Review Article Interferons and Interferon Regulatory Factors in Malaria

Sin Yee Gun,^{1,2} Carla Claser,¹ Kevin Shyong Wei Tan,² and Laurent Rénia^{1,2}

¹ Singapore Immunology Network, Agency for Science, Technology and Research (A^{*} STAR), Singapore 138648

² Department of Microbiology, Yong Loo Lin School of Medicine, National University of Singapore, Singapore 119228

Correspondence should be addressed to Laurent Rénia; renia_laurent@immunol.a-star.edu.sg

Received 19 April 2014; Accepted 18 June 2014; Published 15 July 2014

Academic Editor: José C. Rosa Neto

Copyright © 2014 Sin Yee Gun et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Malaria is one of the most serious infectious diseases in humans and responsible for approximately 500 million clinical cases and 500 thousand deaths annually. Acquired adaptive immune responses control parasite replication and infection-induced pathologies. Most infections are clinically silent which reflects on the ability of adaptive immune mechanisms to prevent the disease. However, a minority of these can become severe and life-threatening, manifesting a range of overlapping syndromes of complex origins which could be induced by uncontrolled immune responses. Major players of the innate and adaptive responses are interferons. Here, we review their roles and the signaling pathways involved in their production and protection against infection and induced immunopathologies.

1. Introduction

Malaria, a mosquito-borne infectious disease transmitted by Anopheles mosquito, remains as one of the leading causes of morbidity and mortality worldwide, particularly in Africa, South-East Asia, and parts of South America [1]. When infected mosquito feeds on a human, the infective form of the Plasmodium parasite, sporozoites, is inoculated into the dermis of the host. Most of the motile sporozoites then leave the skin, travel through the blood circulation, and settle in the hepatocytes. During this liver phase, sporozoites undergo several asexual multiplications to form merozoites. Vesicles containing mature merozoites, merosomes, are released into the peripheral blood circulation and ruptured in the lungs to release thousands of merozoites into the blood circulation. These parasites infect red blood cells and initiate the erythrocytic phase [2]. Due to the exponential growth of the parasite, followed by massive destruction of erythrocytes, this stage is responsible for the common clinical manifestations of malaria such as fever, headaches, chills, and diaphoresis [3]. Usually the host immune response can control and eliminate the parasite, yet in some circumstance, patient's conditions deteriorate and develop severe systemic or organ-related pathological conditions such as anemia [4], hypoglycemia, febrile illness, respiratory distress [5], or cerebral malaria (CM) [6].

2. Innate Immunity to Pathogens

For the past decades, it was shown that the host immune response plays an important role in controlling the progression of malaria infection. The adaptive immunity, developed through repetitive infections during childhood, is pivotal in the elimination of *Plasmodium* parasite [7-10]. Yet, studies suggest that the host's ability to control the growth of parasites also relies on the innate immunity [11, 12]. Recent analysis of clinical records from neurosyphilis patients who underwent malaria therapy showed a controlled parasite density, irrespective of parasite strain, during the first and the second parasite inoculation which suggested the presence of a stable innate response [13]. In addition, peripheral blood mononuclear cells (PBMCs) from patients who had no prior exposure to malaria were able to produce proinflammatory cytokines, such as TNF- α , IL-12, and IFN- γ , within 10 hours of exposure to infected red blood cells (iRBCs) [14] demonstrating the activation of innate immune response against malaria parasite. However, proinflammatory cytokines are a doubleedged sword. Under normal circumstances, they are essential for the control of parasite growth and sustained protection against the disease pathology, yet excessive and dysregulated production can lead to several immunopathologies [15, 16].

Human genetic diversity, parasite variability, and immune status of host generate various disease profiles of malaria infections. Fortunately, only a fraction of malaria infection in human leads to pathologies [17]. This diversity in phenotypes is always associated with differences in measured biological and immune parameters. In addition, due to obvious ethnical reasons, analyses of these parameters are largely confined to peripheral blood (serum, plasma, and circulating cells). In most studies, only association but not causal mechanisms can be determined. Thus, malaria research mainly relies on mouse models to investigate the host immune response during malaria infection. Although these models cannot reflect all aspects of human infections, they allow the study of controlled experimental infections. There are 4 rodent malaria species, P. berghei, P. chabaudi, P. vinckei, and P. yoelii, 13 subspecies, and various strains and cloned lines [18]. These parasites were isolated from African thicket rats in Central and West Africa more than 50 years ago [19]. Depending on the host and parasite combinations, different disease profiles can be induced and host immune response will determine the outcome of infection (Table 1). These models, when used together with genetically deficient mice, allow in-depth study on protection against infection or immunopathogenesis. For example, the study of CM is hampered by the limited access to tissue samples and difficulty to perform in vivo experiments. Susceptible mice infected with P. berghei ANKA (PbA) manifest neurological abnormalities similar to human CM. In this model, termed experimental cerebral malaria (ECM), high production of proinflammatory cytokines, sequestration of parasite [20-23] and leukocytes, in particular CD8⁺ T cells [24-26], and presentation of parasite antigen by brain microvessels [27] lead to the damage of the blood-brain barrier (BBB) and death. However, the role of innate immune responses in this pathology still remains to be determined.

