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2 **Review**

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Plasmodium malariae: the persisting mysteries of a persistent parasite

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6 *Plasmodium malariae* is a 'neglected malaria parasite' in as much as the amount

7 of research conducted on it pales into insignificance when compared to that

8 pertaining to Plasmodium falciparum and Plasmodium vivax, its more notorious

and pathogenic cousins. There has, however, been an increase in interest in this

10 parasite over the past decade. Principally, this is because of the increasing use

11 of sensitive molecular detection techniques that have revealed a wider than pre-

- viously recorded prevalence in some regions (particularly in Africa), and high
- 19 numbers of chronic, asymptomatic infections.

15 A brief history

At the end of 1930 Robert Knowles, Ronald Senior White, and Biraj Mohan Dasgupta published Q10 Q9 an extensive monograph [1] in which they reviewed the current knowledge of the global distribu-17 tion of the three malaria species that infect humans (P. falciparum, P. vivax, and P. malariae; the 18 specific status of the recently discovered Plasmodium ovale was still in question). Their conclu-19 sion: 'Despite the length of this Memoir our final conclusion is that our present-day knowledge 20 of malaria is remarkably meagre'. Whereas much has been learned since a similar conclusion 21 could still be justifiably applied to P. malariae today. In this review, we present an overview of 22 23 the idiosyncrasies of this globally successful species and highlight interesting gaps and possible misconceptions in our knowledge of its biology and speculate as to their potential significance. 24

Quartan fevers (see Glossary), in which febrile episodes recur every fourth day, have been dis-Q11 tinguished from other types of fever since antiquity. Following the acceptance by the Italian 26 27 workers of Laveran's discovery in 1880 of the protozoan parasites that cause malaria, Camillo Golgi was the first in 1885 to associate the parasites' forms in the blood with the evolution of 28 the paroxysm. His detailed microscopical observations led him to differentiate between the par-29 asites of the tertian fever and the quartan parasites [2], which were then named by Giovanni 30 Grassi and Raimondo Feletti as Hæmamæba vivax [3] and Hæmamæba malariae [4] 31 32 (Hæmamæba = Plasmodium).

It was noted by early malariologists that guartan fevers were rare and only exceptionally associ-33 ated with mortality. The characteristic low-grade parasitaemias (often close to the limit of micro-34 scopic detection with peaks rarely exceeding 10 000 parasites/µl) were ascribed to the 72-h 35 erythrocytic cycle and a low number (from six to 12) of merozoites per schizont, yet infections 36 37 were persistent, confirming the old Roman adage that 'quartana te teneat' (quartan fever is tenacious). Indeed, a primary infection often left the patient suffering over many weeks with regular 38 paroxysms, and recurrent (though shorter) episodes over the ensuing years. In contrast to 39 P. vivax and P. falciparum, early attempts at experimental mosquito transmission of P. malariae 40 from one person to another proved elusive [5]. Prevalence was found to be patchy, with specific 41 42 localities showing high levels with those close by devoid of any P. malariae cases. Such observations left malariologists perplexed, as pithily stated by Marchoux 'll existe d'ailleurs au sujet de la 43

Highlights

Plasmodium malariae, the quartan malaria parasite of man, is a neglected species.

Advances in molecular detection techniques are revealing a much greater prevalence of this species than previously thought.

There remain many mysteries surrounding its biology and epidemiology, including its true prevalence, and the nature of its interactions with coinfecting malaria species.

We review some outstanding mysteries and dogmas concerning the biology and epidemiology of *P. malariae*.

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fièvre quarte une sorte de mystère non encore pénétré' [6] (There is a mystery yet to be elucidated
about quartan fever).

46 Humans as an experimental model

The advent of malariotherapy in the early 1920s, whereby a remarkable and unique cure for 47 tertiary syphilis was obtained by multiple malarial paroxysms in patients deliberately infected 48 with parasites, provided a means to investigate the biology of P. malariae, as it did that of the 49 other species [7,8]. The globally preferred species throughout the malariotherapy era was 50 Q12 P. vivax, the parasite first used by Wagner-Jauregg to treat neurosyphilitics. P. malariae, though tested with success in 1924, was used mainly to obtain infection in patients who were or became 52 immune to P. vivax, and in the USA to infect patients of African descent who were found to be 53 broadly insusceptible to infection by P. vivax. Nonetheless, the observations on experimental 54 P. malariae spanned more than 40 years (1924–1968); of the 67 biologically informative articles 55 we identified 11 from England, 22 from Romania, and 22 from the USA. Mosquito transmissions 56 having finally been achieved in 1933, these records include cases of induced infections by sporo-57 zoites as well as by infected blood inoculation. Successful adaptation of P. malariae to New World 58 monkeys (Aotus and Saimiri) in the late 1960s provided further scope for observations. Two other 59 guartan species, Plasmodium brasilianum of South American primates and Plasmodium rodhaini 60 of African Apes, which are both considered to be synonymous with P. malariae, provided additional 61 scope for experimentation (Box 1). Altogether, these data have provided the basis on which the Q13

63 clinical and epidemiological reports on *P. malariae* are currently perceived.

