



Review

Historical review: Does falciparum malaria destroy isolated tribal populations?



G. Dennis Shanks ^{a,b,c,*}

^a Australian Army Malaria Institute, Enoggera, QLD 4051, Australia

^b University of Queensland, School of Population Health, Brisbane, QLD 4006, Australia

^c Department of Zoology, University of Oxford, Oxford, UK

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Summary Many isolated populations of tribal peoples were nearly destroyed when they first contacted infectious diseases particularly respiratory pathogens such as measles and smallpox. Surviving groups have often been found to have declining populations in the face of multiple social and infectious threats. Malaria, especially *Plasmodium falciparum*, was thought to be a major cause of depopulation in some tribal peoples isolated in tropical jungles. The dynamics of such host parasite interactions is unclear especially since most such populations would have had long histories of exposure to malaria. Three groups are individually reviewed: Meruts of Borneo, Yanomami of Amazonia, Jarawas of the Andaman Islands. The purpose of this review is to examine the role of falciparum malaria in the depopulation of some isolated tribal groups in order to understand what measures, if any, would be likely to prevent such losses.

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It is not often that the exact fashion in which malaria affects a native tropical community has been described.
S R Christophers 1912 [1].

Plasmodium falciparum is likely to have coevolved with humans and our primate ancestors in tropical Africa [2]. This understanding is based on the discovery in gorillas of parasites indistinguishable from *P. falciparum* [3–5]. It is not obvious that malaria was a major cause of primate mortality in pre-historic tropical Africa or in gorillas today. Human mortality due to malaria may have been greatly magnified as part of the agricultural revolution that brought

the three species of plasmodium parasite, human host and anopheles vector into effective combination [2]. The resulting mortality shift generated by lethal falciparum malaria may have occurred only during the last few millennia of co-evolution as marked by the selection of balanced genetic polymorphisms in West Africa such as that seen in sickle cell anemia caused by hemoglobin S.

Populations with long histories of exposure to lethal malaria have adapted over time. This includes such isolated tribes as the various Pygmies (Yaka, Bawta etc) of central Africa who have genetic markers of malaria resistance such as glucose-6-phosphate dehydrogenase deficiency (G6PD) and Hemoglobin S [6]. Although more isolated than their Bantu neighbors, Pygmies do not appear to have comparatively increased mortality due to malaria [7]. Malaria parasites migrated down the Melanesian island archipelago

* Australian Army Malaria Institute, Enoggera, QLD 4051, Australia. Fax: +61 7 3332 4800.

E-mail address: dennis.shanks@defence.gov.au.

with their human hosts more than ten millennia ago. Malaria risk is partitioned in Melanesia away from coral islands without *Anopheles* mosquitoes and mountainous areas where cold temperatures limit parasite development [8]. Coastal populations on volcanic islands (e.g. Solomon Islands) have coevolved with falciparum malaria with the isolated populations developing a wide range of polymorphisms such as Southeast Asia ovalocytosis [9]. In Vanuatu on the edge of Melanesia, G6PD forms a north-south gradient reflecting the decreasing malaria evolutionary pressure [10]. So for some tribal groups that have long co-existed with malaria, falciparum extracts its mortality toll from the young but does not cause destabilizing population losses.

There are exceptions to the long coevolution of man with malaria in Melanesia. Ontong Java is a Polynesian outlier north of Santa Isabel in the Solomon Islands. It is a coral archipelago and not volcanic like the rest of the Solomon Islands. It is said that malaria was only introduced on Ontong Java in the 1880s and was a major if not primary cause of reducing the peak population by 80% in 1939 [11]. Malaria was considered holoendemic on Ontong Java based on spleen surveys in the 1940s and parasite surveys in the 1950s. Once malaria control measures through residual insecticide spray were initiated, malaria decreased and the population returned to near pre-contact levels by 2000 [11,12].

But does falciparum malaria kill truly isolated tribal groups that have no previous history of malaria exposure?

Since it is impossible to be sure what pathogens might have existed in a pre-contact situation, it is necessary to examine historical records of isolated groups soon after the end of their relative separation from global pathogen circulation. In three cases such information exists and will be reviewed in order to gain insight into what may have happened more broadly across the tropics. See Fig. 1 for approximate geographic locations.

1. Meruts of Borneo

The Meruts of North Borneo are a jungle Dyak tribal group related to their near neighbors the more agriculturally settled Dusuns. See Fig. 2. Depopulation labeled as “racial extinction” was an acute concern of the colonial era government by a chartered company when it was found that the number of Meruts were rapidly decreasing compared to the Dusuns [13]. Early investigators of the Merut long-house environment in the deep jungle identified several health problems associated with isolated tribes but thought that chronic ill health due to malaria was the primary cause of their falling population. The plausible hypothesis put forward was that imported Javanese rubber plantation workers had brought *P. falciparum* into close contact with a disturbed jungle eco-system causing localized malaria epidemics in the previously isolated Meruts [13]. Introduction of a new lethal pathogen had destabilized the population and in the absence of any effective chemotherapy (e.g.



Figure 1 Map showing approximate location of tribal groups discussed as examples of falciparum malaria in tribal peoples.

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