When pathogens breach the skin or mucosal barriers, innate immune cells such as macrophages, mast cells, dendritic cells, and fibroblast, as well as circulating leukocytes, including monocytes and neutrophils, sense foreign agent using pattern recognition receptors (PRRs) that identify conserved pathogen-associated molecular patterns (PAMPs) on pathogens [28-30]. PRRs are either membrane-bound, such as toll-like receptors (TLRs) [28, 31-33] and C-type lectin receptors (CLRs) [28, 34-36], or free in the cytosol, such as NOD-like receptors (NLRs) [37-39] and RIG-I-like receptors (RLRs) [32, 40]. These PRRs are distinctly expressed on different cell populations which in turn influence the immunological repertoire elicited by a particular antigen. Professional antigen presenting cells, such as macrophage, B cells [41, 42], and dendritic cells [41, 43, 44], are well equipped with a wide spectrum of PRRs which enables this surveillance team to recognize a great variety of PAMPs and induce specific responses against each class of pathogens. For instance, in human, myeloid dendritic cells (mDCs) express all TLR1-10, but not TLR7, whereas plasmacytoid dendritic cells (pDCs) exclusively express TLR7 and TLR9 [41, 43, 44]. When activated, mDCs preferentially induces IL-12 while pDCs mainly produces IFN- α [44]. Other PRRs, such as dendritic cell-specific intracellular molecule-3-grabbing nonintegrin (DC-SIGN) [45] and DNGR-1 (Clec9A) [46], members of CLRs, expressed on immature DC were implicated in tolerogenic responses in some studies [47-49].

Besides professional antigen presenting cells, some epithelial cells are also furnished with PRRs. TLR2, TLR4, and TLR5 are widely found on pulmonary [50–53] and intestinal [54–56] epithelial cells. Since these surfaces are in continuous exposure to microbial challenges, strategic expression of these TLRs on these surfaces enables prompt recognition and response against bacterial infection. Vascular endothelial cells that line the entire circulatory system express also TLR4 [57, 58], RIG-I [59], and NOD-1 [60].

Upon positive PAMPs recognition, PRRs trigger a cascade of downstream signaling pathways that leads to nuclear translocation of transcription factors such as nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B), activating protein-1 (AP-1), and interferon regulatory factors (IRFs) into the nucleus. These transcription factors modulate the production of inflammatory cytokines, chemokines, type I interferon (IFN-I), and some interferon-stimulated genes (ISGs) [127, 128], which in turn mobilize immune cells to target pathogens and eliminate infections. Most of these mechanisms have been identified for viral or bacterial infections [129, 130]. However, the precise mechanism by which the innate immune receptors and their signaling trigger the systemic inflammation and immune cells trafficking during malaria infection has yet to be fully uncovered. Here, we review the knowledge of the role of TLR-dependent and TLRindependent pathways and the modulation of IRFs in the activation of interferons (IFN) during malaria infection.

3. Recognition of Malarial Ligand by Host Receptors

Malaria parasite travels undetected in the circulation as it is encapsulated in the red blood cells. However, rupture of the matured forms of infected red blood cells exposes the parasite and releases malarial products which trigger host immune response [131–133]. This is evident by the paroxysms of fever and chills which coincide with the time of schizonts rupture [134]. The asexual erythrocytic stage of Plasmodium life cycle begins when merozoites are released from infected hepatocytes into the circulation. These merozoites infect red blood cells for source of nutrients and possibly also as a form of sanctuary from peripheral immune cells. Invasion is initiated by the initial contact of the parasite with red blood cells. Weak interactions of some glycosylphosphatidylinositol membrane anchors (GPIs) on the surface of merozoites [135] with receptors on red blood cells [136] trigger mechanisms that further commit the parasite to invasion [137, 138]. During invasion, most GPIs are shed from coat to facilitate entry into the target cells [139, 140]. As the parasite multiples and feeds on erythrocyte hemoglobin, it detoxifies hemoglobin heme by-product into Hemozoin (Hz) which is kept in the digestive vacuole (DV) [141-143]. Eventually, this DV, together with leftover host hemoglobin, is discharged into the circulation during egress of infective merozoites at the late schizonts stage in an explosive manner [138, 144]. Throughout this process of invasion and egress, the Plasmodium parasite continually scatters malarial products which could trigger the immune system.