Thus, *P. malariae* is presented as a parasite of humans, with an overall low – though unevenly variable – prevalence [9–13], that is potentially zoonotic in Africa as *P. rodhaini* and in

b0.2 Box 1. The *P. malariae* parasites of nonhuman primates

b1.3 The genomes of *P. malariae* parasites collected from humans harbour much lower levels of pairwise nucleotide diversity than **b1.4** those identified in the so-called malariae-like parasite collected from chimpanzees in Gabon $(3.2 \times 10^{-4} \text{ vs. } 6.5 \times 10^{-3})$ [17], a

b1.5 situation akin to that noted for P. falciparum and P. reichenowi [90]. This Gabonese parasite may correspond to P. rodhaini, a

b1.6 species found in gorillas and chimpanzees that is indistinguishable morphologically from *P. malariae* [91].

b1.7 Further analysis of *P. malariae* type sequences from both captive and wild African apes revealed the presence of three clades; (i) *P. malariae* of humans (sometimes also found infecting captive, but not wild apes), (ii) a *P. malariae*-like parasite
b1.9 of wild apes (the Gabonese parasite from above), closely related to but distinct and separate from the human infecting linb1.10 eage, and (iii) a distinct and distantly related species infecting chimpanzees and gorillas in west and central Africa, with the

b1.11 proposed name *Plasmodium celatum* [92].

b1.12 The above analyses also revealed that the genetic diversity of the *P. malariae* clade infecting humans globally is significantly
b1.13 lower than that of the clade infecting wild chimpanzees and apes in Africa. This suggests that *P. malariae* became a parb1.14 asite of humans as the result of a host-switch from African nonhuman Hominidae.

Investigations of P. brasilianum, another species restricted to New World monkeys that is morphologically identical to b1.15 b1.16 P. malariae, found that their genomic sequences were almost identical [19]. This supports the view that P. brasilianum repb1.17 resents the outcome of a host-switch of P. malariae from humans to a lower primate. Detailed analysis of a larger collection of samples should help to establish whether P. malariae and the two malaria-like species above are part of a single species b1.18 b1.19 or are distinct Plasmodium species. This is of some interest because humans are susceptible to infection by all three parb1.20 asite types, as are the African apes and the New World monkeys to P. malariae [93,94]. Further targeted genomic analyb1.21 ses, for example, comparisons of the repertoire of proteins implicated in red blood cell invasion might illuminate the origin and the dynamics of the zoonotic infections [95]. b1.22

b1.23The availability of complete reference genomes has made it possible, for the first time, to determine a true phylogeny for theb1.24human-infecting malaria species [17]. A maximum-likelihood tree based on 1000 evolutionary conserved single-copy pro-b1.25teins from each of the twelve *Plasmodium* genomes provided distinct evidence that *P. malariae* forms a unique clade sep-b1.26arate from those of the other primate- and rodent-infective species. Although this phyletic position contrasts with thatb1.27derived from previous phylogenomic datasets [16,96,97], it concords with one based on apicoplast sequences [98].

Glossary

Gametocyte: the sexual stage of malaria parasites.

Hypnozoite: latent liver stage of malaria parasites.

Malariotherapy: the treatment of neurosyphilis, a syphilis complication affecting the central nervous system, and other neurological disorders by induction of fever through controlled inoculation of malaria parasites and their subsequent clearance by drug treatment.

Merozoite: red blood cell-invasive form of the malaria parasite.

Normocyte: mature red blood cell. Oocyst: form of the malaria parasite resulting from the encystation of an ookinete on the midgut epithelium of the mosquito. A replicating stage that results in the production of numerous sporozoites

Paroxysm: a sudden and acute attack of a disease. Malaria paroxysms are tvoically associated with fever onset.

Pyrogenic threshold: the density of parasites in the blood sufficient to cause fever onset.

Quartan fever: a fever that recurs every third day. Associated with malaria parasites, such as *Plasmodium malariae*, that replicate in the blood every 72 h. **Reticulocyte:** immature red blood cell, characterised by the presence of a reticular network of ribosomal RNA. **Schizont:** multinucleate, replicating stage of the malaria parasite, producing

numerous merozoites.

Sporogonic cycle: the part of the malaria parasite's developmental cycle that occurs in mosquitoes, initiated by the fusion of male and female gametes and ultimately resulting in the production of sporozoites.

Sporozoite: the form of the malaria parasite inoculated into vertebrates via the bite of infected mosquitoes. **Syphilis:** a sexually transmitted disease

caused by the spirochete bacterium Treponema pallidum.

Tertian fever: a fever that recurs every second day. Associated with malaria parasites such as *Plasmodium falciparum*, *P. vivax*, and *P. ovale* that replicate in the blood every 48 h.

Tertiary syphilis: the third phase of infection with *Treponema pallidum* in which severe damage to the central nervous system (neurosyphilis) and internal organs (cardiovascular **syphilis**) occurs.



South America as P. brasilianum. The hepatic phase is lengthy by comparison with the other 86 species, with a minimum of 15 days required for maturation. P. malariae is considered not to 87 form **hypnozoites**, though this has been recently guestioned [14,15]. Following a variable, 88 89 often lengthy, prepatent period, clinical symptoms appear when the parasitaemia is very low (<500 parasites/µl) and can persist for months in primary infections of naïve subjects. The py-90 rogenic threshold is the lowest among the species that infect humans, with the first rise in 91 fever or clinical signs often declaring when the parasites are barely detectable (500 parasites/µl 92 or less). Parasite levels rarely peak above 10 000 parasites/ul, and when untreated the parasite 93 94 can persist for months at low and often submicroscopically detectable levels. Infections lasting asymptomatically for several decades have been recorded in persons who had migrated from an 95 endemic area to a malaria-free country; however, the proportion of those where the infection 96 was extinguished without radical cure is unknown. The characteristically low parasite burdens 97 are ascribed to a 72-h ervthrocytic cycle, the low number of merozoites per schizont (from six to 98 12), and a strict preference for mature erythrocytes. P. malariae is reported as non-sequestering 99 since both young and mature forms can be seen in peripheral blood samples. The infection is 100 considered benign in that directly attributed mortality or clinical severity has been rarely reported. 101 but it has been associated with guartan nephropathy, whose aetiology remains to be elucidated. 102 Mosquito transmission is hindered by low **gametocyte** numbers, few **oocysts**, and a rather 103 lengthy extrinsic period of development. A critical survey of the available observations suggests 104 to us that the strength of some of these notions on *P. malariae* might deserve reappraisal. Recently, 105 large-scale and whole-genome sequences of the malariae group of parasites have become 106 available [16-19], but the functional significance of tantalising differences within and between 107 other *Plasmodium* species remains speculative. Knowledge of the genetic diversity of this 108 species still lags far behind that of P. falciparum and P. vivax (Box 2), but it is expected to 109 110 expand in future.

