Malysia were asked about this topic, the majority of people understood that mosquitoes transmit the disease and almost half of the participants related transmission to the presence of non-human primates near households, knowledge which is negatively correlated with prevalence of disease (Munajat et al. 2021). Indigenous hunters and gatherers are routinely exposed to malaria. Assessing their knowledge of zoonotic routes of transmission is as important for eradication as understanding the traditional and other methods they use in prevention and treatment of the disease. A recent study involving four ethnic groups in Nigeria analyzed ILK about zoonotic diseases and interactions with 44 different animal species as well as a survey of zootherapeutics (Friant et al. 2022). This study reported that these four communities had knowledge of 172 medicinal uses for animals and animal parts, involving 44 different species of wild and domesticated animals, including zootherapies for malaria. Contact with animals mitigates and may exacerbate exposure risks for zoonotic spillover particularly when human groups are seeking out non-human primates for their use as medicine, and particularly when seeking those that are already exhibiting symptoms of disease.

Scholars have also begun documenting ILK about zoonotic spillover and disease prevention through human-plant interactions. For example, a recent survey of rural communities in Sabah, Malaysia that are dealing with malaria infections caused by *P. knowlesi* revealed they had no misconceptions about this disease, its relationship to local primates, and how to effectively use local plants to prevent spread of the disease (Naserrudin et al. 2022). Interviews with local people demonstrated their understanding that the disease was related to environmental factors, including agricultural expansion and deforestation that had increased contact with macaques and risk of mosquito bites. The community also had an extensive repertoire of traditional and other preventative practices already in place, from preventing stagnant water to burning leaves and coconut fiber to produce smoke and repel mosquitoes. They reported planting specific species around their homes to act as mosquito repellants and using some plants, such as lemongrass, as a lotion to repel mosquitoes.

ILK systems are also slowly being operationalized into public health efforts to control the spread of malaria as well. In Zimbabwe, ILK about the relationship between malaria, weather (temperature and rainfall), and environmental indicators (plant and animal behavior and cosmological variables) have been used to create an early warning system to prevent epidemic malaria (Macherera et al. 2017). This kind of hybrid knowledge formation is critical not just for management of diseases but for widespread disaster mitigation in general (Mutasa 2015). There is a lot of potential for ILK systems (past and present) to inform efforts to treat malaria more effectively in the global context, to control malaria's spread, avoid zoonotic spillover, and understand all of these vulnerabilities more completely. This is an important growth area for policy makers and organizations seeking to have an impact on this disease in the Anthropocene.

Conclusion

Appreciating the long history of malarial infection and the deep value of ILK systems will be pivotal for creating an equitable sustainable future. These often-overlooked systems hold the key to understanding social determinants of health and well-being, biological evolution, and climate-driven interactions. This chapter reviewed selected literature to describe a planetary health approach to malaria that could integrate anthropological, biological, and climate science evidence for the transmission and spread of the disease in the past, present and future. Interdisciplinary approaches are not just beneficial but will be essential to understand the longstanding relationship and complex interactions between malarial pathogens, their vectors, and the human-environmental nexus. Biological anthropology has a lot to offer in regard to understanding human-pathogen evolution, risks related to zoonotic spillover, and the natural history of malaria as we integrate ancient textual sources (Newfield 2016; Perry and Gowland 2022; Shin et al. 2018; Wilson et al. 2023), molecular evidence for infection and co-evolutionary processes (Brickley 2024; Escalante and Ayala 1994; Hedrick 2011; Loy et al. 2017; Schats 2023; Taylor et al. 2012), and direct evidence from ancient human remains (Llanos-Lizcano et al. 2024; Wilson et al. 2023) to provide a deep source of data for predictions about the future of health in human societies.

