BP 60: Physics of Parasites - Joint Focus Session (BP/DY) organized by Holger Stark

Time: Friday 9:30–12:15 Location: SCH A251

Invited Talk BP 60.1 Fri 9:30 SCH A251

Spontaneous curvature and membrane curling for malaria-infected erythrocytes — •Manouk Abkarian[1,2], Octavio Albarran Arriagada[2], Gladys Massiera[2], Cyril Claudet[1,2], Andrew Callan Jones[2], Vladimir Lorman[2], and Catherine Braun Breton[3] — [1]Centre de Biochimie Structurale, Montpellier, France — [2]Laboratoire Charles Coulomb, Monptellier, France — [3]Dynamique des Interactions Membranaires Normales et Pathologiques, Montpellier, France

The culminating step of the intra-erythrocytic development of P. falciparum, the causative agent of malaria, is the spectacular release of multiple invasive merozoites upon rupture and curling of the infected erythrocyte membrane in a split second. We rationalized curling eversion by the acquisition of a high (negative) natural curvature c0 by the iEM, at a moment during parasite development. In this presentation, we will discuss our current investigation on curling both experimentally and theoretically. In particular, we will show with recent data that c0 is acquired several hours before maturation, by inducing a metastable curled and opened pore state in the iEM. I will discuss such stability using a more sophisticated model of the iEM taking into account its axisymmetry, the pore line tension and the iEM shear elasticity. Our model captures such a metastability and predicts the dynamics during egress when considering the internal and external viscous dissipations of the iEM. In particular, our approach underlines the importance of the membrane viscous flow thanks to the study of macroscopic elastic naturally curved ribbons.

BP 60.2 Fri 10:00 SCH A251

Shape and adhesiveness of malaria-infected red blood cells — Anil Kumar Dasanna, Marco Linke, Mailin Waldecker, Christine Lansche, Sirikamol Srismith, Marek Cyrklaff, Cecilia P. Sanchez, Michael Lanzer, and •Ulrich S. Schwarz — Heidelberg University

An infection of a red blood cell by the malaria parasite takes approximately 48 hours and during this time, the host cell is completely remodelled by the parasite. In particular, the parasite induces an adhesive structure on the host cell surface that keeps the infected red blood cell (iRBC) in the vasculature for a longer time and thus avoids clearance by the spleen. At the end of the infectious cycle, the iRBC ruptures and around 20 new parasites are released into the blood stream. Using fluorescence microscopy and image processing, we have found experimentally that during this process, the surface area of the iRBC is relatively constant, while the volume increases by 60 percent due to increased osmotic pressure, leading to a final reduced volume of 1 and thus to a spherical shape. This shape transition becomes apparent at the schizont stage (40 hours after infection). Using flow chamber experiments, we show that at the same time, the movement of iRBC under flow on endothelial monolayers changes from flipping to rolling adhesion. Using adhesive dynamics simulations, we systematically predict the effect of the adhesive structure on the rolling adhesion of schizont-stage iRBC, in good agreement with our experimental results.

BP 60.3 Fri 10:30 SCH A251

Deadly microswimmers - how trypanosomes move in blood and navigate in the tsetse fly — Sarah Schuster, Tim Krüger, and •Markus Engstler — Department of Cell and Developmental Biology, Biocenter, University of Würzburg, Würzburg, Germany

Trypanosomes are flagellate microswimmers and causative agents of deadly human diseases. The parasites swim freely in the blood and tissue fluids of their mammalian hosts, where they employ hydrodynamic drag to escape immune destruction. We found that different trypanosomes species reveal distinct motion patterns, which allows adaptations to diverse infection niches. Cell motility is essential for trypanosome survival, not only in the mammal, but also in the transmitting insect, the blood sucking tsetse fly. Within the tsetse, the parasites pass through different microenvironments and undergo several developmental transitions. This involves crossing various barriers and confined surroundings, concurrent with major morphological changes. This lecture introduces the trypanosome microswimmer system and focuses on the tsetse fly stages. Light sheet fluorescence microscopy is presented as a powerful tool for the 3D analysis of geometries within the tsetse fly's digestive tract. High spatio-temporal resolution microscopic analyses reveal how the different forms of trypanosomes exploit obstacles and borders for navigation in a complex environment. Transitions between solitary swimming and swarming mark the 30 days long journey of the trypanosomes through the fly. The parasites' behaviours range from self-avoidance to collective motion. We suggest that the trypanosome system is well suited for addressing some fundamental questions related to active motion in the world of low Reynolds numbers.