Rich as they might be, the observations from induced infections in humans (mainly in 111 malariotherapy but also a few in volunteers) should be interpreted with some caveats at hand. 112 In order to deal with the repeated malarial paroxysms, the patients selected for infection had to 113 be in good health, and were monitored daily and protected from further infectious bites. The par-114 asite strains used were selected to be of moderate pathogenicity and susceptible to the available 115 antimalarials; moreover, they were often maintained by repeated human-to-human blood pas-116 sages. The majority of data reported derives from six P. malariae strains acquired locally (one in 117 Germany and The Netherlands, two in the USA, and three in England and Romania). Thus, the 118 data are biased towards P. malariae parasites from temperate endemic regions. The only recent 119 reanalyses of malariotherapy data on P. malariae were based solely on infections by a single strain 120 [20-23]. Finally, the follow-up periods were rarely of sufficient length and frequency to address the 121 longevity of the infection. Thus, the published observations on P. malariae infections that could 122 illuminate the natural history of the parasite are rather disparate, partial, and difficult to interpret. 123 Whereas the available observations provide sufficient support for the current views on 124 P. malariae, they are equally consistent with, but not sufficient to dismiss, alternative views. We 125 126 feel that a paucity of data should promote rather than hinder speculation. In this context, some of the P. malariae canons merit further appraisal. 127

128 Of paradigms and dogmas

129 Do reticulocytes matter?

130 The notion that the malarial merozoite might favour younger rather than older red blood cells was

- first made for *P. vivax* in 1934 [24]. The first investigation on red blood cell selectivity [25] actually
- 132 led to the conclusion that, given an equal availability of either cell type, the penetration of
- 133 a reticulocyte by P. malariae would have occurred 9.5 times as frequently as for a mature



Q3 Box 2. The dawn of *P. malariae* genomic diversity

b2.3 Investigations of the diversity, evolutionary history, and population structure of *P. malaria*e in field-collected samples have
b2.4 been, until recently, restricted to a few genes [99–107]. These studies indicated a degree of genetic diversity and variation
b2.5 akin to those observed for the other malaria parasite species of humans, including a high level of the multiplicity of infection
b2.6 in areas of high endemicity.

In 2016–2017, two independent studies made the genome of this neglected malaria parasite available [16,17]. Ansari and b2.7 colleagues offered the first insight into the genome of P. malariae with a particular focus on the architecture of the exb2.8 panded gene families across seven complete human-infecting Plasmodium genomes that also included the zoonotic mab2.9 laria parasites P. knowlesi and P. cynomolgi. In the following year, a more complete reference-quality genome of b2.10 b2.11 P. malariae was published [17]. The P. malariae genome has a larger nuclear genome compared to other Plasmodium species (by about 30%; ~31.9-33.6 Mb with > ~6500 protein-coding genes). The core P. malariae genome is by and large b2.12 b2.13 shared with that of other species, but there are unique, and in some cases, massive expansions of some gene families b2.14 for example, of the pir, phist, surfin, and fam-a (later denoted as fam-I and fam-m) gene families, which suggests an inb2.15 creased diversity of proteins predicted to be exported to the surface of infected red blood cells (RBCs) [16]. The large proportion of 'pseudogenized' members of the pir family is a distinct characteristic, as is the presence of gene doublets from b2.16 the fam-i and fam-m at the subtelomeric boundaries of the chromosomes, with some evidence that these two families b2.17 coevolved [16], and might be related to a major malaria red cell invasion ligand, RH5, in P. falciparum [108]. The potential b2.18 to uncover the functional significance of these genes is restricted by the inability to cultivate *P. malariae in vitro*. b2.19

b2.20 Over the past 5 years, genome-enrichment techniques, such as selective whole-genome amplification (sWGA), have been b2.21 developed and optimised for the Plasmodium parasites of humans [109-112]. This makes it possible to extend analyses to field samples hitherto excluded by low parasitaemias or the presence of mixed-species infections. A proof-of-concept b2.22 study that applied an sWGA protocol to 18 P. malariae clinical samples [112] yielded a total of 28 899 core-genome SNPs b2.23 that were subsequently used to establish a robust phylogeny. With careful handling of the starting material during DNA b2.24 extraction, high-molecular-weight DNA preparations are now amenable to sWGA-based amplification protocols for b2.25 long-read sequencing using the PacBio or the ONT platforms. Thus, much-larger-scale population-genetics-driven b2.26 studies on P. malariae are now possible. When coupled with recent state-of-the-art ultrasensitive nucleic acid detection b2.27 b2.28 technologies, such as the clustered regular interspaced short palindromic repeats (CRISPR)-based SHERLOCK (specific b2.29 high-sensitivity enzymatic reporter unlocking) platform [113], a quantum leap in our knowledge of P. malariae biology and epidemiology has become possible. b2.30

