

Master's Project Proposal

Title:

Identify Plasmodium immunomodulatory molecules proteins that contribute to the success/failure of vaccination

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Synopsis:

Vaccination is undoubtedly one of the most cost-effective health interventions available. Whole-organism pre-erythrocytic (WOPE) vaccines employing *Plasmodium* sporozoites constitute the most promising approach to vaccination against malaria. WOPE vaccination relies on the natural ability of the immunizing parasites to productively infect the liver of a non-immune host (1). To achieve this, the parasite expresses a diverse repertoire of essential, partially redundant, or redundant genes, which moderate host-parasite interactions, not only scavenging nutrients but also evading and modulating the host's immune system to ensure survival. To develop improved vaccine candidates, we need to better understand how the immunizing parasites present themselves to the host, and which parasite immune modulating molecules can be eliminated in order to increase immunogenicity.

In collaboration with MIMS (Sweden), we aim to use a novel genome wide, high throughput screening assay for gene function to identify *Plasmodium* genes that serve as decoys and hamper the mounting of a successful immune response by WOPE vaccines (2,3).

The Master's student involved in this work will acquire various technical skills, including the use of animal and cell models of *Plasmodium* infection, immunofluorescence microscopy, qRT-PCR, ELISA and flow cytometry (4).

Bibliography (facultative):

1. Book chapter: A.M. Mendes, A. Scholzen, A.K. Mueller, S.M. Khan, R.W. Sauerwein, M. Prudêncio (2017) "Whole Organism Pre-Erythrocytic Vaccines", In: Rodriguez, A. and Mota M.M. (Eds) *Malaria: immune response to infection and vaccination*, Springer International Publishing, Cham, Switzerland
2. R. R. Stanway, E. Bushell, A. Chiappino-Pepe, M. Roques, T. Sanderson, B. Franke-Fayard, R. Caldelari, M. Golomugi, M. Nyonda, V. Pandey, F. Schwach, S. Chevalley, J. Ramesar, T. Metcalf, C. Herd, P. C. Burda, J. C. Rayner, D. Soldati-Favre, C. J. Janse, V. Hatzimanikatis, O. Billker, V. T. Heussler, Genome-Scale Identification of Essential Metabolic Processes for Targeting the *Plasmodium* Liver Stage. *Cell* 179, 1112-1128 e1126 (2019)
3. E. Bushell, A. R. Gomes, T. Sanderson, B. Anar, G. Girling, C. Herd, T. Metcalf, K. Modrzynska, F. Schwach, R. E. Martin, M. W. Mather, G. I. McFadden, L. Parts, G. G. Rutledge, A. B. Vaidya, K. Wengelnik, J. C. Rayner, O. Billker, Functional Profiling of a *Plasmodium* Genome Reveals an Abundance of Essential Genes. *Cell* 170, 260-272 e268 (2017)
4. Prudencio, M.; Mota, M. M.; Mendes, A. M., A toolbox to study liver stage malaria. *Trends in parasitology* 2011, 27(12), 565-74.

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