15 min break

BP 60.4 Fri 11:15 SCH A251

An *in silico* model for the African trypanosome — •Holger Stark — Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstr. 36, 10623 Berlin, Germany

The African trypanosome is the causative agent of the sleeping sickness and there is tremendous interest in understanding all aspects of how it moves forward and how it interacts with its environment. This includes the blood flow in blood vessels and passing the brain-blood barrier. Therefore, in the past years we have developed an *in silico* model for the African trypanosome, which fairly well captures its swimming motion [1-3]. The trypanosome has a conventional eukaryotic flagellum attached to its body. When a bending wave runs along the flagellum, the whole body deforms and is able to swim in the liquid environment, which me model with a particle-based solver of the Stokes equations called multi-particle collision dynamics.

With the help of the *in silico* model, we are able to demonstrate that the helical attachment of the flagellum optimizes the swimming speed [3], which helps the trypanosome to dispose of antibodies. We also simulate different morphotypes that occur during the parasite's development in the tsetse fly [3]. Finally, we address swimming in confinement and demonstrate that nearby channel walls or obstacles help the trypanosome to move forward.

[1] S. B. Babu and H. Stark, New J. Phys. **14**, 085012 (2012).
[2] N. Heddergott *et al.*, PLoS Pathogen **8**, e1003023 (2012).
[3] D. Alizadehrad, T. Krüger, M. Engstler, and H. Stark, PLoS Comput. Biol. **11**, e1003967 (2015).

BP 60.5 Fri 11:45 SCH A251

The development of a novel malaria diagnostic device — •Agnes Orban[1], Adam Butykai[1], Petra Molnar[1], Maria Pukancsik[1], Tivadar Zelles[2], Stephan Karl[3], and Istvan Kezsmarki[1] — [1]Dept. of Physics, Budapest Uni. of Technology and Economics and MTA-BME Lendület Magneto-optical Spectroscopy Research Group, 1111 Budapest, HU — [2]Dept. of Oral Biology, Semmelweis University, 1089 Budapest, HU — [3]Infection and Immunity Division, Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, AU

Although malaria is the most threatening parasitic disease worldwide and a global health issue, the current standard for its detection still remains the microscopic observation of stained blood smears. A novel cost-effective, automated, yet sensitive diagnostic method is needed for malaria detection both as an in-field instrument and as a laboratory tool for malaria researchers.

Our group aims to design such a device based on the detection of the magnetically induced linear dichroism of the malaria pigment crystals (hemozoin) by replacing the conventional polarization-modulation detection scheme with a rotating magnetic field. This concept enables a very high sensitivity detection of both synthetic and natural malaria pigment crystals as tested on suspensions of synthetic hemozoin; on hemozoin produced by *in vitro Plasmodium falciparum* cultures and on *in vivo* mouse models and human samples.

My brief introduction into the technological background will be followed by the presentations of the test results by my colleagues.

BP 60.6 Fri 12:00 SCH A251

Pre-clinical testing of a novel malaria diagnostic device — •Petra Molnar[1], Agnes Orban[1], Adam Butykai[1], Maria Pukancsik[1], Istvan Kezsmarki[1], Tivadar Zelles[2], Istvan Kucsera[3], Jetsumon Prachumsri[4], and Stephan Karl[5] — [1]Dept of Physics, Budapest Uni. of Technology and Economics and MTA-BME Lendület Magneto-optical Spectroscopy Research Group,

1111 Budapest, HU — [2]Dept of Oral Biology, Semmelweis Uni.,1089 Budapest, HU — [3]National Center for Epidemiology, 1097 Budapest, HU — [4]Mahidol Vivax Research Center (MVRC) of Mahidol Uni., Bangkok, TH — [5]Infection and Immunity Division, Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, AU

We have developed a compact and inexpensive rotating-crystal magneto-optical diagnostic (RMOD) device based on the detection of hemozoin crystals, a metabolic byproduct of all *Plasmodium* species. The first step of the in-field validation had been carried out in Thailand. To assess the diagnostic performance of the RMOD technique, 50 field-collected frozen human blood samples were measured at the MVRC. The RMOD method was also tested in collaboration with Dr. Stephan Karl, using field samples (n≈800) previously collected from symptomatic children prior to treatment and following combination therapies at Modilon Hospital in Papua New Guinea. These samples, well characterized by light microscopy and quantitative PCR, have offered an ideal opportunity to i) assess the diagnostic capability of the RMOD method and ii) study the hemozoin clearance kinetics in patient samples.