3

Mouse strain	Infection	Infection/pathology/protection	Ref.	
	P. berghei ANKA		[61–76]	
C57BL/6 C57BL/6I	P. berghei ANKA-luc (231c11)		[21, 77]	
C57BL/6J C57BL/6N	P. berghei ANKA-GFP		[78, 79]	
C57BL/6AnNCr 129/Ola x C57BL/6 129P2Sv/Ev	P. berghei ANKA clone 15cy1	ECM	[80, 81]	
	P. berghei ANKA-GFP clone 15cy1		[82]	
	P. berghei ANKA clone BdS		[26, 83]	
29 Sv/Ev x C57BL/6	P. berghei ANKA sporozoite		[73]	
	<i>P. berghei</i> ANKA clone 15cy1 sporozoite		[80, 84]	
	P. berghei K173	Protection from ECM	[67]	
	P. yoelii nigeriensis N67C	Lethal hyperparasitemia and severe anemia	[85]	
	P. yoelii 17XNL		[86]	
	<i>P. yoelii yoelii</i> 265 BY uncloned line	Protection from lethal hyperparasitemia and severe anemia	[87]	
	P. yoelii nigeriensis N67	severe anenna	[85]	
C57BL/6	, ,	Liver injury	[88]	
	P. berghei NK65	Malaria-associated acute respiratory distress syndrome	[76]	
	P. berghei NK65-GFP	Placental malaria	[89]	
	P. chabaudi chabaudi AS		[77, 90]	
	P. chabaudi AS	Protection in uncomplicated malaria	[76, 91]	
	P. berghei ANKA-luc sporozoite			
	<i>P. berghei</i> NK65 sporozoite	Liver-stage malaria	[92]	
	<i>P. yoelii</i> 17XNL sporozoite			
C57BL/6.C- <i>H2^d</i> /bBy	<i>P. berghei</i> ANKA-GFP sporozoite	Liver-stage malaria	[93]	
	P. berghei ANKA	ECM	[75]	
CBA/J	P. yoelii 17X	Protection from lethal hyperparasitemia and		
	P. yoelii 17XNL	severe anemia	[94]	
	P. berghei ANKA	ECM		
CBA/T6	P. berghei K173	Protection from ECM	[95]	
CBA/CaH	P. chabaudi adami 556 KA	Protection against blood-stage malaria	[96]	
		Protection from ECM		
DBA/2	P. berghei ANKA	Acute lung injury	[84]	
20.6 /F	P. berghei ANKA clone 1.4	ECM	[97]	
29 Sv/Ev	P. chabaudi chabaudi AS	Protection against blood-stage malaria	[98]	
	P. berghei ANKA	0 0	[65, 70, 74, 75, 84]	
BALB/c	<i>P. berghei</i> ANKA clone BdS	Protection from ECM	[26]	
	P. berghei ANKA-GFP		[79]	
	P. yoelii 17XL	Lethal hyperparasitemia and severe anemia	r 1	
BALB/cByJ		Protection from lethal hyperparasitemia and	[94]	
SW	P. yoelii 17XNL	severe anemia	r1	

TABLE 1: Combinations of different mouse backgrounds and parasite strains combinations allow the study of many disease profiles.

Extensive research has identified a few host receptors agonists from *Plasmodium* parasite which promote proinflammatory responses [61, 85, 99, 100, 102–106, 111, 112]. For the liver stage of the infection, *Plasmodium* RNA is the only malarial ligand discovered so far [92]. In the blood stage, several ligands have been identified, such as GPI

[62, 99–103], Hz [63, 104, 145], CpG DNA bound on Hz [105], host fibrinogen [106], heme [107, 108], microparticles [109], AT-rich motifs in malarial genome [61], *Plasmodium* DNA/RNA [85], *P. falciparum* tyrosyl-tRNA synthetase (*Pf* TyrRS) [111], and *P. falciparum* high mobility group box protein (*Pf* HMGB) [112]. All the different malarial ligands

TABLE 2: List of malarial ligands that stimulate different signaling molecules to trigger diverse immune responses and affect disease outcome in various experimental models.

