Compounding Vulnerabilities: Syndemics and the Social Determinants of Disease in the Past

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Abstract

Objective: This article explores the theory and utility of a syndemic approach for the study of disease in the past. Syndemic principles are examined alongside other theoretical developments within bioarchaeology. Two case studies are provided to illustrate the efficacy of this approach: Tuberculosis and vitamin D deficiency in 18th and 19th century England, and malaria and helminth infections in Early Medieval England. **Materials:** Public health studies of present syndemics, in addition to published bioarchaeological, clinical and social information relating to the chosen case studies. **Methods:** The data from these two historical examples are revisited within a syndemic framework to draw deeper conclusions about disease clustering and heterogeneity in the past.

Results: A syndemic framework can be applied to past contexts using clinical studies of diseases in a modern context and relevant paleopathological, archaeological, and historical data.

Conclusions: This approach provides a means for providing a deeper, contextualised understanding ancient diseases, and integrates well with extant theoretical tools in bioarchaeology

Significance: Syndemics provides scholars a deep-time perspective on diseases that still impact modern populations.

Limitations: Many of the variables essential for a truly syndemic approach cannot be obtained from current archaeological, bioarchaeological, or historical methods.

Suggestions for Further Research: More detailed and in-depth analysis of specific disease clusters within the past and the present, which draws on a comprehensive analysis of the social determinants of health.

Keywords: syndemics, tuberculosis, vitamin D deficiency, malaria, helminth infections, Great Britain

- 1 1.1 Introduction
- 2

3 Paleopathology has contributed substantially to global understandings of disease, 4 providing long-term perspectives and revealing the biocultural patterns and complexities 5 in human/pathogen interactions. Study of ancient disease must rely on an assumption of biological and ecological uniformitarianism, allowing extrapolation of factors such as 6 7 disease transmission and virulence to different cultures, ecologies, and time periods. By 8 contrast, the actual complexities of ancient disease are easily downplayed as 9 confounders, exceptions, and idiosyncrasies in our often incomplete and patchy skeletal data. Within populations these complexities can take the form of 'hidden 10 11 heterogeneities', which have formed the basis of considerable interpretive challenges in 12 the discipline (Wood et al., 1992). Here we suggest that a syndemic approach allows 13 bioarchaeologists to think more deeply about the social and economic, in addition to the 14 biological, contexts associated with disease.

The SARS-Cov-2 virus exemplifies the heterogeneity of risk and outcomes 15 experienced by different subsections of a population exposed to the pandemic. COVID-16 17 19 very quickly became a global disease, but its effects were locally disparate. A particular pattern was the high levels of morbidity and mortality amongst low socio-18 economic status and minoritized ethnic groups. Initially this was linked to the high 19 20 frequency of comorbid conditions in the communities hardest hit, such as obesity, 21 diabetes mellitus, and hypertension. Public health researchers, however, soon rejected 22 the biological determinism that underpinned these initial assessments, arguing instead 23 that SARS-Cov-2 should be understood in relation to existing health disparities rooted in 24 long-term structural inequalities (Gravlee, 2020; Pirtle 2020; Singer et al., 2021). The 25 virus was not landing on a level playing field – instead it was interacting with individuals 26 who had varying inherent vulnerabilities due to intersectional, inter-generational and 27 socio-cultural inequality. COVID-19 thus exposed the fault lines within society (Wade 28 2020). To understand the patterns of morbidity and mortality associated with the 29 pandemic, it is essential to do so in relation to existing diseases, but also, crucially, the 30 socio-cultural and historical milieu.

1 Understanding disease processes and prevalence in terms of the synergistic 2 interaction between a pathogen and existing morbidities within specific socio-economic. 3 cultural and natural environments has been coined the 'syndemic' approach 4 ('Synergistic Epidemic, Singer 1996, 2009). Syndemics is a concept developed by Singer in the 1990s for explaining the relationship between substance abuse, violence 5 6 and HIV/AIDS (known as the SAVA syndemic). It is defined as "a set of enmeshed and 7 mutually enhancing health problems that, working together in a context of noxious social 8 and physical conditions, can significantly affect the overall disease burden and health status of a population" (Singer, 2009, xiv). Syndemics are not restricted to infectious 9 10 diseases and can involve the spectrum of disorders, including psychiatric or psycho-11 social conditions (Singer et al., 2017; Tsai, 2015). These elements synergistically 12 compounded biological and social ills, with AIDs essentially classified as an opportunistic infection within that context. 13

14 When Singer (1996) applied this concept to HIV/AIDS it facilitated understanding of the complex interactions and vulnerabilities associated with this condition; for 15 16 example, co-infection of HIV and tuberculosis resulted in a synergistic interaction between the bacterium and virus, which exacerbated the rapid progress of each. These 17 18 co-infections were syndemic because they disproportionately occurred amongst minoritized and impoverished groups living within specific socio-political contexts 19 20 (Singer 2017, p. 941). Likewise, the heterogeneity of impacts of COVID-19 are best 21 understood within a syndemic framework because the pandemic hit communities with 22 socially determined patterns of chronic disease, and these pre-existing conditions 23 interacted synergistically with COVID-19 to produce greater morbidity and mortality risk. 24 The syndemic approach has been applied across health-related disciplines to other 25 "syndromes" that cluster in particular environments: childhood sexual abuse, depression, and partner violence and HIV in men who have sex with men (Stall et al., 26 27 2003), alcohol use, illicit drug use, depression, childhood sexual abuse, and intimate 28 partner violence in men who have sex with men (Tomori et al., 2018), metabolic 29 disease, mental illness, poverty, and infectious diseases such as HIV (in Kenya), tuberculosis (in India), and depression (in South Africa) (Mendenhall et al., 2017), and 30 31 violence, immigration, depression, type II diabetes, and abuse (or the VIDDA syndemic) in Mexican female immigrants in the U.S. (Mendenhall, 2012) (for a recent summary of
examples, see Singer et al., 2021).

3 Paleopathology has recently moved towards a deeper theoretical and 4 methodological analysis of sources of disease heterogeneity – paying attention to the many shades of gray to explore the meaning within. This exploration has been assisted 5 6 by the sociological turn over the last two decades within the discipline, including an 7 increased emphasis on osteobiographical narratives, and a consideration of the 8 interplay between aspects of identity and disease over the life course (Argawal 2016, 9 Baker and Argawal 2017). The recent incorporation of perspectives relating to the 10 Developmental Origins of Health and Disease (DOHaD) framework have further 11 emphasized the key role of developmental, biographical and inter-generational 12 dimensions when interpreting disease risk and expression. The discipline has also adopted a more 'particularized' biocultural analysis through the adoption of Margaret 13 14 Lock's (1993) concept of 'local biologies', which emphasizes the need to interpret 15 disease/body interactions in terms of local entanglements of history, culture, geography, 16 and ecology (Lock 1993, Niewöhner & Lock, 2017, p. 687). Finally, recent work has also 17 drawn upon Black feminist research on the intersectionality between identities such as 18 gender, low socio-economic status and ethnicity, and how these exacerbate or mitigate 19 exposure to disease risk and biological responses (Crenshaw 1989, Geller 2021, Mant 20 et al. 2021, Yaussy 2019, 2022). What all these perspectives have in common is that they each emphasize the socio-cultural and historical embeddedness of disease risk 21 22 and the consequent heterogeneity of individual responses within populations.

23 Medenhall et al. note (2022, p. 2) "Everyone concerned with past health would 24 gain considerably by viewing epidemic clusters through the lens of syndemic theory" 25 (see also Newfield, 2022). With this in mind, we outline here the potential and application of the syndemic framework for bioarchaeological and paleopathological 26 27 analyses. We start with the present-day pandemic as an exemplification of syndemic effects and follow this with two examples of past diseases (tuberculosis and malaria), 28 29 illustrating how the interpretation of each within specific geographic and temporal contexts can be substantially enhanced by a syndemic approach. We discuss how this 30 31 framework intersects with other theoretical approaches recently adopted in

palaeopathology, including the life course and inter-generational insights provided by
the Developmental Origins of Health and Disease hypothesis, and the need to ground
biological effects within an understanding of intersectional, socio-cultural environments
that shape disease clustering and interaction (Gravlee, 2020; Singer et al., 2017, 2022).

