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Malaria Parasites **Saving Lives, Buying Time Malaria Control During Mass Population Movements and Natural Disasters Breaking the cycle: attacking the malaria parasite in the liver World Malaria Report 2019** *Advances in Malaria Research* Malaria *Endogenous Insulin-like Peptides and Control of Malaria Parasite Infection in the Mosquito Host Disease and Mortality in Sub-Saharan Africa* **CDC Yellow Book 2018: Health Information for International Travel Investigations Into Aspects of Central Metabolism in the Human Malaria Parasite Plasmodium Falciparum** *Malaria Immunology Heat Shock Proteins of Malaria* **Mouse Model for Exoerythrocytic Stages of Plasmodium Falciparum Malaria Parasite** Malaria Parasites: Diverse Topics Malaria **The Garki Project** Malaria The Biology of Malaria Parasites Metabolic Systems Biology of the Malaria Parasite **Avian Malaria Parasites and other Haemosporidia** Malaria **Local Mate Competition and the Sex Ratios of Malaria Parasites, with a Focus on Plasmodium Mexicanum** Malaria Parasites *Heat Shock Proteins of Malaria* Malaria Parasites *Current Topics in Malaria* Regulation of Malaria Parasite Development **Comparative Genome Analysis of Malaria Parasite Species** *The Unconventional Amino Acid Starvation Response of the Malaria Parasite, Plasmodium Falciparum* **Atlas of Human Malaria** *An Exploration of Transcriptional Regulation in the Human Malaria Parasite, Plasmodium Falciparum Malaria Methods and Protocols* **Immunology and Immunopathogenesis of Malaria** *Bioinformatic Analysis and in Vitro Expression of Malaria Parasite Translocon and Ribonuclease Binding-like Rhoptry Genes* An Alternative Secretory Pathway in the Malaria Parasite 'Plasmodium falciparum' **CDC Yellow Book 2020** *Exploring the Roles of Phosphoinositides in the Biology of the Malaria Parasite Plasmodium Falciparum* **Cloning of Malaria Parasite DNA** *Raman Spectroscopic Techniques for the Detection of Malaria Parasite Infection*

Heat Shock Proteins of Malaria Feb 09 2022 This new edition describes the role of heat shock proteins in the life cycle of malaria parasites, particularly in the context of intracellular parasite stages. Thoroughly revised, this work provides a general introduction to the structural and functional features of heat shock proteins with a special focus on their role as molecular chaperones in ensuring protein quality control. The emphasis is on the heat shock protein families from Plasmodium falciparum, and their role in proteostasis and the development of malaria pathology. Moreover, the authors explore the latest prospects of targeting heat shock proteins in antimalarial drug discovery either directly or in combination therapies. Readers will experience a functional analysis of the individual families of heat shock proteins and their cooperation in functional networks, including both the parasite-resident proteome and the exportome released into host cells during intracellular stages. Subcellular and extracellular organelles such as the apicoplast and the Maurer’s Clefts associated with Plasmodium species are discussed in detail. The book highlights the role of heat shock proteins in the development and function of these structures. Biochemical expertise and the inclusion of novel therapeutic solutions make this collection a unique reference for experts in heat shock protein research, parasitology and infectious diseases, cell stress, molecular biology and drug discovery. Not least, advances in malaria control will contribute to ending epidemics and ensuring healthy lives in line with the UN Sustainable Development Goals.

Malaria Aug 15 2022 Malaria causes more death and disease than any other parasitic pathogen known today. This multiauthored text covers the important areas of malaria research, particularly focusing on those sectors which are of clinical importance for the understanding of the disease, the parasite, and its vector. The chapter authors are all leading experts within their own particular fields. The biology and molecular biology of the parasite, the clinical spectrum of the disease, the pathogenesis of malaria, and the immunology and emergence of malaria vaccines are some examples of the scientific spheres that are discussed. The book is suitable as a text for graduate students and clinicians as well as researchers at universities and companies involved in treating or studying infectious diseases.

Raman Spectroscopic Techniques for the Detection of Malaria Parasite Infection Oct 13 2019

Malaria Parasites Feb 21 2023 Malaria is a global disease in the world today but most common in the poorest countries of the world, with 90% of deaths occurring in sub-Saharan Africa. This book provides information on global efforts made by scientist which cuts across the continents of the world. Concerted efforts such as symbiont based malaria control; new applications in avian malaria studies; development of humanized mice to study P.falciparium (the most virulent species of malaria parasite); and current issues in laboratory diagnosis will support the prompt treatment of malaria. Research is ultimately gaining more grounds in the quest to provide vaccine for the prevention of malaria. The book features research aimed to bring a lasting solution to the malaria problem and what we should be doing now to face malaria, which is definitely useful for health policies in the twenty first century.