Ligand	Signalling molecules involved	Cell types/mice	Immune responses/functions	Ref.
	TLR1-TLR2 heterodimer	BMDM, PBMC		[99]
GPI	TLR2/TLR1, TLR4, MyD88, ERK1/2, p38, JNK1/2, NF-κB, AP-1 (c-Jun, ATF-2)	BMDM, PBMC, HEK, MPM	Stimulates production of TNF- α , IL-12, IL-6, and NO	[62, 100, 101]
	MAPK2	BMDM	Stimulates production of TNF-α Controls production of IL-12	[102]
	ΙκΒ-ζ	BMDM	Involved in IL-12 expression	[103]
	TLR9, MyD88	Murine splenocytes, BMDDC	Stimulates production of TNF-α, IL-12p40, MCP-1, and IL-6	[104]
Hz (<i>Pf</i> 3D7)/ synthetic Hz		Knockout C57BL/6 or 129/Ola x C57BL/6	Increases serum level of MCP-1 and IL-6	[104]
synthetic riz	TLR2, TLR9, MyD88	Knockout C57BL/6	Involved in ECM development Promotes parasite and leukocyte sequestration in brain sections Stimulates production of IFN- γ , TNF- α , and IL-12p40	[63]
Malarial CpG DNA (<i>Pf</i> 3D7)	TLR9, MyD88	BMDDC	Stimulates production of IL-12p40 and Rantes	[105]
Host fibrinogen	TLR4, CD11b/CD18-integrin	РВМС	Stimulates release of ROS, TNF, and MCP-1	[106]
Heme	TLR4, CD14, MyD88, IκΒ-α, ERK1/2, NF-κΒ	MPM, BMDDC, human monocyte-derived macrophages, PBMC	Stimulates production of TNF- α and KC Controls release of PGE ₂	[107, 108]
MPs from infected mouse	TLR4, MyD88	BMDM	Upregulate expression of CD40 Stimulate production of TNF	[109]
Malarial AT-rich motif	STING, TBK1, IRF-3, IRF-7	BMDM, HEK293, knockout C57BL/6	Involved in ECM development Stimulates production of IFN-I, TNF-α, IL-6, and IL-15	[61]
Plasmodium DNA/RNA	MDA5, MAVS, RIG-1, CD14/IL-1R, p38	Knockout C57BL/6, RAW264.7	Stimulates production of IFN-I Controls parasitemia Prevents parasite sequestration in the brain capillaries and apoptosis in the spleen Promotes phagocytosis activity of macrophages	[85]
Unknown in PbA infection	TLR2/4, MyD88	Knockout C57BL/6	Involved in ECM development initiated with sporozoites Partially involved in ECM development initiated with iRBCs Regulates production of IFN- γ , MCP-1, TNF- α , and IL-10	[80]
Unknown ligand in <i>Py</i> 17XNL infection	TLR9, MyD88	Knockout C57BL/6	Controls parasitemia and promotes survival Essential Th1 development and cell-mediated immunity Stimulates production of TNF- α and IL-12 by DC Controls production of IL-10 and IL-4 by DC Induces cytotoxic activity in NK and CD8 ⁺ T cells	[86]

Ligand	Signalling molecules involved	Cell types/mice	Immune responses/functions	Ref.
Unknown	TLR7, TLR9	NK cells, $\gamma\delta$ T cells, CD4 ⁺ T cells	TLR7 mediates IFN- γ production by NK cells 24 h after infection TLR7 stimulates production of IFN-I, IFN- γ , IL-10, and IL-12 TLR9 mediates IFN- γ production by CD4 ⁺ cells and stimulates production of TNF 6 days after infection	[110]
Plasmodium RNA	MDA5, MAVS, IRF-3, IRF-7	Knockout C57BL/6J, BMDDC, MPH	Stimulates production of IFN-I Controls leukocyte recruitment which limits parasite growth in the liver and induction of erythrocytic stage infection	[92]
<i>Pf</i> TyrRs	Unknown	Mouse splenocytes, PBMC, RAW 264.7, THP-1	Stimulates production of TNF- α , IL-6, IL-1 α , and IL-1 β which upregulate expression of ICAM-1 and VCAM-1 receptors	[111]
<i>Pf</i> HMGB Unknown		Mouse splenocytes, RAW 264.7	Stimulates production of TNF- α , IL-6, IL-8, and IL-1 β and upregulates mRNA expression of iNOS	[112]

