BBB Seminar (BMED380)

SCAN ME

Thursday, March 14. 14:30 at the BBB, Auditorium 4

Genetic screens in a malaria parasite reveal the deadly secrets of a divergent eukaryote

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Malaria is caused by protozoan parasites of the genus Plasmodium, which is transmitted between hosts by a mosquito vector, causing more than half a million deaths annually, with 70% of deaths occurring in African children under the age of seven. Malaria parasites are divergent eukaryotes with a complex life cycle, whose asexual replication in erythrocytes is responsible for disease, but whose transmission by mosquitoes depends entirely on sexual reproduction.

In a tractable rodent model, we have scaled up the targeted disruption of parasite genes to the point of enabling genome scale genetic screens at different life cycle stages. This has revealed how genes essentiality have evolved differently in different parts of the genome. It has also allowed us to map how parasite metabolism is reorganized as the parasite moves between different hosts and tissues, exposing changing drug vulnerabilities throughout the life cycle.

Sexual reproduction is essential for malaria parasites to infect mosquitoes, and our screens identify hundreds of parasite genes involved in the process. An analysis of fertility genes leads us to propose potential targets for transmission blocking interventions among some of the unique aspects of parasite sex. It also reveals unexpected, conserved aspects of developmental regulation, sperm biogenesis and gamete fusion that may represent ancestral mechanisms present already close to the last eukaryotic common ancestor.

Chairperson: Inari Kursula, Department of Biomedicine