Quantifying the gametocyte kinetics in *P. falciparum*-infected humans based on data from a malaria human infection study

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Malaria causes approximately half a million deaths every year, predominantly in children under 5 years old and mainly due to the strain *P. falciparum*. Gametocyte is the product of malaria parasite's sexual development in the host and primarily responsible for transmission from humans to mosquitoes. Therefore, developing effective strategies for blocking malaria transmission requires a quantitative understanding of the within-human kinetics of gametocyte. In this talk, I will present our recent work on quantifying the gametocyte kinetics in humans by fitting (within Bayesian hierarchical framework) a mechanistic model of within-host malaria infection to the time series data of total parasite concentration from patients in a clinical trial [1]. I will show that the model is not only able to reproduce (i.e. fit to) the time series of total parasite concentration in the blood but also able to accurately predict the time series of gametocyte concentration, which is crucial for the determination of human-to-mosquito transmission probability and in turn the coupling of within-host and population-level dynamics. Key kinetic parameters of *in vivo* gametocyte development are estimated based on posterior distributions and compared with the literature. The model will facilitate both the design of future clinical trials and the optimisation of drug regimens for treatment and can also be scaled up to population-level to predict more effective interventions to block malaria transmission.

⋆Mini-Symposium: Immuno-epidemiological models

References

[1] Collins KA, Wang CYT, Adams M, Mitchell H, Rampton M, et al. 2018. A controlled human malaria infection model enabling evaluation of transmission-blocking interventions. J Clin Invest 128(4): 1551-1562.