5 6

1.2 A syndemic perspective of COVID-19

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8 Well over two years into the COVID-19 pandemic, statistics on disease mortality, now 9 exceeding 6 million deaths globally, have become a familiar part of the news cycle. 10 Early messages from the government suggested that COVID-19 was an 'equal 11 opportunities' virus - it did not discriminate between rich or poor. This myth was 12 promptly dispelled when public health researchers soon noted the increased mortality risk from COVID-19 for those with underlying health conditions (e.g., cardiovascular 13 14 disease) (Bambra et al., 2021; Bambra et al., 2020). The pre-pandemic pattern of 15 chronic disease is strongly linked to the social determinants of health, such as 16 occupation, living conditions, nutrition, exposure to pollutants, marginalization and 17 subsequent psycho-social stress. Furthermore, those in low-income jobs, often on 18 contracts with no sick pay or holiday pay, or those classed as essential workers, could 19 not 'lockdown' and socially isolate (Bambra et al. 2020; Gravlee 2020), The synergistic 20 interaction between COVID-19 and pre-existing health problems, in concert with 21 socially-conferred vulnerabilities and risks, meant that at a local level the pandemic was 22 experienced syndemically (Mendenhall, 2020)

23 In the U.S., Hispanic/Latino, Native American, and Black individuals have been disproportionately represented among those with poorer COVID outcomes in relation to 24 25 their representation in the population throughout the pandemic. CDC age-adjusted data 26 from late winter 2022 indicate that risks for hospitalization and death due to COVID-19 27 are anywhere from 1 to almost 4 times higher for Native Americans, Black, and Hispanic persons than for White, non-Hispanic individuals (Centers for Disease Control, 2022). 28 29 Age-adjusted data from the UK from February 2022 also demonstrate that during the 30 Omicron surge, Bangladeshi and Pakistani males and females were over two times 31 more likely to die from COVID-19 than White British individuals, statistics that have not

changed dramatically from before Omicron became the main variant (Ahmad et al.,
2022). Even adjusting for the presence of pre-existing medical conditions that increase
the risk of COVID-related mortality, deaths of BAME (Black, South Asian, mixed, or
other ethnicities) individuals of all ages were up to 1.5 times higher compared to Whites
in the UK (Mathur et al., 2021; Williamson et al., 2020).

6 Biological and racial determinism, often prevalent in medical research, does not 7 provide a sound or useful approach to COVID-19 (Gravlee, 2020). Instead, these statistics reflect the coalescence of multiple, historically routed, intersectional social 8 9 disadvantages and their impact on disease risk and biological response to SARS-Cov-2 10 (Bambra et al. 2020; Pirtle 2020). The synergistic interaction between COVID-19 and poverty-associated chronic disease elevated mortality in vulnerable communities. 11 12 Legacies of structural violence and inequalities over the centuries have been highlighted, which for the USA pointed to the root causes of slavery (Gravlee 2020). 13 14 This was exacerbated by a culture of systemic racism and biased treatment of people of 15 color by doctors and other medical practitioners and assumptions regarding genetics 16 and race (Gravlee, 2020, 2009). Meanwhile, in the UK the chief medical officer 17 Professor Chris Whitty highlighted the similarities between the map of COVID-19 mortality and areas with high child mortality (linked to poverty) in the 19th century 18 19 (Jeavans, 2021). The importance of a historical perspective on the social determinants 20 of health have come into stark focus during the course of this pandemic.

The disparate impact of COVID-19 across communities have lead 21 22 epidemiologists, public health researchers, and anthropologists to argue that, due to the 23 diverse experiences with the disease in some contexts, COVID-19 is not actually 24 pandemic, but a series of different, localized syndemics (Bambra et al., 2020; Freeman, 25 2020; Gravlee, 2020; Mendenhall, 2020; Mendenhall et al., 2022). Thus, while COVID-19 has been described as a 'global syndemic' (Horton, 2020, p. 874), Medenhall et al. 26 27 (2020) and Singer et al. (2021, 2022) argue that the biological and social interaction, 28 and clustering of COVID-19 are driven by different factors both locally and between 29 countries. Instead, Singer et al. (2021, p. 8) refer to COVID-19 as a 'syndemogenic disease' in that it forms adverse syndemic interactions with many other infectious and 30 31 non-communicable diseases. In order to understand these interactions, however, it is

essential to understand the localized and historically embedded drivers of disease
 ecology and health inequalities. Our lived experience of this pandemic reveals the utility
 of the syndemic perspective and here we discuss the usefulness of this application
 within paleopathology.

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6 2.1 Syndemics and Bioarchaeology

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8 Anthropology provides a holistic view of human experience, and anthropological 9 approaches to health and disease have always emphasized the importance of social, 10 economic, ecological, and cultural contexts and how these interact with human biology (Dimka et al. 2022). Evidence of this holism is seen in the anthropological relevance of 11 12 disease ecology (Brown et al., 1990; Inhorn and Brown, 1990), biocultural anthropology (Singer, 2015; Wiley and Cullin, 2016; Zuckerman and Martin, 2016), the One World + 13 14 One Health approach (Brown and Nading, 2019; Craddock and Hinchliffe, 2015; 15 Woldehanna and Zimicki, 2015; Wolf, 2015), Developmental Origins of Health and 16 Disease (DOHaD) (Gluckman et al., 2005, 2010, 2008; Gowland, 2015), and critical 17 medical anthropology (Baer et al., 1986; Goodman and Leatherman, 1998; Leatherman 18 and Goodman, 2020, 1997; Singer and Baer, 1995). Despite the apparent 19 interconnectedness of these approaches, in many ways they have been siloed rather 20 than integrated in the anthropological study of disease both past and present (Dimka et al. 2022; Leatherman and Goodman, 2020; Singer, 2015). 21

22 The syndemic model seeks to incorporate all aspects - biological, social, 23 environmental - that lead to high prevalence of certain diseases within a particular 24 population. The multiple components of the syndemic model include synergism between 25 diseases of all types (infectious or non-communicable), mental health issues, structural 26 racism, environmental toxicity, inadequate nutrition, and co-existing social and 27 economic situations within the community that increase the prevalence of disease and 28 the chance of poor disease outcomes. This "biosocial complex" goes beyond simply 29 noting comorbidities (the biological interaction between diseases) to include how social and economic factors may contribute to increased morbidity and mortality from these 30 31 diseases in the community (Gravlee, 2020; Singer et al., 2017). Identification of a

1 syndemic necessitates a multi-level approach that highlights broad-scale economic, 2 ecological, and social factors affecting the community and the pathways by which they 3 interact (Singer et al., 2017; Tsai et al., 2017). There is as much concern for how the 4 confluence of deleterious factors affects an individual as in how the presence of such factors in the community may exacerbate the problem, even if an individual is not 5 6 directly affected (see Tsai, 2018; Tsai et al., 2017). For example, high rates of home 7 foreclosure in a community could amplify individual-level risk for other elements of a syndemic, such as mental health issues, regardless of whether or not an individual 8 personally experienced home foreclosure (Tsai, 2015). In addition, rather than just 9 10 focusing on blanket variables such as "poverty" the syndemic model seeks to identify 11 the specific pathways in which social contexts and behaviors linked to poverty affect 12 disease. Therefore, clustering of disease alone is not enough to qualify a situation as a 13 "syndemic" (Mendenhall et al., 2022; Tsai, 2018). It is the "additive" adversity of disease interaction that is key (Singer et al., 2021; Tomori et al., 2018) (see Table 1). 14

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Table 1: Examples of disease interactions classified as "syndemic" according to
 Tsai (2018)

Disease Interaction	Definition	Example
Mutually Causal Epidemic	Diseases within the syndemic have shared etiologies	The SAVA syndemic: substance abuse, HIV acquisition, and violent victimization (Singer, 1996)
Synergistically interacting epidemics	Diseases within the syndemic have synergistic effects	HIV and tuberculosis, HIV and hepatitis B (Singer and Clair, 2003)
Serially causal epidemics	Diseases or health risks accumulate through time (potentially utilizing a DoHAD or life history approach)	Political violence, humanitarian crises, gender discrimination, PTSD and depression in former female child soldiers in Nepal (Kohrt and Carruth, 2022)

18

19 The syndemic approach has only rarely been applied by medical scholars to

20 historical contexts; for example, Sawchuk and colleagues' (2022) study of the 19th

century syndemic in Gibraltar, driven by cholera and smallpox, within the context of 1 2 overcrowding, poor sanitation, and the regular influx of pathogens due to the island's 3 strategic location. Paleopathologists have begun recognizing the value of a syndemic 4 approach, although in depth applications are relatively limited to date (e.g., DeWitte and Wissler 2022; Larsen and Crespo, 2022; Robbins Schug and Halcrow, 2022). This is 5 6 perhaps surprising given the embeddedness of this discipline within biocultural 7 perspectives. Larsen and Crespo (2022) argue for the value of a 'paleosyndemic' lens 8 for understanding 'how epidemics end' in the past, focusing on leprosy in Medieval 9 Europe, and the Black Death in Europe in the 14th century. While paleopathological 10 evidence can be especially challenging, the discipline is well placed to provide valuable 11 insights into disease interactions and clustering within specific socio-cultural contexts 12 and over time.