There are limitations to paleopathological understanding of malaria, including the challenges of differential diagnosis in the skeleton (Brickley 2024), finding evidence for the plasmodia in ancient human remains, and the interpretation of textual sources (Mitchell 2017). The porotic lesions we use to diagnose the possibility of malaria in human remains are widespread in archaeological human skeletons; they result from a variety of different diseases and other disruptions to homeostasis; and there is thus no consensus on their diagnostic specificity. Assessments of *cribra orbitalia* and porotic hyperostosis are more effective when combined with paleoclimate and paleoenvironmental data and archaeological information about population density and anthropogenic changes to the landscape (Bourbou 2020; Gowland and Western 2011; Robbins Schug 2020b; Robbins Schug et al. 2023; Schats 2023; Vlok et al. 2021). For skeletal lesions and in the case of textual sources, a deeply contextualized analysis is critical because anemia or recurrent fevers are not necessarily due to malaria. Combining the assessment of skeletal lesions with evidence for marrow hypertrophy is also useful in distinguishing acquired anemia from other conditions that can cause porotic lesions and for individuals who have anemia but do not develop porotic lesions (Brickley 2024). Using original texts (not modern translations) and being clear about limitations to different sources of evidence is an important part of rigor in our discipline (Mitchell 2017).

Local and Indigenous Knowledge systems about the nature of a disease, its transmission, treatment, and relationship to environmental and climatological factors have been and will be critical for the future of infectious disease eradication, including malaria (Agozino 2017; Cáceres et al. 2017; Cohen 2019; Frausin et al. 2015; Kader Maideen et al. 2022; Macherera, Chimbari, and Mukaratirwa 2017; Malatji 2022; Munajat et al. 2021; Munguti 1997; Odonne et al. 2021; Phoobane and Masinde 2023; Tabuti et al. 2023; Zakariya et al. 2021). There is a lot of work to be done if paleopathology is to contribute knowledge in a way that is useful to public health and PH communities. These projects will necessarily be large in scope and will require dedicated resources of time and effort. One example of a promising research agenda can be found in recent work by Leal Filho and colleagues (Leal Filho et al. 2022), who conducted a literature review of ILK about climate change and adaptation strategies for food security. They tabulated ILK for its direct application for policy purposes. Such work has yet to be conducted for ILK about disease and its impacts but such an effort has promise for ensuring a more equitable sustainable approach to health in the face of a changing climate.

Malaria is a growing threat to human health, but it is not a standalone issue. It is part of a suite of significant challenges that humanity is now facing, including a growing human population faced with urbanization, socioeconomic inequality, structural violence, habitat loss and fragmentation, and a mass extinction event that is accelerating. Loss of plant diversity and forest destruction has an impact on malaria transmission (Biswas et al. 2023; Burkett-Cadena and Vittor 2018; Ellwanger et al. 2022; Gottdenker et al. 2014; Guégan et al. 2020; Mancini et al. 2024; Ortiz et al. 2021; Whitmee et al. 2015; Yasuoka and Levins 2007). Ethical, equitable, sustainable solutions to this nexus of problems have been difficult to enact, particularly in the face of changes driven by a corposystem in opposition to the biosystem, over consumption, growth, and greenwashing false solutions to the crisis (Lamoreux and Bennett 2024). Community engaged anthropological research can report solutions to the growing malaria crisis that are designed and implemented in conjunction with Indigenous communities and under their leadership. Indigenous people not only steward the land and ecosystems of malarial areas, but they are also frequently the most affected by communicable diseases like malaria. Participant observation can develop sustainable anti-malaria interventions that protect broad swaths of a country's population because they are designed with respect and honor to cultural beliefs and traditions about religious, magical, and natural elements of malaria (Cáceres et al. 2017).

We urgently need to reprioritize our actions toward sustainability, ethical cooperation and engagement, and peaceful political and economic forms and PH offers a vehicle for doing this. Public health is not just a sector; it is also a powerful vehicle for communicating the urgency of the threats posed by global warming and for catalyzing social change. We must leverage it to its full potential. In conclusion, we must remember that rapid climate change and comprehensive societal reorganization is not just possible, it has been a pivotal part of human history. It is not a question as to whether it is possible to change; rather, it is a question as to when we began to doubt our ability to adapt and overcome. Resilience is a key feature of human evolution and our future depends on respect for and acknowledgement of the adaptable nature of our species.

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