BMDM: mouse bone marrow-derived macrophages (C57BL/6 unless otherwise stated); BMDDC: mouse bone marrow-derived dendritic cells; PBMC: human peripheral blood mononuclear cells; HEK: human embryonic kidney epithelial cells; Hz: Hemozoin; iNOS: inducible nitric oxide synthetase; KC: keratinocyte chemokine; MCP-1: monocyte chemoattractant protein-1; MP: microparticles; MPH: mouse primary hepatocytes; MPM: murine peritoneal macrophages; PGE₂: prostaglandin E2; *Pf*TyrRS: *P. falciparum* tyrosyl-tRNA synthetase; *Pf*HMGB: *P. falciparum* high mobility group box protein; RAW264.7: murine macrophage-like cell line; ROS: reactive oxide species; THP-1: human monocytic leukemia cell line.

and their respective signaling molecules involved to induce an immune response are listed in Table 2. However, the exact roles of each of these factors remain to be established.

3.1. TLR-Dependent Signaling. TLRs are central in the sensing and responding to pathogens during innate immunity. Members of TLRs were originally identified in embryo of Drosophila melanogaster more than 20 years ago [146]. Later, Medzhitov et al. reported the first human homolog of the Drosophila toll protein that is involved in the activation of adaptive immunity [147]. To date, ten TLRs have been identified in human and twelve in mice [148]. In both human and mouse, TLRs 1, 2, 4, 5, and 6 are expressed on cell surface whereas TLRs 3, 7, 8, and 9 are found within the endosomal compartments. TLR10 is uniquely expressed in human [149] and localized on the surface of plasma membrane. TLRs 11, 12, and 13 are only functionally expressed in mice and expressed on the membrane of endosomes [150]. These TLRs recognize PAMPs ranging from DNA and RNA to bacterial products [151]. Subcellular localization of TLR ensures that different pathogenic antigens are promptly recognized by the correct receptor in order to induce proper immune responses and, at the same time, minimize accidental trigger of an autoimmune response. Upon ligand-receptor interactions, TLR signal transduction is initiated leading to production of interferons and induction of proinflammatory cytokines [31, 148, 151, 152].

3.1.1. TLR Polymorphism and Malaria. Studies on genetic epidemiology revealed that TLR polymorphism is associated

with outcome of malaria infection (Table 3). A population study in the Amazonian region of Brazil demonstrated that single nucleotide polymorphisms in TLR1 and TLR6 are associated with incidence of mild malaria [114]. Genetic variations in TLR1 are also capable of influencing susceptibility to placental malaria in Ghanaian mothers [113]. Case control studies demonstrated that common polymorphism in TLR2 and TLR4 can affect CM development [115, 119]. Variants in TLR2 amongst uncomplicated malaria children in Uganda were associated with altered proinflammatory responses [115] and a particular single nucleotide polymorphism in TLR4 amongst African children is correlated with an altered responsiveness to the malarial ligand, GPI, which in turn determine risk to severe malaria [119]. On the other hand, another TLR4 variant assessed in Iran (Baluchi) [116], Burundi [117], Brazil [114], and Ghana [118] was not found to be involved in malaria infection or disease severity.

Effects of TLR9 polymorphism in malaria infection have been most extensively studied amongst all the TLRs. Human genetic studies in endemic regions found a strong correlation in most of TLR9 variants with parasite load in the peripheral circulation [114, 120]. However, association of TLR9 alleles with susceptibility to malaria infection and disease severity varies according to the single nucleotide polymorphism and the regions studied [114, 116–121]. For example, TLR9 T1237C rs5743836 was associated with susceptibility to malaria infection amongst people in Burundi but not in Ghana or Iran. And amongst Ghanaians, susceptibility to mild malaria was correlated with TLR9 T1486C rs187084, but not with TLR9 G2848A rs352140.