erythrocyte. This was later contradicted by two investigations [26,27] that sealed the notion that 134 P. malariae is restricted to mature red blood cells, because in the samples collected, parasites 135 were nearly all observed in normocytes. One possible explanation for these discrepant observa-136 tions might lie in the time at which the blood samples are collected. Robert William Hegner based 137 his conclusion of a reticulocyte preference on a single slide obtained soon after the chill, that is, 138 soon after invasion. Given their lengthy cycle, the P. malariae ring stage extends for a long period, 139 during which the reticulocyte would have had the time to mature [11]. An accelerated transition 140 from reticulocyte to normocyte has been demonstrated for P. vivax [28], and it is likely that 141 such a phenomenon would occur for all malaria parasites that invade reticulocytes. We propose 142 that P. malariae might actually have a predilection for reticulocytes. This would account for the low 143 parasite burdens and could explain the failure to achieve in vitro cultivation [29-31] where ervth-144 rocytic maturation occurred but with little re-invasion of the plentiful mature red blood cells. 145

146 Does sequestration play a role?

Sequestration, defined here as a withdrawal from the peripheral circulation for a period during the 147 148 erythrocytic cycle, is stated not to occur for P. malariae parasites. This conclusion is based on observations of parasites at all developmental stages in blood smears. The question arises as to 149 whether this represents a valid demonstration that sequestration does not occur. The matter pri-150 marily rests on what observers define as a schizont as well as on the actual duration and extent of 151 sequestration, should it occur. The term 'schizont' has often been used loosely, and rarely de-152 153 fined, to encompass the whole or only the ultimate period following the initiation of nuclear division. In P. falciparum, nearly all the parasites sequester from 18-36 h post-invasion, with 154 multinucleate schizonts usually absent from the peripheral circulation. However, should 155

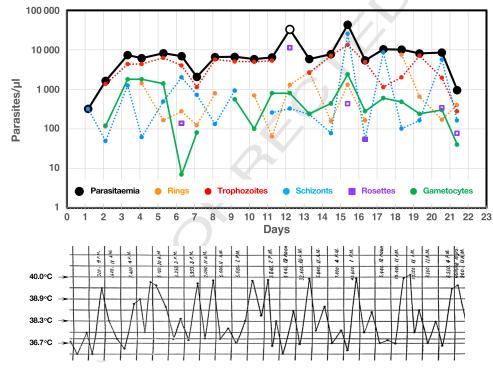


Q14 sequestration occur for only the last few hours of the cycle, concern only a proportion of the par-

157 asites, or a combination of both, then all parasite stages would be observed at any one time in the 158 peripheral blood. Evidence for sequestration would require careful analysis of the parasite stages

peripheral blood. Evidence for sequestration would require careful analysis of the parasiteat close intervals throughout successive erythrocytic cycles in a synchronous infection.

From the data on the course of infection in naturally and experimentally inoculated persons 160 (mostly for the initial episode) we could only identify 19 patients where parasitaemia was pre-161 sented over time before treatment (Figure 1, and see Figures S1-S3 in the supplemental informa-162 tion online): in a single volunteer inoculated with sporozoites [32], in three naturally infected 163 persons during the chronic phase [33,34], and in 15 patients or volunteers inoculated with in-164 fected blood [10,12,22,32,34]. These data are clearly insufficient to derive an estimate of multipli-165 cation rates [35]. To our knowledge, the only record of daily differential counts of parasite stages 166 [33] was obtained from a neurosyphilitic patient inoculated with infected blood and followed up 167 daily for 3 weeks (Figure 1). Two aspects are noteworthy. First, whereas the parasitaemia re-168 mained at relatively constant levels (5000-10 000 parasites/µl), there were two curious sharp 169 peaks when parasite numbers increased five- to sixfold in 24 h and reverted to the original levels 170 the next day. On neither occasion was the fever particularly high. Second, fully mature schizonts, 171 known as rosettes, were observed on only 6 of the 21 days, mostly as a very minor fraction of the Q15



Trends in Parasitology

Q2 Figure 1. Daily course of parasitaemia in a case of blood-induced *Plasmodium malariae* infection. The course of infection with daily differential counts of parasite forms over a period of 21 days, derived from a neurosyphilitic patient of 35 years of age, who was inoculated intramuscularly with 5 ml of *P. malariae*-infected blood '...showed a fair number of rings and growing trophozoites and scanty schizonts and gametocytes' on 17 February. Scanty parasites were observed on 4 March, the first temperature rise was recorded on 5 March (D0 in the graph) and full patency was observed from 6 March onwards. The patient was administered an antimalarial only after 29 March. The authors define the parasite stages as follows: 'rings, still preserving the ring outline, and with the vacuole present; growing trophozoites, with chromatin undivided, schizonts, showing the division of the chromatic, mature rosettes in which the merozoites have developed fully, and are distinguishable as different individuals, gametocytes'. The graph is derived from the data presented in [33].





total parasitaemia. Interestingly, free merozoites were seen only during the first peak when they Q16 accounted for ca. 60% of the total number of parasites. To our knowledge, only one other author 196 distinguished fully mature schizonts (the characteristic daisy-head rosette) from maturing schiz-197 198 onts in his observations. In an article summarizing 4 years of observations on P. malariae in Panama [36], William McCully James specifically notes that he has found 'the perfect segmenting 199 form to be uncommon in the peripheral blood'. He further remarks that, in well-marked parox-200 ysms, 'the youngest form of the parasite is first observed about two hours after the temperature 201 begins to rise' with their number increasing over the next hours. These observations suggest that 202 203 the mature or nearly mature P. malariae parasites sequester for a few hours, with reinvasion taking place away from the peripheral circulation. This would also be consistent with the paucity of 204 observations of P. malariae rings in reticulocytes. 205

206 The first of these two observations is consistent with a cryptic cycle in which a significant propor-

tion of the *P. malariae* biomass multiplies in the vasculature of internal organs away from the peripheral circulation. A single observation from a post-mortem examination of a chronic *P. malariae*

case (who died accidentally) seems to support this possibility [37]. The concept of such a cryptic

cycle has been recently made evident for *P. vivax* and *P. falciparum* [38,39] and it would seem

211 logical to assume that the same phenomenon could occur for *P. malariae*.