A syndemic perspective requires a deep understanding of the potential biocultural and environmental pathways involved in the clustering and comorbidity of particular diseases. Some of these factors may be invisible in the archaeological and skeletal record, and thus impossible to integrate into the model. Many

bioarchaeologists, however, regularly contextualize their results within the social and
natural environment and explore the antagonistic effects of co-morbid or multi-morbid

19 diseases that could provide the basis for a syndemic approach. In addition,

bioarchaeology often utilizes multi-scalar analysis through which individual life histories
or osteobiographies have been used to generate population- or group-level

characterizations of disease burdens in a community. Paleopathologists have frequently explored comorbid conditions and the co-occurrence of epidemics in the past, but often from the perspective of 'cumulative adversity' (Tsai, 2018). Essential components of the syndemic approach would include an analysis of the synergistic interaction of these disease processes with each other, and crucially, in concert with socio-cultural inequities.

Bioarchaeologists furthermore have called for understanding the sources of inequity that create heterogeneous experiences, risks and outcomes of disease. Intersectionality in bioarchaeology and bioanthropology seeks to construct how the interplay of identities result in systematic oppression and social inequity that impacts

1 biology (Blakey 2001; DeWitte and Yaussy, 2021; Dimka et al, 2022; Franklin and 2 Wilson 2020: Torres-Rouff and Knudson 2019; Watkins 2012, 2020; Yaussy 2019). The 3 syndemics model approaches disease much in the way intersectionality approaches 4 inequity - more than just the sum of its parts, but instead fully embracing the "intersectional experience", (Crenshaw, 1989, p. 140), or the cumulative effects of each 5 6 element that uniquely build upon and magnify the other(s). One critique of this approach 7 argued that syndemic theory provides no additional value to that supplied by intersectionality and, worse, fails to analyze the forces creating inequity 8 (Sangaramoorthy and Benton, 2022). These sentiments have been countered, however, 9 10 by others who argue that "intersectionality-informed syndemics may offer entry into settings that perpetuate invisibilization of people with multiple identities that are 11 12 subjected to forms of oppressions" (Kline, 2022). By turning away from the concept that the poor are to blame for their problems, syndemics theory "seeks to identify the role of 13 14 power and structural injustices in creating pathology and recognizing how pathology can 15 intensify inequalities and multiple forms of oppression' (Bulled et al., 2022).

16 Other recent theoretical innovations within medical anthropology yield further synergies with the syndemic perspectives that are applicable to disease in the past. For 17 18 example, the focus on 'local biologies' (Lock 1993) underscores the simultaneously 19 biological and cultural materiality of the skeleton, which can only be understood within 20 its specific historical, social and ecological relationships. Linked to this, the Developmental Origins of Health and Disease (DOHaD) framework emphasizes the 21 22 importance of life histories, and in particular the sensitivity of early life and inter-23 generational adversity for later life frailty and disease risk (Barker 2012). Intrauterine 24 circumstances are closely linked to social and environmental variables and if maternal 25 health is compromised via malnutrition, this can have repercussions for subsequent generations (Barker 2012, Gowland 2015). Jonathan Wells (2010) highlights the 26 27 importance of 'maternal somatic capital' for interpreting links between social inequality and health, arguing that mothers living in poverty may have low 'somatic capital', 28 29 leading to disadvantageous consequences for their off-spring, such as low birth weight and increased risk of chronic disease later in life. Wells (2010) refers to the transmission 30

of the effects of poverty across the generations in this way as a form of 'metabolicghetto'.

3 Crespo (2021) and McDade et al. (2012; 2010) note the sensitivity of the immune system to ecological and social factors during the first 1000 days of life and the impact 4 of this for longer-term inflammatory responses. Crespo (2021) highlights the utility of a 5 6 syndemics in addition to a DOHaD perspective for interpreting inflammatory skeletal 7 responses (described as a skeletal inflammatory index - SINDEX). He argues that because of the 'complex heterogeneous biosocial landscapes' (2021, p. 87) there will 8 9 be no uniform inflammatory model yielded by the SINDEX. Indeed, such rampant 10 heterogeneity is observed in many paleopathological studies, such that interpreting 11 pathological skeletal lesions can be extremely challenging. The reason, of course, is 12 that like COVID-19 today, diseases are not landing on an equal playing field, but are 13 interacting with bodies that have their own socio-culturally, biographically and 14 intergenerationally subscribed biological response.

15 Dimka and colleagues' (2022) provide a model for understanding differential risks 16 in morbidity and mortality in recent historical epidemics using three different episodes as examples (the 1918 influenza epidemic, the 2009 influenza epidemic, and COVID-19). 17 18 They found similar patterns but different magnitudes of heightened risk for disease by sex/gender, race/ethnicity/indigeneity, and comorbidities/disabilities across all three 19 20 epidemics. They imply that this intersectional approach should be the beginning of understanding "local biologies" and interconnected variables related to health, and 21 22 greater engagement with syndemic theory will move this type of investigations forward.

DeWitte and Wissler (2022) approach the 14th century Black Death in England as 23 24 a syndemic, during which certain communities were disproportionately impacted by agricultural crises of the 13th and 14th centuries. This could have led to intergenerational 25 health disparities that continued until the Black Plague epidemic, resulting in a 26 27 disproportionate mortality amongst individuals of lower socioeconomic status. The survivors of the epidemic had reduced frailty and higher survivorship than pre-Black 28 29 Death groups (DeWitte 2014, 2018), highlighting the long-term impacts of disparate 30 susceptibility.

1 While Battles and Gilmour (2022) and Franklin and Wilson (2020) do not 2 explicitly take a syndemics approach in their studies on ancient disease, they include a 3 multitude of socioeconomic and other biological factors impacting disease outcomes. 4 Battles and Gilmour (2022) focus on the after-effects of infection, providing one example of how cessation of an infection can either prolong a syndemic or initiate a new one. 5 6 They focus on the experiences of polio survivors with lingering disability and the stigma 7 they face as a result of the infection, and how these individuals may have increased 8 mortality as a consequence. As they note this can have a group-level impact in a 9 community.

10 Franklin and Wilson's (2020) research exploring the confluence of sexism. 11 racism, economic subjugation, migration, and poverty in African American communities 12 after emancipation and their impacts on health also closely aligns with a nuanced syndemic approach. They found that choosing to stay in the rural South versus moving 13 14 to urban areas resulted in disparate patterns of morbidity and mortality reflecting the 15 unique social, environmental, and economic contexts of each experience. 16 Bioarchaeologists clearly recognize the compounded effects of biological and socio-17 economic variables on health, but often do not "close the circle" by exploring the specific 18 pathways by which these factors result in disease clustering. Upon recognizing a cluster 19 of diseases affecting the skeleton, a syndemics approach encourages a deeper 20 exploration of the biological interactions between these conditions, and how local social 21 and environmental determinants of health will further exacerbate the effects (Figure 1). 22 23 3.1 The Rickets-Tuberculosis-Poverty Syndemic in 18th and 19th Century

24 England

25

26 Vitamin D deficiency has been implicated as a risk factor in the current COVID-19

27 pandemic and has been linked to the severity of the disease (e.g., Dror et al. 2022).

28 Vitamin D therapy provided to certain groups infected with COVID, such as older adults,

has improved mortality risk and disease outcomes (Annweiler et al. 2022). The

30 mechanism behind this relationship largely lies in the impact of vitamin D on the

31 immune system, particularly the cells involved in fighting respiratory infections. Another

example of a respiratory disease that has a synergistic relationship with vitamin D 1 2 deficiency is the one caused by the *Mycobacterium tuberculosis* (MTB) complex. MTB 3 and vitamin D deficiency are both conditions that can affect the human skeleton and 4 have been reported on extensively in the paleopathological literature. They have been found to co-occur in some historical and archaeological contexts, particularly 18th and 5 6 19th century Britain (Donoghue, 2017; Redfern et al., 2015; Roberts et al., 2016; 7 Roberts and Brickley, 2019; Snoddy et al. 2016). Employing a syndemic approach 8 allows paleopathologists to better understand the underlying interactions of these two 9 diseases, the social environment that increases poor disease outcomes, and possible 10 undernumeration of individuals with the condition.