Immunology and Immunopathogenesis of Malaria Apr 18 2020 Malaria is still a major global health problem, killing more than 1 million people every year. Almost all of these deaths are caused by Plasmodium falciparum, one of the four species of malaria parasites infecting humans. This high burden of mortality falls heavily on Sub-Saharan Africa, where over 90% of these deaths are thought to occur, and 5% of children die before the age of 5 years. The death toll from malaria is still growing, with malaria-specific mortality in young African children estimated to have doubled during the last twenty years. This increase has been associated with drug resistance of the parasite, spread of insecticide resistant mosquitoes, poverty, social and political upheaval, and lack of effective vaccines. This collection of reviews addresses many of these important issues of malarial immunity and immunopathology. They are of interest not only to malariologists, but hopefully also to the broader immunological community. Strong interactions with, and feedback from immunologists working in other infectious diseases and in basic immunology will help us to move the field of malaria immunology and therapeutic intervention forward more quickly.

World Malaria Report 2019 Oct 17 2022 The World Malaria Report 2019 provides a comprehensive update on global and regional malaria data and trends. The report tracks investments in malaria programs and research as well as progress across all intervention areas: prevention, diagnosis, treatment, elimination, and surveillance. It also includes dedicated chapters on the consequences of malaria on maternal infant and child health the "High Burden to High Impact" approach as well as biological threats to the fight against malaria. The 2019 report is based on information received from more than 80 countries and areas with ongoing malaria transmission. This information is supplemented by data from national household surveys and databases held by other organizations.

Current Topics in Malaria Nov 25 2020

Saving Lives, Buying Time Jan 20 2023 For more than 50 years, low-cost antimalarial drugs silently saved millions of lives and cured billions of debilitating infections. Today, however, these drugs no longer work against the deadliest form of malaria that exists throughout the world. Malaria deaths in sub-Saharan Africaâ€"currently just over one million per yearâ€"are

rising because of increased resistance to the old, inexpensive drugs. Although effective new drugs called "artemisinins" are available, they are unaffordable for the majority of the affected population, even at a cost of one dollar per course. Saving Lives, Buying Time: Economics of Malaria Drugs in an Age of Resistance examines the history of malaria treatments, provides an overview of the current drug crisis, and offers recommendations on maximizing access to and effectiveness of antimalarial drugs. The book finds that most people in endemic countries will not have access to currently effective combination treatments, which should include an artemisinin, without financing from the global community. Without funding for effective treatment, malaria mortality could double over the next 10 to 20 years and transmission will intensify.

An Alternative Secretory Pathway in the Malaria Parasite 'Plasmodium falciparum' Feb 15 2020 Doctoral Thesis / Dissertation from the year 2014 in the subject Biology - Diseases, Health, Nutrition, grade: 1.3, University of Marburg (European virtual Institute for Malaria Research), language: English, abstract: This study focuses on the discovery of an alternative secretory pathway to the ER/Golgi route in the malaria parasite P. falciparum in infected RBCs. Two proteins appeared to be promising candidates of an alternative secretory pathway: the PfADP-ribosylation factor 1 (ARF1) and the Pfadenylate kinase 2 (AK2). Both proteins contained an N-myristoylation site at their N-terminus, which is indicative for N-myristoylation. N-myristoylation is a co-translational modification of a protein, whereby a fatty acid (myristate) is irreversibly attached to the glycine residue at the N-terminus of a protein via the PfN-myristoyltransferase (NMT). A preceding proteomic analysis of the parasitophorous vacuole and a reporter construct study proposed for both PfARF1 (determined by a proteomic study) and PfAK2 (determined by a reporter construct study) PV localization although both proteins lacked a signal peptide. That’s why it was hypothesized whether or not N-myristoylation would drive protein secretion across the parasite plasma membrane (PPM). The subcellular localization of the PfARF1/GFP parasites and the PfAK2/GFP parasites, respectively, were analyzed via epifluorescence microscopy and biochemical methods. In parallel, another batch of reporter constructs were generated and analyzed, where the N-myristoylation site of PfARF1 (this study) and PfAK2 (Ma et al., 2012), respectively, was removed (PfARF1G2A/GFP and PfAK2G2A/GFP). Live cell imaging showed that the fusion protein ARF1/GFP was localized as dot-like structures in the parasite. In contrast, the phenotype of the fusion protein of the PfARF1G2A/GFP parasites showed an evenly distributed signal in the parasite cytosol. Further analysis of the subcellular localization of the PfARF1 strongly supports its localization to compartments of the early secretory pathway of the parasite, but no localization in the PV. In contrast, the fusion protein PfAK2/GFP localized to a ring-like structure around the parasite indicating PV localization. The PfAK2G2A/GFP parasites showed a cytosolic localization of the fusion protein (Ma et al., 2012). Biochemical analyses revaled that the fusion protein PfAK2/GFP was secreted into the PV when the N-myristoylation site was present. Furthermore, it could be shown that the N-terminus of the PfAK2 protein is sufficient for parasite plasma membrane targeting, stable membrane anchoring and subsequent protein translocation across the PPM.