212 The vexed question of dormancy

213 The longevity of *Plasmodium* infections is not novel per se, as the parasites have often been found

to persist throughout the life of their animal natural hosts. The longevity of *P. vivax* infections is as-

cribed to the activation of persisting dormant liver stages, hypnozoites, that also occur in a few other species (*P. ovale*, and *Plasmodium cynomolgi*, *Plasmodium fieldi*, and *Plasmodium simiovale*

other species (*P. ovale*, and *Plasmodium cynomolgi*, *Plasmodium fieldi*, and *Plasmodium simiovale* in macagues). The persistence of *P. malariae* over many years, and that of *P. falciparum* [40], is as-

cribed to continued erythrocytic parasite multiplication since neither species is considered to pro-

duce hypnozoites, based on the fact that relapses are not observed in sporozoite-induced

220 *P. falciparum* or *P. malariae* sporozoite infections following chemotherapeutic clearance of the pri-

221 mary episode. However, a recent report of a traveller treated successfully for *P. falciparum* in

222 Germany, who then experienced a P. malariae episode 4 months later, led the authors to propose

the existence of P. malariae hypnozoites [14]. Similar cases of such late recurrences of P. malariae

a few months after return to Germany despite adequate prophylaxis had been reported [41-43],

prompting the authors to re-evaluate the question of dormant stages in *P. malariae*.

It should be noted that in vivo investigations of the liver stages of P. malariae are very limited indeed. 226 The first set of observations was made when sporozoites obtained from naturally infected humans in 227 Liberia were inoculated into four recipient chimpanzees [44], and the pre-erythrocytic stages were 228 sought in liver biopsies taken over the next 8-12.5 days, when about 1500 nuclei were noted in 229 the oldest schizonts. The second study was made using the sporozoites from a Romanian strain 230 (VS) that were inoculated into a splenectomised chimpanzee [45]. The resulting liver forms were ex-231 amined from days 12 to 14 by which time an estimated 15 000 merozoites in mature schizonts were 232 observed, and their rupture on day 15. A liver biopsy, made on day 87, proved negative for parasites. 233 Finally, liver biopsies from a person who died accidentally 3 months after inoculation with the same 234 P. malariae VS strain also failed to reveal any parasite forms [37]. These meagre observations are 235 clearly insufficient to exclude the possibility of a P. malariae hypnozoite, not least as the number of 236 sporozoites inoculated in the human subject was probably too low to allow meaningful interpretation 237 (the bite of 50 mosquitoes that were not uniformly infected). 238

Two other possibilities exist. First, the notion of a secondary excervit cycle. The hypothesis that some hepatic merozoites invade a fresh hepatocyte to maintain a liver cycle was



proposed by Henry Edward Shortt and Percy Cyril Claude Garnham in 1948 [46] and was only 241 abandoned with the discovery of the hypnozoite in 1980 [47]. This hypothesis remains unex-242 plored. A single observation of growing Plasmodium chabaudi and Plasmodium yoelii hepatic 243 244 schizonts in the livers of naturally infected Thamnomys rutilans [48,49] supports a secondary exoerythrocytic cycle, though it is insufficient as proof. Second, the existence of quiescent erythro-Q17 cytic forms, which was invoked in the 1890s by Italian malariologists to explain latent malaria. 246 Investigations of rodent malaria parasites suggested the existence of latent merozoites [50]. Initial 247 observations of free parasites in the lymphatic circulation of infected mice [51] and intact merozo-248 249 ites within lymphocytes [52] led to the discovery of merophores, a term coined to denote groups of intact merozoites, often enclosed in a sack or within a lymphocyte, which were found mainly 250 in the spleen and the lymphatic circulation of infected mice [53]. The occurrence of parasites 251 in a state of arrested development was suggested by observations on in vitro-cultured 252 P. falciparum subjected for a few days to fully inhibitory doses of pyrimethamine but that then 253 reappeared when the drug was removed [54]. A similar phenomenon was discovered for the 254 ring stages of P. falciparum in artesunate-exposed cultures [55], and it was later confirmed that 255 such parasites could remain 'dormant' for up to 25 days [56]. There is no biological impediment 256 to discount the possibility that such quiescent, possibly metabolically minimally active, P. malariae 257 parasites could remain viable for substantially lengthier periods. 258