[114, 117]

[122]

[116]

Burundi, Amazon

Vietnam, Kenya

Gambia,

Iran

TLRs/ adaptors	SNPs	Association	Region	Ref.
TLR1	S248N rs4833095	Placental malaria and anemia	Ghana	[113]
	I602S	Susceptibility to malaria infection	Amazon	[114]
TLR2	Δ22	No association with serum cytokines (TNF, IFN- γ , IL-1 β , IL-6, IL-10) levels		
		Susceptibility to cerebral malaria	Uganda	[115]
	GT_n	No association with serum cytokines (TNF, IFN- γ , IL-1 β , IL-6, IL-10) levels		
		No association with cerebral malaria		
	Dance	No association with susceptibility to malaria infection	Burundi, Amazon, Ghana, Iran	[114, 116–118]
	D299G rs4986790	No association with risk of placental malaria		
TLR4	101900790	Maternal anemia	Ghana	[118]
		Severe malaria		[119]
	T399I	No association with mild malaria	Iran	[116]
	13991	Severe malaria	Ghana	[119]
TLR6	S249P	Susceptibility to mild malaria	Amazon	[114]
		No association with susceptibility to malaria infection	Burundi	[117]
		Susceptibility to mild malaria	Ghana	[120]
	G1174A	Level of parasitemia		[120]
	rs352139	No association with serum $TNF\alpha$ level		
	T1237C rs5743836	No association with serum IFN- γ level in mild malaria children	Uganda	[121]
		Level of serum IFN- γ level in CM children		
		No association with susceptibility to malaria infection	Ghana, Iran	[116, 118, 120]
		No association with disease severity	Ghana	[119]
TIDO		No association with placental malaria		[118]
TLR9		Susceptibility to malaria infection	Burundi	[117]
		Level of parasitemia	Amazon, Ghana	[114, 120]
		No association with serum $TNF\alpha$ level		
		No association with serum IFN- γ level in mild malaria children	Uganda	[121]
	T1486C rs187084	Level of serum IFN- γ level in CM children		
		No association with susceptibility to malaria infection	Burundi, Ghana, Iran	[116–118, 120]
		No association with disease severity		[119]
		No association with placental malaria	Ghana	[118]
		No association with level of parasitemia		[120]
		Level of parasitemia	Amazon	[114]
	G2848A rs352140	No association with level of parasitemia Susceptibility to mild malaria infection	Ghana	[120]
	13332140	Susceptionity to mild mataria infection		

TABLE 3: Association of TLRs and adaptor molecules gene polymorphisms with susceptibility to malaria or pathology in human.

CM: cerebral malaria; $\Delta 22$: 22 base pair deletion in the first untranslated exon; GT_n: GT dinucleotide repeat in the second intron; mild malaria: patients suffer fever with temperature greater than or equal to 38°C, malaise, muscular pain, headache, and parasite load greater than or equal to 5000 parasite/ul of blood; severe malaria: patients who suffer anaemia, prostration, respiratory distress, convulsions, and/or impaired consciousness; cerebral malaria (CM): patients who experience coma with *P. falciparum* on blood smear and have no other cause for coma.

No association with susceptibility to malaria or severity

of infection

Mild malaria

Mild malaria and severe malaria

S180L

rs8177374

TIRAP

Besides TLR, effects of single nucleotide polymorphism of coadaptor molecule, TIR domain-containing adaptor protein, TIRAP, on malaria infection were also investigated. A particular TIRAP variant was correlated with mild malaria amongst people living in Iran [116], Gambia, Vietnam, and Kenya [122]. However, when the same TIRAP alleles were sampled in Burundi and Amazon, no association with susceptibility to malaria or disease severity was observed [114, 117]. These findings suggest that variants in TLR are capable of altering disease outcome during malaria infection but polymorphism in the strains of *Plasmodium* in different regions could also account for the different association.

3.1.2. TLR in Malaria Infection. Purified GPI from P. falciparum iRBCs [153] was preferentially recognized by TLR2/TLR1 or TLR2/TLR6 heterodimer and, to a lesser extent, TLR4 in vitro [99, 101]. TLRs-GPI interactions trigger the recruitment of MyD88, which phosphorylates a series of mitogen-activated protein kinases (MAPKs) including extracellular-signal-regulated kinases 1/2 (ERK1/2), p38 MAPK, and c-Jun N-terminal kinases 1/2 (JNK1/2) [62, 100, 101]. Following that, nuclear translocations of transcription factor such as NF- κ B and AP-1, comprising the activation of transcription factor-2/c-Jun (ATF-2/c-Jun) [100, 102], stimulate production of proinflammatory cytokines such as TNF- α , IL-6, IL-12, and nitric oxide (NO) [100, 102, 154]. Interaction of nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta (I κ B- ζ) with NF-kB, promotes IL-12 production [103]. However, the concentration of GPI on the surface of merozoites is too low to account for this potent stimulatory effect observed [155].