Exploring the Roles of Phosphoinositides in the Biology of the Malaria Parasite Plasmodium Falciparum Dec 15 2019 Plasmodium falciparum belongs to the phylum of Apicomplexa and causes the most severe form of malaria. In endemic areas of sub-Saharan Africa, most of the victims are among children under the age of five. P. falciparum relies on proteins released from sophisticated invasion organelles called micronemes, rhoptries and dense granules to enter human erythrocytes. The mechanism of biogenesis of invasion organelles and the coordinated release of their contents during invasion are mostly unknown. It has been shown that proteins targeted to the apical organelles

accumulate in microdomains of the Golgi apparatus with specific lipid and protein composition that determine the final destination of their cargo. To date, the mechanisms of transport of the cargo molecules to the invasion organelles and their release mechanism are mostly unknown. We proposed that phosphoinositides (PIPs) and their effector proteins could be involved in these processes in P. falciparum. PIPs are seven minor phosphorylated lipids in cellular membranes. Each subcellular membrane contains a characteristic species of PIPs that are specifically bound by PIPinteracting proteins. A wide range of biological processes regulated by PIPs such as vesicular trafficking, ion channels, pumps, and transporters and control both endocytic and exocytic processes. Based on previous reports five out of seven PIP species have been detected in P. falciparum. In my first project, we have studied the distribution of six PIPs namely PI3P, PI4P, PI5P, PI(4,5)P2, PI(3,4)P2 and PI(3,4,5)P3 using expression of specific reporters made up of human PIP-binding domains fused to a fluorescent protein. Here, we have confirmed previous reports on PI3P localization to the food vacuole membrane, small vesicles close/on the parasite plasma membrane and the apicoplast. Also, we have reported for the first time the presence of PI5P in P. falciparum and showed that it localizes to the PM, nucleus and potentially transitional ER. PI4P shows localization to the PM and Golgi and PI(4,5)P2 localizes to the PM all over the erythrocytic cycle. The resulting map of the subcellular distribution of PIPs will now be a great tool to further decipher the roles of these lipids in P. falciparum, In the second project, we have characterized a Pleckstrin Homology domain-containing protein (PfPH2) conserved in all apicomplexan parasites. Using the knock sideways strategy to conditionally inactivate the protein, we show that PfPH2 is involved in an early step of the invasion process, when the merozoites initially attach to red blood cells. We further demonstrate that this is due to the abrogated secretion of a specific population of micronemes. Finally, we reveal that recombinantly expressed PfPH2 binds PIPs with a broad specificity. Taken together, our results present evidence for the role of PI in invasion and propose a mechanistic model for the exocytosis of micronemes.

CDC Yellow Book 2020 Jan 16 2020 The definitive reference for travel medicine, updated for 2020! "A beloved travel must-have for the intrepid wanderer." -Publishers Weekly "A truly excellent and comprehensive resource." -Journal of Hospital Infection The CDC Yellow Book offers everything travelers and healthcare providers need to know for safe and healthy travel abroad. This 2020 edition includes: · Country-specific risk guidelines for yellow fever and malaria, including expert recommendations and 26 detailed, country-level maps · Detailed maps showing distribution of travel-related illnesses, including dengue, Japanese encephalitis, meningococcal meningitis, and schistosomiasis · Guidelines for self-treating common travel conditions, including altitude illness, jet lag, motion sickness, and travelers' diarrhea · Expert guidance on food and drink precautions to avoid illness, plus water-disinfection techniques for travel to remote destinations · Specialized guidelines for non-leisure travelers, study abroad, work-related travel, and travel to mass gatherings · Advice on medical tourism, complementary and integrative health approaches, and counterfeit drugs · Updated guidance for pre-travel consultations · Advice for obtaining healthcare abroad, including guidance on different types of travel insurance · Health insights around 15 popular tourist destinations and itineraries · Recommendations for traveling with infants and children · Advising travelers with specific needs, including those with chronic medical conditions or weakened immune systems, health care workers, humanitarian aid workers, long-term travelers and expatriates, and last-minute travelers · Considerations for newly arrived adoptees, immigrants, and refugees Long the most trusted book of its kind, the CDC Yellow Book is an essential resource in an ever-changing field -- and an ever-changing world.

Investigations Into Aspects of Central Metabolism in the Human Malaria Parasite Plasmodium Falciparum Apr 11 2022 This thesis combines four published research papers and a book chapter investigating aspects of central metabolism in the human malaria parasite Plasmodium falciparum. The publications are preceded by a statement which explores features of the research not fully described in the published texts, incorporates a review of the development over time and the present state of relevant scientific knowledge, and discusses the place of the individual papers and book chapter within malaria research. An assessment of the impact of each publication on its field of study is also included. A general discussion of the combination of papers as representative of the progress of research into the metabolism of malaria parasites concludes the statement section. The first publication is a chapter from a book, which describes detailed methods for the in vitro cultivation of P. falciparum. Such methodology, both robust and reliable, is a prerequisite for any investigation of parasite metabolism. The following publications are all primary research papers. The second publication describes the isolation and characterisation of the gene encoding the glycolytic pathway enzyme enolase from P. falciparum. The inferred amino acid sequence included peptide insertions found only in the enolases of higher plants and other photosynthetic organisms. This raised implications concerning the deep evolutionary history of the malaria parasite and related species. The third is concerned with the elucidation of the molecular basis of resistance to the antimalarial drug sulfadoxine. Resistance was found to result from point mutations within the dihydropteroate synthetase domain of the bifunctional protein hydroxymethylpterin pyrophosphokinase-dihydroptero¬ate synthetase, an enzyme of the parasite folate pathway. Additionally, it was discovered that the presence of exogenous folate has an antagonistic effect on sulfadoxine in some parasites of a defined genotype. This highlighted the importance of folate salvage in parasite metabolism. Fourth is a paper representing the discovery of a novel metabolism in both P. falciparum and the related apicomplexan parasite Toxoplasma gondii. The use of parasite genes in rescuing an Escherichia coli tyrosine auxotroph resulted in a proof of function of the products of these genes as pterin-4a-carbinolaminedehydratases. Pterin recycling, hitherto undetected in apicomplexans, was therefore added to the known metabolic processes of these organisms. The final paper describes an investigation into the subcellular distribution of the folate pathway enzyme serine hydroxymethyltransferase (SHMT) within P. falciparum erythrocytic stage parasites. The use of confocal laser scanning microscopy and immunofluorescent techniques showed that SHMTc, the sole enzymatically active parasite SHMT protein, was found in the cytoplasm but also showed a stage-specific localisation to both the mitochondrion and apicoplast organelles. The otherwise enigmatic, enzymatically inert, SHMTm paralogue revealed a possible function, when in complex, in allowing targeted localisation of SHMTc to the mitochondrion. The spatial distribution of SHMTm also suggested a possible role in the morphogenesis of elongating apicoplasts during schizogony.