259 An unexplored epidemiology

260 Transmission with discretion

The initial difficulties in obtaining mosquito transmission [5] led the early malariologists to propose 261 that P. malariae could thrive only in some special anopheline species. However, further attempts 262 showed this to be incorrect but also revealed that the mean number of oocysts that can be ob-263 tained through experimental feeding rarely exceeds ten and the sporozoite output is conse-264 quently low (e.g., [57-62]). The **sporogonic cycle** at 25°C is about 5 days longer than that of 265 P. falciparum and P. vivax and about 3 days longer than that of P. ovale. These features associ-266 ated with a relative paucity of gametocytes have contributed to considering that P. malariae trans-267 mission is somewhat inefficient, which could incidentally also account for the patchy distribution. 268 However, it is not clear that the paucity of gametocytes should be taken as an indication of poor 269 transmissibility. Indeed, a common feature of those very few reports of experimental transmission 270 is the lack of correlation between the number of gametocytes in the blood and the success of 271 mosquito infection. Moreover, infectivity to mosquitoes could be obtained during the lengthy 272 chronic infection [44,63]. One could legitimately suggest that P. malariae transmission to mosqui-273 toes occurs continuously, albeit at low levels, which would ensure a constant pool of infective 274 mosquitoes throughout the transmission season. Ultimately, there are woefully few detailed ob-275 servations to confirm or invalidate this view. 276

277 The unavoidable underestimation of prevalence

The conundrum of the distinctly mosaic nature of P. malariae prevalence that challenged early 278 malariologists [1,6] remains unsolved, and it is still not clear today whether P. malariae is in fact 279 a rare or a common parasite [13,64]. Sole reliance on microscopic detection is not adequate to 280 capture those harbouring parasites that hover close to the limit of detection over time. When 281 combined with variations due to differing levels of acquired immunity, and to changing transmis-282 sion intensity, it is not surprising that wide variations in prevalence are observed in cross-sectional 283 surveys. Moreover, P. malariae is most likely to be overlooked, even by an experienced micros-284 copist, in areas where infections with other parasite species that lead to higher burdens are pres-285 ent. A potential resolution of this question has become theoretically feasible with the development 286 of molecular amplification techniques that provide a high level of specificity and detection sensi-287 tivity [65]. These brought to the fore the pervasiveness of asymptomatic infections. However, 288



the amplification techniques that are routinely used are not sufficient to provide an accurate pic-289 ture of *P. malariae* epidemiology. Whereas most amplification protocols can detect a single par-290 asite, the true limit of detection is determined by the volume of blood from which the aliguot of 291 292 DNA is added to the assay. A parasitaemia below 1000 parasite/ml is likely to be missed in an assay of 1 µl of blood. Higher limits of detection can be achieved [66], but larger blood volumes 293 requiring special processing would be required. Ultimately, a mere routine cross-sectional survey 294 will, by definition, lead to an underestimate of the true prevalence, and in the case of P. malariae 295 substantially so. Simply put, an infection in a person who is sampled monthly but whose parasites 296 Q18 are detectable for only 10 days over 3 months, is more likely to be missed than if sampling were performed weekly. To quote Leonard Bruce-Chwatt 'The usual single, cross-section Q19 malariometric survey gives about as much information of the natural history of malaria in an 299 endemic area as a few 'frames' taken out at random from a reel of film would of its plot'. Thus, 300 the actual prevalence of *P. malariae* is likely to remain elusive. Given that nearly all cross-301 sectional molecular surveys brought to light higher numbers of P. malariae than were detected Q20 by microscopy, we suggest that, in all regions of moderate to high endemicity, P, malariae should 303 be considered to have a significant prevalence unless proven otherwise. 304

305 Immunity and premunition

306 Little is known concerning the acquisition of immunity to P. malariae. The current consensus seems

to be that it is established faster, is more effective, and lasts longer than that of the other species.

Nearly all the relevant observations were conducted in Romania [67–69] where the infections were

induced by inoculation of erythrocytic parasites into neurosyphilitic patients from endemic areas.

The Romanian workers, nonetheless, noted that sterilising immunity required more frequent repeat infections than for *P. falciparum* or *P. vivax*. To what extent the acquisition of immunity differs from

that in the other species remains to be determined, as is the molecular basis of antigenic variation.

313 Edmond Sergent, Louis Parrot, and André Louis Donatien in 1924 proposed the term premuni-

tion to describe a state of relative refractoriness to disease and high parasitaemias conferred

315 by the continued presence of a subclinical/subpatent infection when subjected to new infection

316 [70,71]. Given the particularly lengthy chronic nature of *P. malariae* infections, one might specu-

317 late whether premunition plays a significant, if not predominant, role in the control of this parasite

in its human host, and the rapid and long-lasting acquisition of immunity against it.

319 A predominance of mixed infections...with consequences

Given their global distribution, P. malariae parasites invariably circulate in endemic areas where other 320 species predominate. Thus, it is highly likely that P. malariae occurs frequently in mixed-species infec-321 tions. This is equally probable even for areas of low or seasonal endemicity because of the persistence 322 of the asymptomatic malariae infection. It is recognised that microscopic diagnosis is particularly ill-323 adapted in determining the prevalence of mixed infections with P. malariae. The limitation imposed 324 by low parasite numbers is confounded by the morphological similarities with other species, 325 P. falciparum rings in particular and P. knowlesi, and by the 'flexible stopping rule' in which examina-326 327 tion of slides ceases following the discovery of a single parasite or following the enumeration of a set number of fields or cells in a blood smear [1,72]. The extent to which this prevalence can be 328 underestimated was shown in one of the first epidemiological surveys where diagnosis by amplifica-329 tion revealed P. malariae in 44/107 positive samples of which 43 were a mixed infection [73]. Since 330 then, the increasing number of molecular surveys in diverse endemic settings are confirming that 331 the significant prevalence of *P. malariae* is predominantly represented by mixed infections. 332