A study by Pichyangkul et al. described an unknown, heat labile, malarial product in the schizont-soluble fraction that is able to upregulate expression of CD86 and stimulate IFN- α production by human plasmacytoid dendritic cells. When mouse bone marrow-derived dendritic cells (BMDDC) were stimulated with the same schizont fraction, upregulated expressions of CD40, CD86, and IL-12 production were observed [156]. Later, this ligand was proposed to be a metabolic by-product, Hemozoin (Hz), that is present in P. falciparum schizont lysate [157]. It is recognized by TLR9 to induce production of proinflammatory cytokines such as TNF- α , IL-12p40, MCP-1, and IL-6 [104]. However, this discovery was refuted by Parroche et al. who suggested that Hz only serves as a vehicle to deliver the malarial DNA, a TLR9 ligand, to the endosome for TLR9 sensing [105]. Similarly, Barrera et al. also supported the claim that Hz is only a vehicle for other malarial ligands, such as host fibrinogen. In this case, instead of TLR9, TLR4 and CD11b/CD18-integrin on monocytes were shown to recognize these malarial ligands [106]. In response to these, Coban et al. have recently demonstrated that both DNase-treated natural Hz and synthetic Hz are recognized by TLR9 and able to elicit an immune response via MyD88 [145]. These highly discordant results are likely due to different methodologies adopted by each group to purify the malarial Hz. Parroche et al. and Sharma et al. purified free Hz biocrystals using a magnetic separator [61, 105], whereas both Barrera et al.

and Coban et al. utilized different protocols that largely consist of various chemical and mechanical procedures to obtain the natural Hz [104]. Despite disagreement on the ligand that stimulates the immune response, *in vitro* studies by both Parroche et al. and Coban et al. agreed upon the importance of TLR9 in *P. falciparum* infection. During *P. falciparum* infection, activation of TLR9 mediates production of IL-12 and IFN- γ . These proinflammatory cytokines in turn enhance expression of TLR and prime the signaling pathway to be more sensitive to TLR agonist [158].

Heme is released into the circulation when cell-free hemoglobin, from ruptured schizonts, is oxidized by reactive oxygen species (ROS) or other free radicals present in the plasma. The prosthetic group is recognized by TLR4, along with coreceptor CD14 [107, 108]. This interaction triggers MyD88 recruitment, $I\kappa B\alpha$ degradation, ERK1/2 phosphorylation, and eventually NF-*k*B activation. Endotoxin contamination was abolished through the use of polymyxin B, anti-TLR4/MD2, and lipid A antagonist which inhibit effect of lipopolysaccharide (LPS) [108]. A study on a population of P. vivax-infected Brazilians discovered a correlation between high concentrations of heme in the plasma with disease severity. This is mediated through the activation of antioxidant enzyme Cu/Zn superoxide dismutase (SOD-1) which impairs production of anti-inflammatory mediators, such as Prostaglandin E2 (PGE₂) and TGF- β , by PBMCs [107]. In the same study, plasma level of proinflammatory cytokine, TNF- α , was found to be positively correlated with total heme and SOD-1 [107]. Heme can be detrimental in other ways such as its toxic effects on endothelial cells [159-161] and hepatocytes [162]. At the same time, it promotes survival [163], activation [164], and migration [165] of polymorph nuclear cells. Taken together, it seems to suggest that free heme in the plasma could engage in multiple signaling pathways to promote a proinflammatory immune response, which possibly exacerbates the malaria infection.

Microparticles (MPs) are submicron vesicles produced through membrane budding during immune-activation or cell death. Extensive studies revealed that MPs are capable of influencing biological functions such as expression of adhesion molecules by endothelial cells [166] and leukocyte recruitment [167]. In addition, these minute vesicles also play a part in pathology, for instance, by inducing nitric oxide synthesis [168, 169] and delivering mRNA into other cells [170, 171]. During malaria infection, MP derived from iRBCs affects disease progression by strongly inducing bone marrow-derived macrophages (BMDM) to produce TNF [109, 172]. In vitro study revealed that MP, and not LPS contamination, engages in a TLR4-MyD88 signaling pathway to induce this immune response. Since MP could contain other parasite proteins, like GPI and Hz, in the vesicles, it was not surprising that both TLR2 and TLR9 were also found to be involved in the induction of this MP-mediated signaling pathway. In fact, synergic engagement of all these TLRs with MP and other parasite ligands stimulated a proinflammatory response stronger than that induced by iRBCs [109].