CDC Yellow Book 2018: Health Information for International Travel May 12 2022 An up-to-date, definitive guide to staying safe and healthy anywhere in the world. Completely updated for 2018 with expanded guidelines for Zika virus, cholera vaccine, and more.

The Garki Project Oct 05 2021

Comparative Genome Analysis of Malaria Parasite Species Sep 23 2020 With over 200 million infections and up to one million deaths every year, malaria remains one of the most devastating infectious diseases affecting humans. Over the last few years, complete genome sequences of both human and non-human malaria parasite species have become available, adding comparative genomics to the toolbox of molecular biologists to study the genetic basis of human virulence. In this thesis, I computationally compared the published genomes of seven malaria parasite species with the aim to gain new insights

into genes underlying human virulence. This comparison was performed using two complementary approaches. In the first approach, I used whole-genome synteny analysis to find genes present in human but not non-human malaria parasites. In the second approach, I first clustered virulence-associated genes into gene families and then examined these gene families for species-specific differences. Both comparisons resulted in interesting gene lists. Synteny analysis identified three key enzymes of the thiamine (vitamin B1) biosynthesis pathway to be present in human but not rodent malaria parasites, indicating that these two groups of parasites differ in their ability to synthesize vitamin B1 de novo. My gene family classification exposed within the largest and highly divergent surface antigen gene family pir a group of unusually well conserved orthologs, which should be considered as high-priority targets for experimental characterization and vaccine development. In conclusion, this thesis highlights genes and pathways that are different between human and non-human malaria parasites and therefore could play important roles in human virulence. Experimental studies can now be initiated to confirm virulence-associated functions and to explore their potential value for drug and vaccine development.

Regulation of Malaria Parasite Development Oct 25 2020

Malaria Apr 30 2021 Malaria is spread by infected mosquitoes. Millions of people are infected by malaria each year. Read this book to learn more about the history of this infectious disease.

Malaria Immunology Mar 10 2022 Despite extensive efforts to control it, malaria is still one of the most devastating infectious diseases worldwide. This book, now in its second edition, provides a broad and up-to-date overview of the rapidly expanding field of malaria immunology and its importance in the control of this disease. The first section deals with the malaria parasite and its interactions with both the vertebrate host and the mosquitoes which transmit the disease. In the second part, the mechanisms of immunity and their regulation by environmental and genetic factors are discussed. Finally, this volume contains several chapters on malaria vaccine development, describing the application of the most recent vaccine technologies as well as ongoing and planned vaccine trials. Authored by well-recognized experts, this volume not only demonstrates the rapid progress being made in the search for vaccines against malaria, but also broadens our understanding of immunity to infection in general. It is therefore highly recommended reading for all scientists and professionals in the fields of immunology, infection and vaccine development.

Cloning of Malaria Parasite DNA Nov 13 2019

Avian Malaria Parasites and other Haemosporidia Jun 01 2021 When studying the effects of parasites on natural populations, the avian haematozoa fulfills many of the specifications of an ideal model. Featuring a multitude of tables and illustrations, Avian Malaria Parasites and Other Haemosporidia summarizes more than a century of research on bird haemosporidians. For a long time, bird blood parasites served

Malaria Sep 04 2021 Malaria is a mosquito-borne disease caused by parasitic protozoa that belong to the genus Plasmodium. This disease imposes a significant global health burden, claiming the lives of several thousand children and pregnant women each day. Increasing antimalarial drug resistance and the complexity of the Plasmodium life cycle, among other factors, have made eradication difficult. Written and edited by experts in the field, this collection from Cold Spring Harbor Perspectives in Medicine examines the biology, pathology, and epidemiology of malaria, as well as ongoing efforts to treat infections and manage their spread. Contributors discuss the Plasmodium life cycle, focusing on the molecular mechanisms by which the various parasitic stages induce clinical symptoms, interact with the immune system, and lead to further transmission of malaria. They also explore topics such as the interaction between mosquito reproduction and Plasmodium development, epigenetic regulation of malaria-associated genes, and unique features of malaria in pregnant women (e.g., parity-dependent susceptibility) and

describe how an improved understanding of these phenomena may lead to novel intervention strategies. The driving forces behind antimalarial drug resistance are covered, as is progress in developing an effective vaccine and controlling mosquito populations. This volume is therefore an essential reference for all scientists, clinicians, and public health professionals interested in understanding malaria and reducing its devastating effects.