11

12 3.1.1 Tuberculosis (MTB)

13 Tuberculosis (MTB) is a droplet infection tied to mycobacteria mostly included within the 14 Mycobacterium tuberculosis complex. Primary infection can occur in the lungs or the 15 gastrointestinal system, and only a small fraction of those infected develop symptoms 16 after initial infection (Roberts and Buikstra, 2019). The bacilli can lie latent for many 17 years until either additional exposure or a decline in immune system functioning 18 reactivates the pathogen, resulting in a delayed emergence of symptoms (secondary or 19 post-primary TB). Infection with *M. tuberculosis* complex pathogens may result in the 20 development of skeletal lesions in 3 - 5% of untreated cases (Jaffe, 1972). MTB bacilli travel to bone through the circulatory system and favor areas of hematopoietic marrow 21 22 in the skeleton such as the vertebral bodies and long bone epiphyses in adults with 23 additional foci in flat bones of the crania and diaphyses of long bones in children (Lewis, 24 2018; Roberts and Buikstra, 2019). The common diagnostic lesions of skeletal MTB are 25 resorptive foci in the vertebral bodies and joint regions, with the less-specific abnormal bone formation on the pleural surface of ribs providing an additional indicator (Roberts 26 27 and Buikstra, 2019). The extraction and identification of *M. tuberculosis* complex DNA in 28 skeletal remains has provided an additional pathway to diagnosis (Harkins et al., 2015; 29 Kerudin et al., 2019; Müller et al., 2014; Sabin et al., 2020; Zink et al., 2003), and has demonstrated that MTB diagnosis based on skeletal lesions alone undercounts the 30 31 number of people infected in ancient communities.

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2 3.1.2 Vitamin D Deficiency

3 Vitamin D is a prohormone critical for metabolism of the essential bone minerals 4 calcium and phosphorus. A deficiency in vitamin D triggers the release of stored calcium from the skeleton causing osteomalacia, pseudofractures, poor bone density, and 5 6 biomechanical-related shape deformities (Brickley et al., 2020). Vitamin D primarily is 7 obtained through UVB exposure that initiates the synthesis of the vitamin from 7-8 dehydrocholesterol (Holick, 2007, 2005). Diet and nutritional supplements also provide 9 a source of vitamin D for the body. Vitamin D synthesized through UVB radiation or 10 ingested via dietary sources undergoes hydroxylation in the liver to form the circulating form of the vitamin, 25(OH)D. A second hydroxylation in the kidney by the enzyme $1-\alpha$ -11 12 hydroxylase (CYP27B1) produces the active form, 1,25(OH)₂D₃ (calcitriol), which regulates calcium and phosphate levels in the skeleton, gut, and kidneys (Chanchlani et 13 14 al., 2020; Holick, 2007).

15 Vitamin D deficiency impacts bone mineral metabolism by increasing PTH 16 activity that stimulates renal tubular reabsorption of calcium, increases production of 1,25(OH)₂D₃ in the kidney, increases renal excretion of phosphorus 17 18 (hypophosphatemia), and stimulates osteoblast activation (Holick, 2007). This last 19 process triggers RANKL expression, causing preosteoclasts to transform into 20 osteoclasts that dissolve the bone matrix to release calcium and phosphorus into the blood (Brickley et al., 2020, p. 93). Genetic polymorphisms affecting phosphorus 21 22 regulation (hypophosphatemic rickets) (Bitzan and Goodyer, 2019), calcium-sensing 23 receptors (CaSR) (Wu et al., 2017), or VDR function (vitamin D-resistant rickets) 24 (Liberman, 2007) can also result in skeletal rickets. Many diseases and iatrogenic 25 factors also affect the bioavailability, synthesis, or metabolism of vitamin D, such as hyperparathyroidism, celiac disease, cystic fibrosis, chronic kidney disease, or 26 27 medications used to treat high cholesterol (Holick, 2007).

A "deficiency" of vitamin D clinically depends on having a serum 25(OH)D level below 30 nmol/L, and an "insufficiency" is marked by levels between 30 to 50 nmol/L (Munns et al., 2016). Vitamin D deficiency manifests skeletally in non-adults as rickets, or poorly mineralized bone subject to biomechanically-caused shape changes due to the pull of gravity as well as connective tissue during movement (Brickley et al., 2020,
pp. 97–105). Adults with active vitamin D deficiency also have bone with low mineral
content ("osteomalacia") and thinned cortices susceptible to repetitive microfractures
(Brickley et al., 2020, pp. 117–121).

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6 3.1.3 Interactions between Vitamin D Deficiency and MTB

7 The benefits of vitamin D and UVB radiation for management of MTB arose early in the 8 search for its treatment. Vitamin-D-packed cod liver oil (Grad, 2004) and sunlight 9 exposure (Roberts and Buikstra, 2003, p. 228) were important elements of the 10 sanitarium regime in the U.S. and Britain in the 19th and 20th centuries. Current clinical 11 research has identified vitamin D deficiency as a risk factor for tuberculosis infection, 12 particularly pulmonary tuberculosis, and is linked to a higher bacillus load, reactivation of latent MTB, and poor disease outcomes (Aibana et al., 2019; Chocano-Bedova and 13 14 Ronnenberg, 2009; Jaimni et al., 2021; Jolliffe et al., 2017; Talat et al., 2010). MTB is 15 held in latency by macrophage-filled granulomas that surround bacilli-infected cells. 16 which must be maintained at some cost (Wilson et al., 2019). Failure of the granuloma 17 results in unfettered spread of the bacilli. $1,25(OH_2)D_3$ is essential for development of 18 the antimicrobial peptide cathelicidin located in macrophages that limits the growth of 19 MTB bacilli (Liu et al., 2007; Prietl et al., 2013) and 1,25(OH₂)D₃ prevents MTB bacilli 20 from hindering macrophage maturation (Hmama et al., 2004; Houben et al., 2006). 21 Maintenance of adequate vitamin D levels thus is essential for maintaining the 22 macrophage-filled granulomas that keep the MTB bacilli in check.

23 Conversely, infection with granulomatous diseases such as MTB can cause 24 interferon gamma (IFNy) to up-regulate the VDR and $1-\alpha$ -hydroxylase genes 25 (CYP27B1), resulting in increased production of $1,25(OH_2)D_3$ and hypercalcemia (Holick, 2007; Moloney et al., 2018; Sharma, 2000). This would presumably prevent 26 27 worsening of vitamin D deficiency during an MTB infection. However, hypercalcemia in 28 TB patients can result in renal failure, which has been documented in clinical settings 29 (Rajendra et al., 2016). In addition, an individual suffering from an active MTB infection often has insufficient nutritional intake (Feleke et al., 2019), which may result in vitamin 30 31 D deficiency and allows MTB to progress more guickly.

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3.1.4 Environmental Contexts of Vitamin D Deficiency and MTB in 18th and 19th century England

4 In addition to the synergistic impacts of vitamin D deficiency and MTB on the immune system and lesion progression, demographic and environmental factors indicate why 5 6 they also thrive in the same contexts. Tuberculosis often is referred to as a "disease of 7 poverty" (Roberts and Buikstra, 2003, p. 55), with many of the social determinants of the disease linked to poor living conditions and economic inequity, usually crowded and 8 9 unsanitary housing and poor nutrition (Lönnroth et al., 2009). Researchers point to 10 social improvement and economic growth as primary factors for reduction in MTB in 11 many regions (e.g. McFarlane, 1989; McKeown and Record, 1962), although others 12 suggest innate immunity through successive MTB exposures across generations or acquired immunity through Mycobacterium bovis or other mycobacteria exposure 13 14 played a role (Davies et al., 1999; Grange et al., 2001).

