and *Plasmodium gaboni* recently given to haplotypes of malaria parasites of apes are not available (*nomina nuda*). These haplotypes could well be shown to be previously undescribed species but, by the current rules, morphological data and the selection of type specimens are essential in the descriptions of new species. Obviously, DNA sequences will continue to accumulate much faster than it will be possible to describe species. These diverse entities could be assigned acronyms as a temporary solution, as already accepted in avian malariology [10].

We call for a marriage of advanced molecular and microscopical approaches in mammalian malariology similar to the established practice in current studies on malaria parasites of reptiles and birds [9,10]. These combined approaches are essential for reliable comparative studies.

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#### References

- 1 Ollomo, B. *et al.* (2009) A new malaria agent in African hominids. *PLoS Pathogens* 5, e1000446
- 2 Liu, W. et al. (2010) Origin of the human malaria parasite Plasmodium falciparum in gorillas. Nature 467, 420–425

- 3 Krief, S. et al. (2010) On the diversity of malaria parasites in African apes and the origin of *Plasmodium falciparum* from bonobos. *PLoS Pathogens* 6, e1000765
- 4 Garnham, P.C.C. (1966) Malaria Parasites and other Haemosporidia, Blackwell Scientific Publications
- 5 Valkiūnas, G. (2005) Avian Malaria Parasites and other Haemosporidia, CRC Press
- 6 Ferrell, S.T. et al. (2007) Fatal hemoprotozoal infections in multiple avian species in a zoological park. J. Zoo. Wild. Med. 38, 309–316
- 7 Valkiūnas, G. et al. (2009) Nested cytochrome b polymerase chain reaction diagnostics detect sporozoites of hemosporidian parasites in peripheral blood of naturally infected birds. J. Parasitol. 95, 1512-1515
- 8 Palinauskas, V. et al. (2010) Laser microdissection microscopy and single cell PCR of avian haemosporidians. J. Parasitol. 96, 420-424
- 9 Perkins, S.L. and Austin, C.C. (2009) Four new species of *Plasmodium* from New Guinea lizards: integrating morphology and molecules. J. *Parasitol.* 95, 424–433
- 10 Bensch, S. et al. (2009) MalAvi: a public database of malaria parasites and related haemosporidians in avian hosts based on mitochondrial cytochrome b lineages. Mol. Ecol. Res. 9, 1353–1358
- 11 Garnham, P.C.C. and Duggan, A.J. (1986) Catalogue of the Garnham Collection of Malaria Parasites and Other Haemosporidia, Cambridge University Press
- 12 Adl, S.A. et al. (2007) Diversity, nomenclature, and taxonomy of protists. Syst. Biol. 56, 684–689

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## Letters

# Evolutionary parasitology applied to control and elimination policies

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Huijben *et al.* [1] recently suggested that subcurative antimalarial drug treatment of clinical cases might slow the spread of drug resistance through increased competition between drug resistant and sensitive infections. This was further discussed in letters to Trends in Parasitology. Goncalves and Paul [2] raised important questions about the potential use of subcurative treatment: What is the epidemiological and clinical impact of leaving a patient with circulating parasites? How is the correct drug sub-clearance level determined? Hastings [3] added several ethical and operational arguments against such a proposal namely that patients treated with subcurative drug levels could have repeated episodes of recurrent malaria and/or succumb to a secondary infection after being weakened by the primary malaria episode. However, the basic evolutionary argument remains unscathed, in untreated patients, competition between resistant and sensitive infections will benefit the latter as resistant mutations are expected to incur a fitness penalty. The question then arises: Is there any way to exploit competition between infections with different resistance profiles infecting the same host?

Fortunately, the parasite environment that Huijben *et al.* describes does already exist. Asymptomatic parasite carriers, mostly individuals that have acquired immunity owing to repeated infection in high transmission areas, provide an environment where there is no drug pressure as long as they are not treated. In this environment, sensitive parasites can outcompete resistant ones owing to the absence of drug induced selection. Also, the community-wide pressure against sensitive parasites is lower because less individuals need treatment and thus fewer individuals have a low level of drugs, a decisive factor in the spread of tolerance and resistance [4].