Although vertebrate hosts, including humans, are naturally subjected to infections by multiple species, simultaneously or successively, the biological or pathological consequences remain



speculative, with only a few experimental investigations addressing this aspect [74]. Acquired im-335 munity is highly species-specific, and thus, unlikely to contribute significantly to interactions be-336 tween concurrent Plasmodium species. Seasonal alternation of species prevalence and some 337 338 infections due to an unsuspected cryptic species suggested that some form of 'mutual exclusion' might occur when two species are present in the same host. Support for this was provided by the 339 first (and possibly only) detailed description of the course of parasitaemia in two patients moni-340 tored over 140 days following simultaneous inoculation of P. falciparum and P. vivax by mosquito 341 bite [75]. In both cases, P. vivax appeared only after the resolution of the primary peak(s) that were 342 343 fully dominated by *P. falciparum*. It is interesting to note that both species coexisted during the chronic phase in one of the patients but not the other. However, although observations in England 344 confirmed this early dominance, they also indicated that the suppression of P. vivax does not 345 occur if this species is introduced a few days before P. falciparum [76]. The unique observation 346 of a concurrent P. vivax and P. malariae experimental inoculation, using infected blood, showed 347 a dominance of P. vivax in nine of 12 cases where both parasites appeared in the blood, but of 348 P. malariae in three others, while in the four remaining patients, three showed only P. vivax and 349 one only P. malariae [77]. Controlled studies involving the infection of nonhuman primates [78] 350 and rodents [79,80] demonstrate that malaria parasites interact in mixed-species, as well as 351 mixed-strain, infections and that this significantly affects the course of parasitaemia, disease se-352 verity, and parasite transmission. However, at present, it is not possible to predict how and to 353 what extent this will occur, and the underlying mechanisms remain speculative. 354

In nature, P. malariae infections occur under highly variable environmental, epidemiological, and 355 host conditions. A truthful insight into the interplay between coinfecting species will require 356 large-scale longitudinal studies with standardised protocols for sample collection and highly sen-357 sitive parasite-detection methods. Available surveys have been predominantly cross-sectional 358 and have employed variable sampling and detection strategies, making it difficult to derive a co-359 herent picture. Nonetheless, these have provided important indications worthy of further investi-360 gation. A preliminary study on paediatric malaria in an lyory Coast village revealed an inverse 361 relationship between mixed P. falciparum-P. malariae infection and fever in infected children 362 [81]. Similar and additional interesting observations were recently made in two cross-sectional 363 surveys of school children using the same PCR diagnostic approach in the Democratic Republic 364 of Congo [82] and Nigeria [83], P. malariae was less likely to be observed in children with symp-365 tomatic malaria than in those who were asymptomatic (ca. three times less in the Democratic Re-366 public of Congo and ten times less in Nigeria). In both studies, P. malariae was almost exclusively 367 found in coinfections with P. falciparum, and it is assumed that symptoms were caused by the 368 P. falciparum component of the mixed infection. Furthermore, both studies revealed that parasite 369 370 carriage, including that of *P. malariae*, was higher in rural as compared to urban residents. This illustrates the heterogeneous nature of parasite prevalence through space, the basis of which 371 in environmental, vector, or socioeconomic factors remains to be explored. It will also be useful 372 to establish whether such patterns also occur in areas of low endemicity. 373

374 The differential distribution of P. malariae between asymptomatic and symptomatic infections where P. falciparum dominates might suggest a role of the former species in moderating clinical 375 symptoms, which are likely to be due to the higher P. falciparum parasitaemias. However, al-376 though mathematical modelling predicts that an ongoing P. malariae infection could reduce the 377 parasitaemia of a subsequent P. falciparum infection by up to 50% [84], other field observations 378 on the pathological consequence of P. falciparum + P. malariae mixed infections suggest an in-379 crease in anaemia [85]. Alternatively, it is possible that the faster-growing P. falciparum sup-380 presses P. malariae either through P. falciparum-induced nonspecific immune responses that 381 would reduce the already low P. malariae burdens or through competition for host cells (which 382



would be consistent with the preference for reticulocytes proposed above). If this were the case,

then P. malariae prevalence will likely increase in areas where that of P. falciparum becomes re-

duced. This was observed in Tanzania in the early 1960s [86], and more recently in Uganda

386 [87]. A further potential consequence of this mixed-species infection is a modulation of gameto-

387 genesis, which would alter the transmission dynamics of the coinfecting species. Indeed, analysis

388 of malariotherapy patients infected by a P. malariae strain (USPHS) and subsequently by a

389 *P. falciparum* strain (McLendon), indicated a significant increase in *P. falciparum* gametocyte pro-

duction [23]. This observation was mirrored in studies in Kenya and Tanzania [88], and Burkina

Faso [89] where *P. falciparum* gametocyte carriage was higher in persons with concurrent

392 *P. malariae* parasites.

393 Concluding remarks

Observations of *Plasmodium* in both vertebrate and anopheline hosts, and of the clinical course 394 and outcome of infections, guides the nature and focus of subsequent laboratory investigations 395 and underlies our perception of a particular species. Plasmodium malariae by virtue of its discrete 396 and long-lived parasitaemias remained under the radar over the decades. This was further exac-397 erbated by a global distribution that overlaps that of other malaria species, making it even less no-398 ticeable among the higher parasite loads of P. vivax and P. falciparum. The application of sensitive 399 and reliable molecular diagnostic techniques is now helping to bring this species to the attention 400 of the research community. Furthermore, the realisation that it is far more prevalent than previ-401 402 ously thought has also attracted the notice of the malaria-control community. In the absence of a routine in vitro cultivation method, or a practical experimental laboratory model, all investiga-403 tions, including those employing state-of-the-art technology, remain reliant on field and clinical 404 sampling. 405

The comparative paucity of observations on *P. malariae* parasites has by equal measure provided the scope for assertions that evolved into dogmas, and speculation as to alternative interpretations, such as some of those presented here. It is hoped that this review will stimulate future investigations (see Outstanding questions) that will not only confirm or invalidate some of these speculations but bring forth new insights into this overlooked parasite species.