15 Vitamin D deficiency, particularly in children, also was a hallmark disease of 16 poverty during the Industrial Revolution in England and other northern European countries. Rickets was particularly entrenched in 17th to 19th century England to the 17 18 point that it was referred to by doctors as the "English disease". The combined effects of 19 low UVB exposure due to living and working conditions, other metabolic deficiencies, 20 and comorbid diseases created a "perfect storm" for high rates of rickets in working class urban industrial communities in Britain and the Netherlands (Ives, 2018; Mays, 21 22 2018; Mays et al., 2009; Snoddy et al. 2016; Veselka et al., 2021, 2015). Nineteenth-23 century British doctors noted links between the condition and early weaning, poor 24 nutrition, bad air, northern climates (although John Snow noted it as more common in 25 southern England, particularly London, than northern England and Scotland), and even heredity (Hardy, 2003). Domestic coal fires for heating and cooking also contributed to 26 27 the extensive air pollution that blocked UVB radiation and the poor air quality sent many 28 individuals indoors (Hardy, 2003). Thus, a multitude of environmental and social risk 29 factors linked to poverty or low socioeconomic status are shared between vitamin D deficiency and MTB. 30

1 The interaction between vitamin D deficiency and MTB and their shared socio-2 economic and environmental factors resulted in a Rickets-Tuberculosis-Poverty 3 syndemic in Industrial-era England (Figure 2). The co-occurrence of these conditions is 4 of no surprise to a paleopathologist or bioarchaeologist, and their high comorbidity rates even led some physicians of the time to postulate TB caused rickets in children (Parry 5 6 1872). Outlining the pathways of exactly how these diseases and their risk factors 7 intertwined provides a deeper perspective of the impacts on communities in urban 18th and 19th century England. In addition, it highlights that MTB cases based on 8 paleopathological evidence alone are likely undercounted, a methodological issue 9 10 already highlighted by recent aDNA research. In addition to the undernumeration of 11 MTB victims based on skeletal lesions alone, skeletal rickets, located at one extreme 12 end of the spectrum of vitamin D deficiency symptoms, may be the "potential tip of an unseen epidemiological iceberg" (Snoddy et al. 2016, p. 193). The environmental 13 14 factors present in this context, and the known interactions between these conditions, also support the likelihood that MTB and rickets were both pervasive conditions in 15

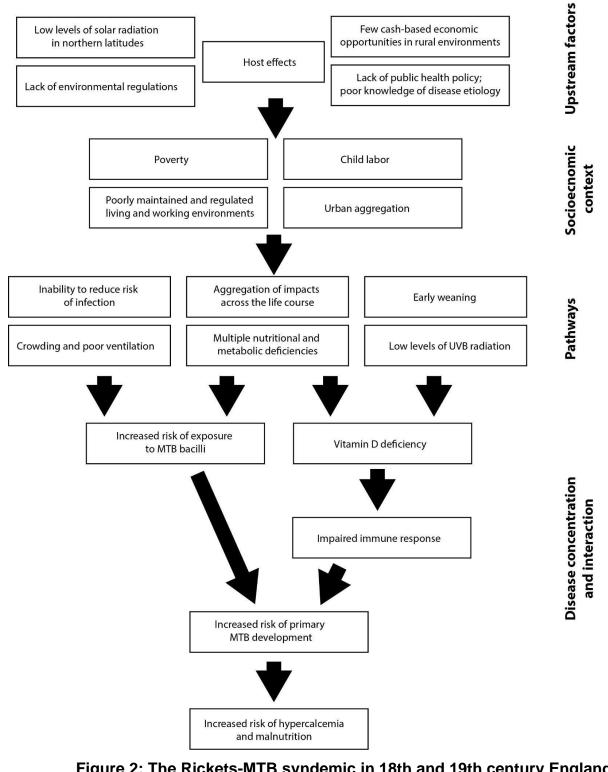


Figure 2: The Rickets-MTB syndemic in 18th and 19th century England (organization based on Gravlee 2020)

 particular socioeconomic and environmental contexts and should be treated as a
syndemic. The syndemic approach then can be used to build a model of disease
interaction and biocultural contexts in antiquity against which to assess the available
paleopathological data and identify additional factors perhaps reducing the synergistic
effects or illuminating methodological limitations (as illustrated in Figures 1 and 2).

6 The longer-term and intergenerational effects of both conditions heighten their 7 impact in this context. Vitamin D-deficient pregnant women have increased risk for 8 pregnancy complications such as eclampsia, preterm births, low birth weight babies, 9 and gestational diabetes (Hollis and Wagner, 2017; Lucas et al., 2008). Maternal and 10 newborn 25(OH)D levels tend to be correlated, and vitamin D deficient mothers give 11 birth to babies with lower vitamin D levels than normal (Lee et al., 2007; við Streym et 12 al., 2013). Epigenetic effects of vitamin D deficiency during critical intrauterine periods may be implicated in abnormalities in lung, bone, liver and immune system development 13 14 and increased risk of Type 1 diabetes (see Ideraabdullah et al., 2019; Zhu et al., 2016).

15 In addition to skeletal rickets, infants with vitamin D deficiency have risk for 16 seizures and convulsions (tetany), delayed motor skills, hyperparathyroidism, underdeveloped musculature, anemia, and even cardiomyopathy or failure (see Pettifor 17 18 et al., 2018). Longer term effects of infant deficiency in vitamin D include impaired 19 immune functioning, persistent hyperparathyroidism, reduced kidney functioning, 20 inhibited expression of vitamin D receptors (VDRs), and an increased risk of Types 1 and 2 diabetes, obesity, some cancers, neurological and behavioral disorders, 21 22 cardiovascular diseases, or multiple sclerosis (Hollis and Wagner, 2017; Ideraabdullah 23 et al., 2019; Jensen et al., 2017; Lucas et al., 2008; Pettifor et al., 2018; Reichetzeder et 24 al., 2014). Some infants whose mothers were vitamin D deficient during pregnancy may 25 not experience its impacts until well after birth. Tetany, convulsions, or cardiac issues can emerge up to 6 months of age in these infants (Pettifor and Prentice, 2011), and 26 27 can have lower than expected bone mineral density from later in infancy through to 28 adulthood (Javaid et al., 2006; Viljakainen et al., 2011; Zhu et al., 2014).

MTB infection during pregnancy also increases the chance for poor outcomes of the mother and fetus. Women with active TB infections have a much higher risk of developing anemia during pregnancy, or having a miscarriage or perinatal death,

18

preterm birth, low birth weight infant, or distressed fetus (Miele et al. 2020). In addition, 1 2 women with latent TB are more likely to develop active infections after giving birth, likely 3 due to the immunological changes that occur with pregnancy (Miele et al. 2020). 4 Congenital TB, while rare, is still a possibility, and breastfeeding may transmit the bacilli from mother to infant (Flores et al. 2021). Results from studies exploring the increased 5 6 risk of infants with vitamin D deficiency developing TB are mixed (Martinez et al. 2022). 7 In 18th and 19th century England, this cycle of infection and deficiency would 8 have contributed to the perpetuation of ill health that characterized many urban

9 environments at the time based on textual data. The intergenerational impact meant

10 that unless the social and environmental determinants of the syndemic shifted, the

11 syndemic would continue. Acceptance of the nutritional foundations of rickets in the

12 early 20th century resulted in a temporary reduction in cases in most regions in

13 England. Similarly, the discovery of the TB bacillus, the development of antibiotics such

14 as penicillin, recognition of living conditions leading to increased transmission, and

15 possibly slight commensalism through repeated infections resulted in a decline in the

16 incidence of active TB cases around the same period. Since then, both diseases

17 experienced a resurgence, rickets in the 1960s with the arrival and subsequent

18 marginalization of immigrants from former British colonies (Bivins 2014; Zhang et al.

19 2016), and TB in the 1980s with immigration from TB-prevalent countries and the rise of

20 HIV/AIDs (Pealing et al. 2013). Despite the reemergence of these conditions, the

21 sociocultural and economic frameworks of these diseases have changed dramatically

from the late 19th century, highlighting that the context rather than the presence of

disease(s) alone is fundamental to the syndemic concept (Singer et al. 2022).