Local Mate Competition and the Sex Ratios of Malaria Parasites, with a Focus on Plasmodium Mexicanum Mar 30 2021 Sex ratio theory is a focus in evolutionary biology that explores how natural selection shapes investment in males and females. It has provided some of the best quantitative evidence of evolution and could find utility in public health efforts through its application to malaria parasites. These parasites have distinct male and female forms that are produced following massive asexual replication, and they mate within the blood-feeding insects that transmit them between vertebrate hosts. A very similar population structure is assumed by local mate competition (LMC), a model from sex ratio theory that predicts female-biased sex ratios dependent on the degree of selfing within a mating patch. In this dissertation, I test a series of predictions from LMC for the lizard malaria parasite Plasmodium mexicanum. These include: (i) sex ratios have heritable variation that is not constrained by other life history traits; (ii) single-genotype infections have female-biased sex ratios that are determined by male fecundity; (iii) multiple-genotype infections have less biased sex ratios than single genotype infections; (iv) if males are limiting, sex ratios may be less biased when there are fewer parasites present (an extension of LMC called fertility insurance); and (v) less biased sex ratios may also be favored if increased female production yields diminishing returns on transmission to a new vertebrate host. To test these predictions, I combined the study of natural and experimental infections, microscopy (parasite density and sex ratio), molecular genetics (infection genetic diversity), and mathematical modeling (of how transmission patterns might affect sex ratio evolution). Overall, the results were qualitatively consistent with both LMC and my new model predictions. Sex ratios showed evidence of heritable variation that was unlinked to other life history traits measured. Sex ratios in single-genotype infections were female biased and consistent with the male fecundity observed, and were lower than sex ratios in experimental multiple-genotype infections, as predicted. Sex ratios were not less biased with lower sexual cell density, suggesting that males were not limiting. In fact, the opposite trend was sometimes observed: sex ratios were less biased with more sexual cells. This pattern has been observed previously in this and other species, and the only model that currently predicts such a trend is the new transmission model I outline. This dissertation contributes to our understanding of sex ratio evolution for malaria parasites in a number of ways. First, it adds evidence to the idea that the selective forces implicated in LMC are at work in malaria parasites and that malaria parasites are able to detect and respond to relevant cues. Second, it helps account for discrepancies in existing data, which have often reached conflicting conclusions. Third, it offers one of the first detailed studies of malaria parasite male fecundity, an essential piece of the sex ratio puzzle. Finally, it outlines a new theoretical extension of LMC that provides novel predictions and highlights areas of study that may be fruitful for future work on malaria parasites and other organisms.

Advances in Malaria Research Sep 16 2022 Thoroughly reviews our current understanding of malarial biology Explores the subject with insights from post-genomic technologies Looks broadly at the disease, vectors of infection, and treatment and prevention strategies A timely publication with chapters written by global researchers leaders

An Exploration of Transcriptional Regulation in the Human Malaria Parasite, Plasmodium Falciparum Jun 20 2020 Approximately half of the world's population is at risk of malaria transmission, and this

number can be expected to grow as drug resistant strains continue to develop. Among the human infectious Plasmodium species, Plasmodium falciparum causes the most severe and lethal form of malaria. This parasite has an extreme AT-rich genome and a complex life cycle that is likely to be regulated by coordinate changes in gene expression. However, the mechanisms behind this fine-tuned gene expression and regulation system remain elusive. For instance, only a limited number of transcription factors have been identified. Recent studies suggest that epigenetic and post-transcriptional regulation may be used as alternative regulation strategies to compensate for the lack of transcription factors in this parasite. Therefore, in this dissertation work, we further explored the transcriptome, epigenome, and the proteome to better understand the transcriptional mechanisms in P. falciparum. In chapter 1, we demonstrated that genes are usually defined by unique nucleosomal features and that nucleosome landscape alone could be used to identify novel genes in organisms with a nucleotide bias. Next, we investigated nascent RNA expression profiles and observed that the majority of genes are transcribed at the trophozoite stage in response to the open chromatin structure of that stage. These results helped us link chromatin reorganization events to transcriptional activity and highlighted the importance of epigenetic and post-transcriptional regulation in this parasite. Therefore, in the latter two chapters, we further examined the proteasome and transcriptome isolated from both nuclear and cytoplasmic fractions to identify potential chromatin regulators. As a result, we identified a large number of chromatin-associated proteins and lncRNAs that are likely to have important roles in chromatin regulation and post-transcriptional and translational regulations. Collectively, data and results from these studies will become stepping-stones for future malaria studies and further assist the identification of promising anti-malarial drug targets.