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416 Declaration of interests

417 The authors declare no competing interests.

418 Supplemental information

419 Supplemental information associated with this article can be found online at https://doi.org/10.1016/j.pt.2022.11.008.

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Outstanding questions

What is the true prevalence of *P. malariae* globally?

Does *P. malariae* preferentially invade reticulocytes?

Do certain forms of *P. malariae* sequester?

Are there dormant tissue stages of *P. malariae*?

Does *P. malariae* modulate the severity or transmissibility of *P. falciparum* pathology?

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Supplementary file

Plasmodium malariae: the persisting mysteries of a persistent parasite

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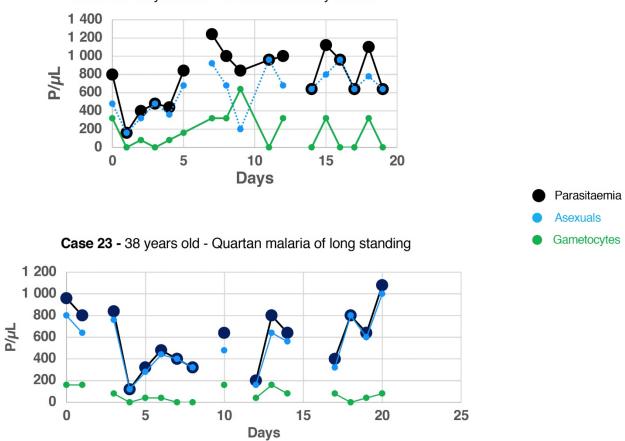


Figure S1. Parasitological course of chronic naturally acquired *P. malariae* infections. Two naturally infected patients with chronic *P. malariae* followed up after admission (Day 0) for 20 days prior to initiation of anti-malarial treatment. $P/\mu L = parasites/\mu L$. $P/\mu L = Parasites/\mu L$. The data are derived from [S1].

Case 22 - 19 years old - 18 months-history of fever

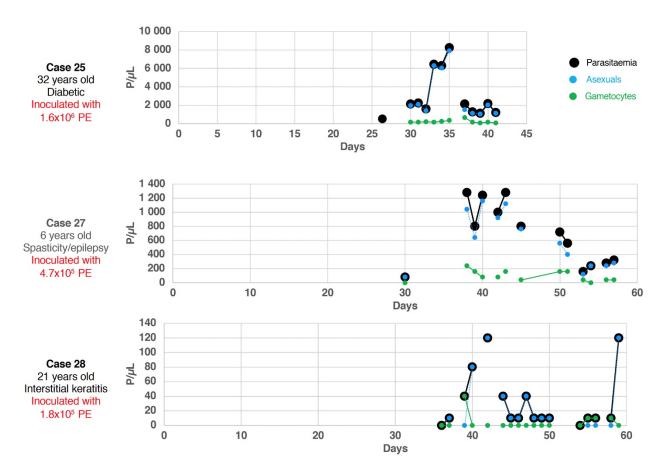


Figure S2. Course of infection following *P. malariae*-infected blood inoculation. Three patients were subjected to malariotherapy through inoculation of *P. malariae*-infected parasitised erythrocytes (PE) on Day 0 and then allowed to experience several paroxysms. The parasitaemias presented are that of the follow-up before the initiation of anti-malarial treatment. $P/\mu L = Parasites/\mu L$. The data are derived from [S1].

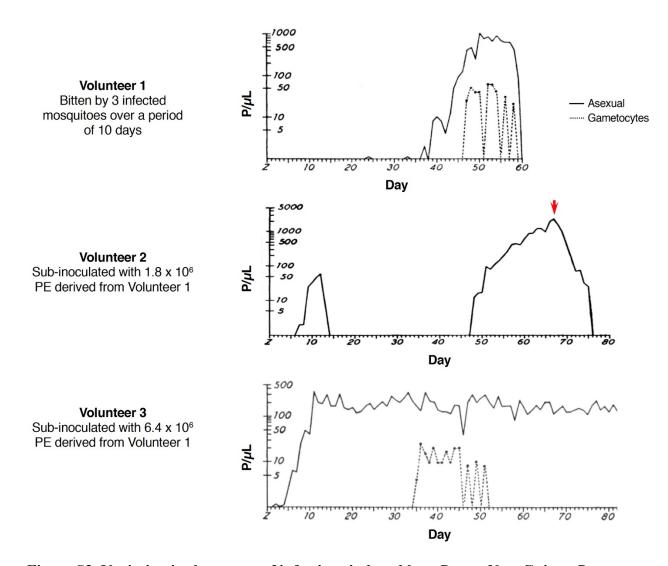


Figure S3. Variation in the course of infections induced by a Papua New Guinea *P*. *malariae* strain. Three volunteers were experimentally infected with *P. malariae*. Volunteer 1 was infected through the bites of mosquitoes that had fed on a *P. malariae* carrier from Papua New Guinea. The two other volunteers sub-inoculated from blood subsequently collected from Volunteer 1. Only Volunteer 2 required anti-malarial treatment (red arrow) before the termination of the follow-up. $P/\mu L = Parasites/\mu L$. Adapted from [S2].

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