24

3.2 The Malaria and Gastrointestinal Parasite Syndemic in Early Medieval England
 26

The current climate crisis is a key factor affecting human health globally, resulting in reemerging infectious diseases, food shortages, fire, floods, damage to housing and infrastructure, population movement and overcrowding. As Singer and colleagues' (2021, p. 8) note, there is "no single climate change syndemic, there are, however, multiple climate change syndemics requiring responses that are informed by locally

grounded assessments". The discipline of bioarchaeology is well-placed to contribute to 1 2 a deeper understanding of human/environment/pathogen interactions in response to a 3 range of climatic fluctuations over time, and this is a growing disciplinary focus (e.g. 4 Robbins Schug, 2021). One disease that features prominently in concerns around climate change is malaria: an infectious disease with one of the highest morbidity and 5 6 mortality rates in the world today. Malaria is caused by the mosquito-borne eukaryotic 7 protozoan parasites of the genus Plasmodium (Plasmodium falciparum, Plasmodium 8 vivax, Plasmodium malariae, and Plasmodium ovale). In many parts of the world 9 malaria, helminths and Giardia are endemic in the same areas and are often co-morbid 10 (Geus et al., 2019). Malaria and helminth/Giardia parasite syndemics today have been linked to climatic shifts, living conditions, subsistence strategies, and low socio-11 12 economic status. Here we revisit an analysis of *Plasmodium vivax* malaria in Eastern England during the early Medieval period by Gowland and Western (2012) using a 13 14 syndemic approach to better understand the social determinants and the potential 15 impact of synergistic co-morbidities. In addition to the early medieval data, we draw 16 upon clinical information relating to: recent and current helminth/Giarda/malaria 17 syndemics; evidence for the higher than expected fatalities from *Plasmodium vivax* 18 recorded in historical documents from England in the 18th to 19th centuries; and the 19 unique social/ecological milieu of the Fenlands.

20

21 3.2.1 Malaria

22 Much has been done to tackle malaria over the last 20 years, resulting in a halving of 23 mortality from malaria during this time. The World Health Organization's Annual Malaria 24 Report from 2021, however, reported an increase in malaria cases (estimated 241 25 million) and deaths (estimated 627,000) during 2020 (WHO Malaria Program, 2021). Disruption associated with COVID-19 was a primary cause of this increase, despite 26 27 efforts to mobilize relief in anticipation of the effects of the pandemic on vital services. A 28 number of authors have highlighted the syndemic interaction between COVID-19 and 29 malaria transmission potential in a number of countries in sub-saharan Africa where malaria is endemic (Shi et al. 2021, Velavan et al. 2021). The symptoms of malaria can 30 31 also, to some degree, overlap with those from COVID-19, leading to diagnostic

complications and under-reporting of co-infections of both diseases (Velavan et al.
2021). The profound effect of COVID-19 on malaria mortality highlights the fragile
nature of such hard-fought progress in tackling this disease and the need for persistent
and holistic strategic health interventions in the face of changing climate and disease
ecologies.

6 Bioarchaeological studies are well-placed to provide longer-term perspectives on 7 malaria prevalence and syndemics over time and in relation to climatic fluctuations, land 8 management strategies and cultural change. There has been a growing interest in the 9 historical and bioarchaeological evidence for malaria over the last two decades (e.g. 10 Sallares 2002; Scheidel 2003; Soren 2003; Gowland and Garnsey 2010, Gowland and Western 2012, Smith-Guzmán 2015, Smith-Guzmán et al., 2016, Newfield 2017, 11 12 Marciniak et al. 2018, Kendall et al. 2020). Such work is hindered, however, by the fact that malaria leaves no specific diagnostic skeletal lesions and historical evidence is slim 13 14 and often vague (Newfield 2017). Direct evidence in the form of pathogenic aDNA 15 evidence of *P. falciparum* malaria has been recovered from archaeological skeletons 16 (e.g. Sallares and Gomzi 2001, Marciniak et al. 2016, Loufouma Mbouaka et al. 2021). These studies have great value in terms of confirming the presence of malaria and 17 18 understanding the particular biosocial pathways of infection (Marciniak et a. 2018). 19 Ancient DNA analyses, as well as immunological assay's to detect antigens associated 20 with malaria (Loufouma Mbouka et al. 2021), are increasingly important to the study of 21 malaria in the past. However the destructive and expensive nature of such techniques 22 mean that they are currently limited in terms of insights into the overall burden of 23 disease and its broader epidemiology.

24 While malaria leaves no diagnostic skeletal lesions, it is known to be a major 25 cause of anemia in malaria endemic regions (Shankar 2000, Rodriguez-Morales et al., 2006; Douglas et al. 2012). *Plasmodium vivax* (endemic in temperate as well as tropical 26 27 climates) has been associated with more frequent and severe cases of anemia than the 28 more fatal *Plasmodium falciparum* (present in more tropical climes). *Plasmodium vivax* 29 results in functional and structural impairment of erythrocytes of infected people (Rodriguez-Morales et al. 2006). There is an established link between malaria, 30 31 haemolytic anemia and subsequent marrow hypertrophy, thus producing lesions known

1 as cribra orbitalia (CO) and porotic hyperostosis (PH) in the skeleton (Gowland and 2 Western 2012). These conditions have multiple etiologies, therefore context is essential 3 to interpreting the epidemiology of both. Paleopathological studies of malaria have 4 relied upon integrating environmental, historical and clinical evidence for malaria endemicity, with skeletal indicators of anemia (CO and PH). For example, Gowland and 5 6 Western (2012) and Smith Guzmán (2016) found correlations between habitats that 7 were known breeding grounds for the mosquito vector in the past and high frequencies 8 of cribra orbitalia. Malaria has long been recognised to exist alongside a range of 9 comorbidities that can also produce anemia and associated skeletal lesions, but 10 bioarchaeological analyses have yet to examine these interactions using a syndemic 11 framework. For example, co-infection with parasites such as helminths is known to 12 contribute to the burden of anemia (e.g. Webb et al. 2020). The multiplied effects of co-13 infection results in a cycle of poor health from which it is difficult to recover, particularly 14 in marginalized social and environmental contexts.

15

16 3.2.2 Interactions between helminth and malaria infections

Clinical studies have shown the detrimental impact of co-infection with parasites such 17 18 as hookworm and malaria in a way that aligns with syndemic principles (Adegnika and 19 Kremsner 2012). For example, Webb (2020) discusses the malaria/hookworm syndemic 20 amongst Chinese and Tamil laborers in British Malaya in the early 20th century. Here, 21 sanitation issues were a key factor in hookworm infestation, while insufficient drainage 22 exacerbated malaria infection: medical investigators were unable to differentiate 23 between anemia caused by either hookworm or malaria (Webb, 2020, 3). These 24 comorbidities each resulted in anemia as part of their own pathological process, and 25 interacted with and mutually enhanced the deleterious effects of the other parasites (Anstey et al 2009:222; Echeverri et al. 2003). 26

Fernandez (2008, 2) noted that working in contact with the soil in rural agricultural areas with endemic malaria (conditions similar to the early medieval Fenlands) carries a greater risk of both malaria and geohelminthiases. Co-infection with malaria and helminths is extremely common in tropical and subtropical regions of the world today (Jepkogei et al. 2016, Geus et al. 2019). One clinical study revealed that

amongst 0-14 year-old children with vivax malaria, 71% exhibited intestinal parasitic 1 2 infections and 100% of those with helminthiasis were anemic (Da Silva et al. 1999). In 3 wetland areas fish consumption is an important source of dietary protein and if 4 undercooked is a known source of parasitic infections. For example, the helminth Diphyllobothrium latum is common in areas of river catchment drainages or lacustrine 5 6 communities (Dick et al. 2001: 67, Peduzzi and Boucher-Rodoni 2001:44). Additionally, 7 Giardia lamblia is a parasitic infection associated with contaminated water supplies from 8 rivers and lakes (Stuart et al 2003). Transmission of the disease occurs through 9 ingestion of the infective, water-borne *Giardia* cysts, which can originate from feces of 10 humans, livestock and wild animals. Infection by either of these parasites has been 11 identified by Walker et al (2009:110, 114-115) as directly causing megaloblastic anemia 12 and thus may result in cribra orbitalia lesions in skeletal remains that would have compounded the anemia of chronic disease associated with vivax malaria. 13

14 This interaction is complex, for while hookworm, for example, has a deleterious impact on the pathogenesis of malaria, some helminths such as Ascaris lumbricoides 15 16 may actually provide protection against the disease (Adegnika and Kremsner 2012). In 17 addition, malaria infection stimulates the production of pro- and anti-inflammatory 18 cytokines such as tumor necrosis factor alpha. Chronic helminth infections stimulate a 19 type 2 and anti-inflammatory immune response that can modulate the high inflammatory 20 cytokine output in response to a vivax malaria infection (Hartgers and Yazdanbakhsh 2006; Mishra et al. 2014). However, chronic infection increases the appearance of 21 22 clinical malaria, particularly early in the disease process. In addition, acute helminth 23 infections have a deleterious effect on the pathogenesis of vivax (Hartgers and 24 Yazdanbakhsh 2006). Finally, it is their dual impact on anemia that results in higher 25 morbidity and mortality. It is the 'multiplicative, not just additive, effects' (Gravlee 2020, 5) of these disease interactions and their shared context that results in increased 26 27 lethality of malaria and falls within scope for a true syndemic.