Breaking the cycle: attacking the malaria parasite in the liver Nov 18 2022 Despite significant progress in the global fight against malaria, this parasitic infection is still responsible for nearly 300 million clinical cases and more than half a million deaths each year, predominantly in African children less than 5 years of age. The infection starts when mosquitoes transmit small numbers of parasites into the skin. From here, the parasites travel with the bloodstream to the liver where they undergo an initial round of replication and maturation to the next developmental stage that infects red blood cells. A vaccine capable of blocking the clinically silent liver phase of the Plasmodium life cycle would prevent the subsequent symptomatic phase of this tropical disease, including its frequently fatal manifestations such as severe anemia, acute lung injury, and cerebral malaria. Parasitologists, immunologists, and vaccinologists have come to appreciate the complexity of the adaptive immune response against the liver stages of this deadly parasite. Lymphocytes play a central role in the elimination of Plasmodium infected hepatocytes, both in humans and animal models, but our understanding of the exact cellular interactions and molecular effector mechanisms that lead to parasite killing within the complex hepatic microenvironment of an immune host is still rudimentary. Nevertheless, recent collaborative efforts have led to promising vaccine approaches based on liver stages that have conferred sterile immunity in humans – the University of Oxford's Ad prime / MVA boost vaccine, the Naval Medical Research Center’s DNA prime / Ad boost vaccine, Sanaria Inc.'s radiation-attenuated whole sporozoite vaccine, and Radboud University Medical Centre’s and Sanaria's derived chemoprophylaxis with sporozoites vaccines. The aim of this Research Topic is to bring together researchers with expertise in malariology, immunology, hepatology, antigen discovery and vaccine development to provide a better understanding of the basic biology of Plasmodium in the liver and the host’s innate and adaptive immune responses. Understanding the conditions required to generate complete protection in a

vaccinated individual will bring us closer to our ultimate goal, namely to develop a safe, scalable, and affordable malaria vaccine capable of inducing sustained high-level protective immunity in the large proportion of the world's population constantly at risk of malaria.

Disease and Mortality in Sub-Saharan Africa Jun 13 2022 Current data and trends in morbidity and mortality for the sub-Saharan Region as presented in this new edition reflect the heavy toll that HIV/AIDS has had on health indicators, leading to either a stalling or reversal of the gains made, not just for communicable disorders, but for cancers, as well as mental and neurological disorders.

Atlas of Human Malaria Jul 22 2020

Heat Shock Proteins of Malaria Jan 28 2021 This book describes the role of heat shock proteins in the life cycle of malaria parasites. The work includes a general introduction on the structural and functional features of heat shock proteins. The main focus is on the role of heat shock protein families from Plasmodium falciparum, their role in protein folding and in the development of malaria pathology. The functions of individual families of heat shock proteins from plasmodium species and their cooperation in functional networks is described. Subcellular and extracellular organelles such as the apicoplast and the Maurer's Clefts which are associated with plasmodium species, are discussed in detail. The role of heat shock proteins in the development and function of these organelles structures are highlighted. Although conceding that heat shock proteins may not be ideal antimalarial drug targets, prospects of targeting heat shock proteins in antimalarial drug discovery either directly and/or in combination therapies are explored.

Bioinformatic Analysis and in Vitro Expression of Malaria Parasite Translocon and Ribonuclease Binding-like Rhoptry Genes Mar 18 2020 Abstract: Malaria caused by the parasite Plasmodium, still remains a significant public health problem worldwide, due to lack of a vaccine and emerging drug and insecticide resistance, among malaria parasites and mosquito vectors, respectively. Rhoptry proteins of Plasmodium enable merozoite invasion of host erythrocytes. However, only a few of these proteins have been characterized. Thirty-six P. yoelii merozoite rhoptry proteins were identified as putative rhoptry proteins by proteome analysis. Some of these proteins have been characterized while others still remain an intense area of active research. Molecular characterization and understanding of these novel proteins may assist in vaccine development, design of diagnostic assays and better control of malaria disease. This study was aimed at characterizing two Plasmodium rhoptry genes; Translocon and Ribonuclease binding-like (RNB-like) genes using bioinformatics analysis and in vitro cell free expression. Bioinformatics analysis was performed using the databases: PlasmoDB, ExPaSy, PSORTb, SWISSPROT-workspace, GeneDB, National Center for Biotechnology Information (NCBI) and COBALT: Multiple Alignment Tool. Both genes were characterized for features such as conservation profiles, domain architecture and alignment of sequences, both within Plasmodium species and among members of the phylum apicomplexa. The RNB protein domains are generally conserved across Plasmodium species but protein identity across species is 30%. The amino acid identity is about 40% across species for the Translocon protein. This study revealed that these genes are expressed early upon merozoite invasion of the host erythrocytes. The expressed translocon protein that is annotated as hypothetical or putative has been shown to be part of a transport complex and the RibonucleaRibonuclea Ribonuclease binding binding - like (RNB) gene expresses a putative RNB -like protein found in all species of Plasmodium . The translocon of Plasmodium falciparum was successfully PCR amplified, cloned and a 23 kDa protein was expressed in vitro. Expression was confirmed with rhoptry specific antibodies.