Elimination attempts, by definition, will have to target all infected humans [5], thus finding and treating asymptomatic carriers is a fundamental part of such efforts. This will jeopardize the reservoirs of sensitive parasites even if the treatment used for elimination is different from the standard first-line therapy. In this best-case scenario, if the elimination attempt fails, the frequency of resistance will probably increase above the pre-intervention frequency as asymptotic carriers, the safe-haven for sensitive parasites, are treated. The worst-case scenario, using the standard first-line therapy for elimination, will drive a dramatic

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## Update

increase in resistance should the elimination attempt not succeed. It is also probable that a failed elimination intervention will have worse consequences, for the spread of resistance, in high-transmission areas as a greater proportion of infections are asymptomatic owing to semi-immunity conferred by repeated infection [6].

On the other extreme of the policy spectrum (i.e. maximizing the number of untreated individuals to increase the relative fitness of sensitive parasites), a more radical approach to sub-clearance treatment would be to provide only palliative care. This would presumably be applied only to uncomplicated malaria cases on a voluntary basis. Analogous situations arise in other infectious diseases such as influenza [7] where not all individuals are treated with antivirals. Most unfortunately, malaria is not influenza, and the patient condition can deteriorate rapidly with complications such as renal failure or even cerebral malaria which can manifest suddenly and have a high mortality rate [8]. Clearly, current adjunctive therapy cannot be seen as a palliative alternative to replace proper malaria treatment [9].

The underlying premise that drug resistant parasites are outcompeted by sensitive parasites in non-treated environments is based in sound evolutionary genetic theory which is consistent, for instance, with the observation in Malawi [10] where Chloroquine removal led to a rather rapid disappearance of Chloroquine resistance presumably owing to a fitness penalty of resistance mutations. Strategies to better exploit this effect are still not clear but rational public health policy should recognize that policies to eliminate and eradicate malaria might conflict with more modest strategies to pursue only control. Decision makers that embark on elimination policies should be reasonably sure that they will be able to meet the desired outcome as excessive optimism might lead to a serious control problem after the failure of well-meaning, but possibly disastrous elimination efforts. Therefore, proper risk analysis encompassing many different factors ranging from donors' ability to maintain funding, transmission intensity, local geopolitical factors of the intervention area and the ability to conduct proper surveillance and monitoring of an intervention among others is fundamental to assure that any elimination attempt will not develop into a difficult-to-control scenario. If the last man standing is indeed the most resistant [11], should there not at least be a Plan B in case we indeed fail to cure him?

### References

- 1 Huijben, S. et al. (2010) Chemotherapy, within-host ecology and the fitness of drug-resistant malaria parasites. Evolution 64, 2952-2968
- 2 Goncalves, B. and Paul, R. (2011) Sub-clearance treatment to slow malaria drug resistance? *Trends Parasitol.* 27, 50–51
- 3 Hastings, I. (2011) Why we should effectively treat malaria. Trends Parasitol. 27, 51-52
- 4 Hastings, I. et al. (2002) The evolution of drug-resistant malaria: the role of drug elimination half-life. Phil. Trans. B 357, 505
- 5 Targett, G. and Greenwood, B. (2008) Malaria vaccines and their potential role in the elimination of malaria. *Malaria J.* 7, S10
- 6 Doolan, D. et al. (2009) Acquired immunity to malaria. Clin. Microbiol. Rev. 22, 13
- 7 Fiore, A. et al. (2011) Antiviral Agents for the Treatment and Chemoprophylaxis of Influenza, Centers for Disease Control and Prevention
- 8 Mishra, S. and Newton, C. (2009) Diagnosis and management of the neurological complications of falciparum malaria. Nat. Rev. Neurol. 5, 189–198
- 9 John, C. et al. (2010) Adjunctive therapy for cerebral malaria and other severe forms of Plasmodium falciparum malaria. Exp. Rev. Anti Infect. Ther. 8, 997–1008
- 10 Laufer, M.K. et al. (2006) Return of chloroquine antimalarial efficacy in Malawi. N. Engl. J. Med. 355, 1959–1966
- 11 Maude, R.  $et\ al.\ (2009)$  The last man standing is the most resistant: eliminating artemisinin-resistant malaria in Cambodia. Malaria J. 8, 31

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