- 28
- 29 3.2.3 Malaria in the Wetlands of England

30 Historical and clinical evidence attests to the presence of endemic malaria in the form of

31 *Plasmodium vivax* in the wetlands of Eastern England from at least the 17th century. In

1 her seminal study, Mary Dobson (1997) noted that the late summer/early autumn 2 seasonal mortality peaks in the wetlands coincided with the life cycles of both the 3 Anopheles atroparvus mosquito vector and the Plasmodium vivax parasite. The origins 4 of malaria in England are debated, although its presence may date to the Roman 5 occupation (1st to the early 5th centuries AD), introduced from the Mediterranean and other regions where the disease was rife (see Newfield 2017, Bankoff 2018). During the 6 7 Roman period in Britain, exploitation of the rich resources of the wetlands increased, 8 aided through the development of land reclamation infrastructure including drains, 9 canals and causeways (Rippon 2000). An unintended consequence, however, was the 10 creation of stagnant pools of brackish water in coastal marshes and fens, which provided an optimum breeding ground for the Anopheles atroparvus vector of malaria 11 12 (Kuhn et al. 2003).

13 Prior to the 19th century, malaria in Britain was variously referred to as 'marsh 14 fever', 'Fen ague', 'spring fever' or 'tertian fever' (Dobson 1997). Earlier historical descriptions of 'ague' closely align with the symptoms and progress of malaria caused 15 16 by *Plasmodium vivax*, which is characterized by intermittent and relapsing fevers, which 17 can reoccur for several years (Reiter 2000). Early twentieth century blood samples 18 provided unequivocal evidence of *Plasmodium vivax* in Fenland dwelling 'ague' 19 sufferers. Vivax malaria is generally held to be less fatal than *Plasmodium falciparum* 20 but unlike the latter can survive and thrive in temperate parts of Europe. There was a sharp decline in malaria in Britain during the latter half of the 19th century in England, 21 22 attributed to improved living conditions and land drainage (James 1929, Shute and 23 Maryon 1974, Reiter 2000, Hutchinson and Lindsay 2006).

24 The early medieval period (AD500-1000) in Britain heralded some climatic 25 fluctuation, including periods of rising sea levels. The earlier Roman drainage systems 26 would have been overwhelmed, resulting in flooding of areas of the coastal wetlands 27 (Cracknell 2005, Rippon 2000). As Gowland and Western (2012) discuss, this would have created an environment in which the anopheles mosquitoes could thrive. Far from 28 29 abandoning this land during the post-Roman period, there is evidence for continued 30 exploitation of the rich natural resources of the wetlands (Higham 2010). People living in 31 this area likely experienced a seasonally transient existence to optimize subsistence

strategies (Rippon 2002). Housing consisted of simple earthen-floored, wooden
structures, and during the winter months the inhabitants would have shared parts of
these modest dwellings with their livestock. They were not alone: one of the mosquito
vectors of malaria, *Anopheles atroparvus*, is also known to over-winter within houses,
thus often infecting multiple inhabitants of the same household (Reiter 2000, Serandour *et al.* 2007). Livestock would have been the preferred blood meal, but if humans are in
close proximity then they too are at risk of being infected.

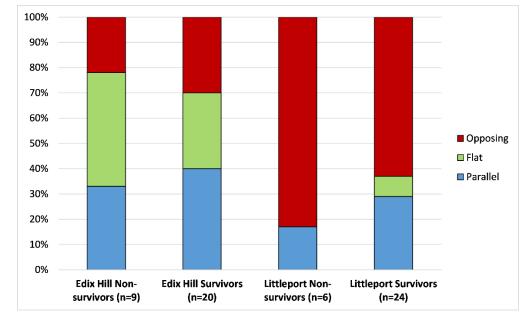
Gowland and Western (2012) found that those areas of the Fenlands associated 8 9 with malaria in the past (identified via historical records of 'aque' and the presences of 10 anopheles) were 'hotspots' for cribra orbitalia in the early Medieval period. They 11 concluded that malaria was a contributing factor to the high levels of anemia observed. 12 In a later study, Kendall et al (2020) undertook incremental dentine stable isotope analysis of individuals excavated from an early medieval site in the Fens (Littleport, Ely) 13 14 where, according to Gowland and Western's (2012) analysis, malaria was likely to have 15 been present. Kendall and colleagues (2020) found evidence of significantly higher 16 levels of *cribra orbitalia* compared to a nearby and contemporaneous site (Edix Hill, 17 Cambridgeshire) where malaria was not endemic. They also found much higher levels 18 of opposing covariance in the δ 13 carbon and δ 15 nitrogen isotope values (δ 15 nitrogen 19 increases and $\delta 13$ carbon decreases) from the site of putative malaria endemicity when 20 compared to the 'non-malarial' site (Figure 2). Opposing covariance in these isotopes is associated with physiological stress such as starvation (Beaumont and Montgomery 21 22 2016) but other forms of stress, such as parasite infection, may produce this effect 23 (Kendall et al. 2020, Kendall and Kendall 2021). This supports the argument that the 24 malarial environment contributed to a complex of stressors, placing the population 25 under significant health strain.

26

27 3.2.4 Social Determinants of Malaria in the Wetlands

The 9th century medical text Bald's Leechbook refers to 'spring fever' – a malaria-type disease manifesting seasonally (Bruce-Chwatt 1976, Cameron 1993). The wetlands of Eastern England during the early medieval period were often described as inhospitable, and ascribed supernatural characteristics (Gowland and Western 2012, 1 Kendall and Kendall 2021). They were the subject of numerous myths and the

- 2 inhabitants of these damp and misty places were often characterized as 'other'. For
- 3 example, the monk Felix recorded that St. Guthlac, who lived in the Lincolnshire
- 4 marshes in the 8th century AD, was forced to ward off supernatural attacks upon his



5

Figure 2: Opposing covariance in the δ13 carbon and δ15 nitrogen isotope values
 from Littleport (malarial) and Edix Hill (non-malarial) (copyright Ellen Kendall).

9 person (Colgrave 1985). These 'attacks' involved extremes of bodily temperature, which
10 could possibly represent fever-induced hallucinations associated with malaria. As Felix

11 records "No settler had been able to dwell alone in this place...on account of the

12 phantoms of demons which haunted it" (Colgrave, 1985: 89).

13 The specificity of local knowledge and skills required to successfully exploit the 14 wetland areas, in combination with local disease ecologies, including malaria, likely 15 contributed to this 'othering' of Fenlanders (Kendall and Kendall 2021). It is worthwhile 16 considering the entanglement of local biologies and the marginalization of Fenlander 17 identities in these uniquely challenging environments. Gowland et al. (2018) argued that 18 these marginal environments forged distinctive cultural identities that manifested as 19 localized variations in the material culture assemblages associated with the early medieval period in the Fens. This marginal view of Fenlanders persists in numerous 20

21 historical records, most notably in first-hand accounts by authors such as Daniel Defoe

in the early 18th century, and is an attitude that continues to this day (Kendall and
Kendall 2021). Such 'othered' identities are important to consider within a syndemic
framework as social isolation and constrained social capital are significant in creating a
cluster of risk factors, which in this instance are derived from the unique environmental,
cultural and biological milieu. This is evidenced in 19th century medical accounts of
Fenlanders, which allude not only to malaria but also the inadequate diet, parasites and
general poor health of the inhabitants (Nicholls 2000).

8 Vivax malaria has widely been considered a non-lethal form of malaria, with a current fatality rate of approximately 0.01% (Phyo et al. 2022). The fatality of vivax 9 10 malaria in Britain is well-attested from mortality records (Dobson 1994) and early clinical 11 studies. For example, James (1929) suggests a fatality as high as 10-12% for malaria in 12 the late 19th century wetlands, based on his direct experience treating patients with the disease. It is worth noting that this figure was likely higher for the preceding period, 13 14 because malaria was already in decline during the time of James' work. The lethality of 15 this condition in the Fens have led others to suggest that the cause of death was 16 instead more likely to be gastrointestinal in origin rather than malarial (Hutchinson and 17 Lindsay 2006). Clinically, the synergistic interaction between malaria and nutritional 18 insufficiencies, helminths and Giardia infections, as well as other infectious diseases, 19 have been observed to thrive in the type of basic housing and unsanitary conditions that 20 were present in the medieval and post-medieval fenlands (Chang and Stevenson, 2004; Anstey et al., 2009). The syndemic interaction between malaria and other comorbidities 21 22 for the Fenland region are likely to have had an additive impact on the lethality of this 23 disease, particularly within the context of poor living conditions and social exclusion.