Malaria Methods and Protocols May 20 2020 The Plasmodium spp. parasite was identified as the causative agent of malaria in 1880, and the mosquito was identified as the vector in 1897. Despite subsequent efforts focused on the epidemiology,

cell biology, immunology, molecular biology, and clinical manifestations of malaria and the Plasmodium parasite, there is still no licensed vaccine for the prevention of malaria. Physical barriers (bed nets, window screens) and chemical prevention methods (insecticides and mosquito repellents) intended to interfere with the transmission of the disease are not highly effective, and the profile of resistance of the parasite to chemoprophylactic and chemotherapeutic agents is increasing. The dawn of the new millennium has seen a resurgence of interest in the disease by government and philanthropic organizations, but we are still faced with compl- ities of the parasite, the host, and the vector, and the interactions among them. Malaria Methods and Protocols offers a comprehensive collection of protocols describing conventional and state-of-the-art techniques for the study of malaria, as well as associated theory and potential problems, written by experts in the field. The major themes reflected here include assessing the risk of infection and severity of disease, laboratory models, diagnosis and typing, molecular biology techniques, immunological techniques, cell biology techniques, and field applications.

Metabolic Systems Biology of the Malaria Parasite Jul 02 2021

Endogenous Insulin-like Peptides and Control of Malaria Parasite Infection in the Mosquito Host Jul 14 2022

The deadliest human malaria parasite, Plasmodium falciparum, is transmitted by mosquitoes of the genus Anopheles, including Anopheles stephensi, the major malaria vector in India and southeast Asia. Recent efforts to enhance malaria control have focused on developing genetically modified Anopheles mosquitoes that are resistant to malaria parasite infection by manipulating proteins that are essential to the immune response, a strategy that requires a detailed understanding of the complex molecular mechanisms underlying immunity. Insulin/insulin-like growth factor signaling (IIS) is highly conserved from invertebrates to humans and a growing body of literature suggests the involvement of this pathway in regulating immunity. In this work, we show that endogenous insulin-like peptides (ILPs) produced during infection can regulate diverse aspects of mosquito physiology to impact malaria parasite growth and transmission. First, we identified five ILPs in A. stephensi, and characterized their tissue-specific expression patterns in response to various physiological conditions. Specifically, we showed that that ILP expression is not highly responsive to dietary changes, starvation, or ageing, but appears fine-tuned to ingested human insulin and infection with P. falciparum. Next, in order to probe the significance of ILP expression during P. falciparum infection, we developed a novel protocol for protein knockdown in the midgut using antisense morpholinos. We confirmed the effectiveness of this method by inhibiting the mitogen-activated protein kinase (MAPK) MEK-ERK signaling pathway, a known regulator of immunity in the A. stephensi midgut. Further, we utilized this knockdown technique to show that two infection induced ILPs negatively regulate mosquito immunity. We demonstrated that P. falciparum induces ILP expression through activation of feed-forward insulin signaling in the midgut to suppress expression NF-KB regulated immune genes and facilitate parasite growth. We also showed that ILP expression during infection regulates host-seeking and feeding behaviors in the mosquito, potentially increasing transmission in addition to parasite growth. Finally, we dissected the dynamics of ILP signaling using synthetic peptides to predict mechanisms by which induced ILPs function during infection to regulate P. falciparum development. We showed that two infection-induced ILPs produce distinct effects on cell signaling, immunity, metabolism, and midgut homeostasis, suggesting that that the kinetics of ILP regulation of P. falciparum infection are controlled through a diverse network of ILP-specific effects on midgut physiology. Collectively, this body of work provides a foundation for understanding a new gene target that could potentially be manipulated to

engineer parasite resistant mosquitoes for disease control, while also unveiling novel aspects of fundamental biology that are controlled by the highly conserved insulin/insulin-like growth factor signaling cascade in a medically important disease vector.

Malaria Parasites Dec 27 2020 Malaria is a global disease in the world today but most common in the poorest countries of the world, with 90% of deaths occurring in sub-Saharan Africa. This book provides information on global efforts made by scientist which cuts across the continents of the world. Concerted efforts such as symbiont based malaria control; new applications in avian malaria studies; development of humanized mice to study P.falciparium (the most virulent species of malaria parasite); and current issues in laboratory diagnosis will support the prompt treatment of malaria. Research is ultimately gaining more grounds in the quest to provide vaccine for the prevention of malaria. The book features research aimed to bring a lasting solution to the malaria problem and what we should be doing now to face malaria, which is definitely useful for health policies in the twenty first century.

Mouse Model for Exoerythrocytic Stages of Plasmodium Falciparum Malaria Parasite Jan 08 2022 Research on the exoerythrocytic (EE) stages of human malaria parasites has been hindered because of the lack of an easily available suitable animal-mode. We report here an approach to produce mature EE-stage Plasmodium falciparum parasites by using severe combined immuno-deficient (scid) mice with transplanted human hepatocytes. Transplantation of human hepatocytes into scid mice (scid hu-hep), their subsequent intravenous infection with P. falciparum sporozoites, and the development of mature liver-stage macrozoites was achieved. Immunofluorescent staining of scid hu-hep kidney tissue sections demonstrated the presence of circumsporozoite protein (early during infection), merozoite surface antigen 1, and liver schizont antigen 1. The scid hu-hep model can serve as a source of human malaria liver-stage parasites, decreasing the need for nonhuman primates. Use of this model will facilitate characterization of EE- stage antigens and the assessment of stage-specific chemotherapeutic agents and candidate vaccines.

Malaria Nov 06 2021 Every 30 seconds a death is caused by Malaria. This book brings together recent advances in our understanding of the basic biology, genetics and pathogenesis of malaria, to facilitate the rapid generation of new insights and interventions. Each chapter is written by a leading expert(s), and serves as both a useful introduction to the area and a helpful set of references. Malaria: Parasite Biology, Pathogenesis and Protection is a useful entry point for graduate and medical students, scientists and individuals engaged in a subspecialty of Malaria research, as well as those who are simply interested in getting a grasp on the present status of this ever burgeoning public health problem.

Malaria Control During Mass Population Movements and Natural Disasters Dec 19 2022 Admittedly, the world and the nature of forced migration have changed a great deal over the last two decades. The relevance of data accumulated during that time period can now be called into question. The roundtable and the Program on Forced Migration at the Mailman School of Public Health of Columbia University have commissioned a series of epidemiological reviews on priority public health problems for forced migrants that will update the state of knowledge. Malaria Control During Mass Population Movements and Natural Disasters- the first in the series, provides a basic overview of the state of knowledge of epidemiology of malaria and public health interventions and practices for controlling the disease in situations involving forced migration and conflict.

Malaria Parasites Feb 26 2021 Malaria is a global disease in the world today but most common in the poorest countries of the world, with 90% of deaths occurring in sub-Saharan Africa. This book provides information on global efforts made by scientist which cuts across the continents of the world. Concerted efforts such as symbiont based malaria control; new applications in

avian malaria studies; development of humanized mice to study P.falciparium (the most virulent species of malaria parasite); and current issues in laboratory diagnosis will support the prompt treatment of malaria. Research is ultimately gaining more grounds in the quest to provide vaccine for the prevention of malaria. The book features research aimed to bring a lasting solution to the malaria problem and what we should be doing now to face malaria, which is definitely useful for health policies in the twenty first century.

The Unconventional Amino Acid Starvation Response of the Malaria Parasite, Plasmodium Falciparum Aug 23 2020 The apicomplexan parasite, Plasmodium falciparum, is the causative agent of the most severe form of malaria, resulting in nearly 1 million deaths each year. The parasite establishes its replicative niche within human erythrocytes, where it degrades massive amounts of host cell hemoglobin, salvaging the released amino acids for its own use. However, human hemoglobin does not contain the amino acid isoleucine, which is one of the most prevalent amino acids in the parasite's proteome. Since P. falciparum cannot synthesize isoleucine, it must acquire this amino acid from human serum. Optimal growth and, ultimately, the survival of P. falciparum depend on the availability of circulating essential nutrients such as isoleucine, which is often scarce in undernourished malaria patients. To understand how P. falciparum responds to isoleucine starvation, we monitored parasite growth in isoleucine-limiting conditions. We observed that in vitro parasite growth is notably slower in medium containing low concentrations of isoleucine, but completion of the life cycle, consisting of steady progression through the ring, trophozoite, and schizont stages, followed by subsequent rounds of re-invasion and gradual expansion of the culture, continues at a reduced rate. However, when subjected to isoleucine starvation, parasites progress only through the trophozoite stage. Interestingly, supplementation with isoleucine restores normal asexual growth, suggesting the involvement of sensory/response elements in the growth control mechanism of the parasite. The focus of this thesis was to characterize the dynamic metabolic properties of this remarkable starvation-induced state in P. falciparum and uncover the molecular basis behind this response. In this work, it was found that isoleucine starvation effectively slows down the metabolic growth of P. falciparum, resulting in cell cycle inhibition, reduced protein translation, and delayed gene expression. Although appreciable parasite growth could be recovered upon isoleucine repletion even after several days of starvation, active proteolysis during extended starvation was required to maintain viability. The canonical amino acid-starvation responsive GCN2/eIF2[alpha] signaling pair is functionally conserved in P. falciparum, exhibiting remarkable specificity in detecting isoleucine availability, however, its activity was not essential to preserving the parasite in a growth-competent state during starvation. These data indicate that the starvation response of P. falciparum is unique: although the parasite maintains an active remnant of a conventional eukaryotic amino acid-stress response pathway, its regulatory role is inconsequential. We conclude that isoleucine starvation induces a hibernating state in P. falciparum, an effective default pathway suitable for its parasitic lifestyle.

The Biology of Malaria Parasites Aug 03 2021

Malaria Parasites: Diverse Topics Dec 07 2021 Malaria is a global disease today but most common in underdeveloped countries of the world. Nearly 90% of deaths due to this fatal disease occur in Sub-Saharan Africa. This book presents information regarding global endeavors undertaken by scientists from across the world. Collaborated efforts such as symbiont based malaria control, latest applications in avian malaria studies, advancement of humanized mice to study P. falciparum (the most virulent species of malaria parasite) and contemporary issues in laboratory diagnosis will aid efficient treatment of malaria. Research has been progressing rapidly in the quest for providing an effective vaccine

for the prevention of malaria. This book presents research aimed at bringing forward abiding solutions to malaria issues and the methods and procedures that should be followed for combating these issues for better implementation of health policies in contemporary times as well as future.

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