24 Crucial to the syndemic interpretation in the early medieval Fenlands is that both 25 helminth and malaria infections were driven by social determinants, including nutritional insufficiency, living conditions and subsistence patterns. Strong parallels can be drawn 26 27 with the hookworm/malaria described in British Malaya discussed above (Webb 2020). 28 Infection with *Plasmodium vivax*, whilst not necessarily fatal on its own, would have 29 presented as relapsing fevers that would have been debilitating for several years. If contracted alongside existing gastrointestinal parasite infections, then the chance of 30 31 fatality is much higher, and this likely contributed to the increased mortality in the

27

malaria endemic parts of the wetlands recorded by Dobson (1997) in post-medievalEngland.

3 Another relevant factor to consider in relation to malaria syndemics is the 4 Developmental Origins of Health and Disease hypothesis. Pregnant women are more susceptible to malaria infection, particularly during the first half of pregnancy. Pregnant 5 6 women and young children are also especially vulnerable to harmful clinical impacts of 7 the disease (Singer 2013, Phyo et al. 2022). Infection during pregnancy adversely 8 affects developing infants, resulting in higher mortality and infants born small for 9 gestational age (SGA) (Chang and Stevenson 2004, Lindsay et al. 2000, Levy et al. 10 2005, Singer 2013). The impact of malaria on mortality in infancy and early childhood has been noted in a number of bioarchaeological studies. For example, Sallares and 11 12 colleagues' (2004) describe the 5th century infant cemetery at Poggio Gramignano, Umbria, where the aDNA of *P. falciparum* was retrieved from skeletal remains: of the 47 13 14 infants recovered, 22 were thought to have been either premature or SGA. Kendall and 15 Kendall (2021) likewise discuss the anomalously high levels of infant mortality in the 16 post-medieval Fenlands, arguing that this was likely due to the risk of being born SGA 17 to a mother infected with malaria and/or direct infection via the *anopheles* vector. The 18 effects of comorbidities in pregnancy, such as between helminths and malaria, provide 19 additional challenges for the mother and her infant. In Africa, malaria and helminths are 20 considered infectious syndemics, with particular susceptibility and risks for pregnant 21 women (Jepkogei et al. 2016). The early and post-medieval Fenlands provide likely environments for this to likewise have been the case. 22

23 The impact of local disease ecologies can therefore affect health even prior to 24 birth, contributing to the very high levels of infant and child mortality recorded historically 25 for the Fenland region and inherent frailities in those who survived to adulthood (Dobson 1997). Slagboom et al. (2022) discuss the intergenerational impacts of 'syndemic 26 27 vulnerability' in a former fishing village in the Netherlands through a combination of 28 shared exposure to social inequities and the clustering of interactive diseases and 29 health conditions. In the Netherlands, these conditions led to early onset of disease and significantly lower life expectancy and increased disease risk, even in offspring removed 30 31 from the direct effects of historical adversity experienced by their grandparents.

Slagboom et al. (2022, pg. 7) define syndemic vulnerability as "a predisposition to the 1 2 development of clustering and interacting diseases or health conditions that results from 3 shared exposure to a set of adverse social conditions". These observations align with 4 the Developmental Origins hypothesis, and can readily be applied to the historical data from the Fenlands. Here, the impacts of malaria and gastrointestinal parasite exposure, 5 6 in concert with social marginalization, created intergenerational vulnerabilities that 7 resulted in markedly higher mortality, as noted in historical documents for the post-8 medieval period (Dobson 1997). Research by Kendall et al. (2020) strongly suggests 9 that similar health stresses were felt during the early medieval period too, evidenced 10 both in terms of skeletal pathologies and opposing covariance in the Nitrogen and Carbon isotope data. 11

12 The impact of the social and ecological determinants of health within the Fenland 13 regions, and the resulting syndemic interaction between these and various 14 gastrointestinal parasitic infections, likely contributed to the cribra orbitalia hotspots 15 observed by Gowland and Western (2012). It is helpful to reflect on the skeletal 16 evidence as more than just the outcome of comorbidities, but instead as a 17 malaria/helminth syndemic, closely tied to the specific societal and ecological 18 constraints of those living within these unique environments. A syndemic perspective in 19 this context has facilitated a deeper understanding of the likely role of helminths and 20 giardiasis in terms of both general health stress and the lethality of the *Plasmodium*. vivax malaria endemic. Through the incorporation of a DOHaD perspective the 21 22 syndemic vulnerability of the local population and intergenerational adversity in health 23 can be more easily understood. This unique socio-ecological niche served to forge 24 particularized Fenland identities, which compounded the marginalization of these 25 inhabitants. This, in turn, contributed to the persistence of conditions which exacerbated the impact of this clustering of diseases. The decrease in lethality of vivax from the late 26 27 19th century may well illustrate what happens when some of the syndemic drivers are 28 removed. The improvement in land management/drainage and living conditions in the 29 Fenland areas at this time, resulted in a documented reduction in both the prevalence 30 and mortality risk from malaria (Dobson 1997). Bioarchaeological studies, therefore,

have the potential to provide longer-term insights into syndemics when one or more of
the contributing factors are ameliorated.

3

4 4.1 Conclusions

5

6 Paleopathological and bioarchaeological research is primed to adopt a syndemic 7 approach, as noted by Crespo and Larsen (2022) and Robbins Schug and Halcrow 8 (2022). Methodological (e.g. paleogenomic and immunological studies) and theoretical 9 (e.g. DOHaD, intersectional and local biologies/disease ecologies) developments have 10 created a more grounded and contextualized paleopathology that goes beyond 11 diagnosis to explore how diseases emerge and are maintained in ancient communities. 12 Singer and colleagues (2021) note a critical yet often missing factor of syndemic 13 applications is the lack of clearly establishing a true relationship between the diseases 14 and understanding how they interact. In other words, what would happen to the 15 syndemic if one of the elements was alleviated or resolved? Bioarchaeological studies 16 have an advantage, as they can provide a longer-term perspective to view how disease 17 prevalence alters when specific social or environmental factors change (e.g. improved 18 drainage of the wetlands and better housing led to a drastic reduction in deaths from the 19 malaria syndemic). Singer and colleagues (2021) also argue for the importance of 20 establishing syndemic pathways beyond just identifying co-occurrence or the presence 21 of deleterious social or economic variables. Likewise, a deeper time perspective may 22 help to illuminate such pathways in some instances.

23 The empirical-based understanding of synergism and interaction between 24 disease and social factors in many ancient contexts may in some situations be limited to 25 a theoretical construct. However, paleopathologists have the tools to identify many of the synergistic elements of past syndemics, and this approach has the potential to 26 27 provide new perspectives on past health, whilst also informing present-day syndemic 28 interactions. The syndemic approach delves deeper into the lived experiences of people 29 in the past, how their quality of life is impacted by the environmental and politicaleconomic change, and perhaps how and whether a past syndemic ever ended. The 30 31 embedded nature of the syndemic concept provides a complementary framework for

1 paleopathologists working within a biocultural theoretical approach. It provides an

- 2 approach that encourages the more seamless integration of the pathophysiology of
- 3 diseases and comorbidities with a deeper understanding of the social determinants of
- 4 health. Information on the social lives of these communities and their lived experiences
- 5 become re-centered alongside, not superseded by the scientific study of their biology,
- 6 as recommended by Lans (2021).
- 7 SARS-Cov-2 laid bare the embedded inequalities that exist in seemingly
- 8 egalitarian epidemic situations and how this manifests biologically and socially in
- 9 humans. Syndemic elements might not all manifest in one individual, however, their
- 10 endemic presence can rupture a community and create instability that reverberates

11 inter-generationally. The syndemic framework helps us better understand the

- 12 heterogeneity of disease through human history and how local biologies are entrenched
- 13 in wider power structures, and why those who are most marginalized suffer such
- 14 adverse health outcomes.
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