The TLR signaling pathway is also involved in the development of placental malaria [89]. Study of *P. berghei* NK65induced placental malaria in mice showed that MyD88 is essential in the production of proinflammatory cytokines such as IL-6, IFN- γ , and TNF- α . In addition, the MyD88 pathway also affects the survival rates of pups from malariainfected mothers [89]. Unfortunately, no specific TLR or malarial ligands were identified to account for the activation of this MyD88 signaling pathway.

3.1.3. TLR in ECM. Optimal production of proinflammatory cytokines can control parasite growth but overwhelming secretion of these soluble mediators can lead to immunopathologies such as cerebral malaria. Human population studies have demonstrated that single nucleotide polymorphism in TLRs can affect susceptibility to cerebral malaria [113–121]. However, no exact mechanism can be derived from such studies. Using the murine model of ECM, specific immune responses upon TLR-ligand interactions can be studied.

TLR2/TLR4, which recognizes malarial GPI, despite playing no role in the early stage of P. chabaudi infection (IFN-I secretion in this model is mediated by TLR7) [110], is important in ECM. The absence of these receptors leads to an attenuated proinflammatory response and protection from ECM lethality [63, 80]. However, different model seems to display varying degrees of reliance on this signaling pathway to induce ECM. Using wild-type (WT) and TLR2knockout (KO) or MyD88-KO in C57BL/6 background mice infected with 10⁶ fresh PbAiRBCs intraperitoneally, Coban et al. [63] showed that ECM pathogenesis totally relies on TLR2-MyD88 signaling pathway. Activation of this pathway led to sequestration of parasites and infiltration of pathogenic T cells into the brain, two important factors responsible for damaging the brain endothelial cells. On the contrary, in this model, TLR4 was shown not to be involved in ECM development. Conversely, Kordes et al. showed that WT and TLR2/4 double knockout (DKO) in C57BL/6 background mice, infected with 10⁴ fresh PbA(clone 15cy1) iRBCs intravenously, trigger a proinflammatory response that is partially dependent on TLR2/4-MyD88 signaling pathway to cause ECM [80]. Unlike blood-stage infection, intravenous inoculation of PbA (clone 15cy1) sporozoites has absolute dependence on MyD88-dependent TLR2/4 pathway to develop ECM [80]. Inconsistency in the involvement of TLR2/4 in these models could be attributed to different infection regimens or the parasite strain/clones used. In a separate study, it was revealed that heme engages with TLR4-MyD88 signaling pathway to secrete TNF- α in mouse peritoneal macrophages and BMDDC. In fact, heme can also engage in a TLR4-independent pathway to induce production of ROS, expression of heme oxygenase-1 (HO-1), and recruitment of neutrophils [108]. Besides TLR2/4, TLR9 is also shown to play a role in ECM [63]. Coban et al. demonstrated that ECM pathogenesis relied on TLR9-MyD88 signaling to induce systemic proinflammatory responses and sequestration of parasite, Hz, and leukocytes in the brain [63].

In addition, TLR9 was discovered to work in synergy with TLR7 to induce IFN-I and IFN-γ production in mice infected with many other strains of *Plasmodium*, like *P. chabaudi*, *P. berghei* NK65, *P. berghei* K173, *P. yoelii* YM (PyYM), *P.*

yoelii 17X (*Py*17X), and *P. vinckei petteri* infection [90, 110]. C57BL/6 mice infected with *Py17XNL* were shown to rely on TLR9-MyD88 signaling pathway to induce production of proinflammatory cytokine and increase commitment to Th1 and cytolytic activity by NK and T cells [86].

Despite all these findings that supported the involvement of TLR2/TLR4/TLR9 in ECM development, Lepenies et al. held a different opinion. Using triple TLR2/4/9 KO mice on C57BL/6 mice, intraperitoneally inoculated with PbA iRBCs that was maintained through alternate cyclic passage in Anopheles stephensi mosquito and BALB/c mice, they demonstrated that ECM induction is independent of TLR2/4/9 [64]. Such disparity in research findings could be due to the unique maintenance of parasite strain/clones used. Similarly, in spite of all these studies that demonstrated the importance of TLR, the study by Togbe et al. [78] casts some doubt on the importance of TLR cascade in the development of ECM. In his study, C57BL/6 mice were infected with a cloned line of PbA tagged with GFP. Results showed that deficiency in TLR did not prevent development in ECM, lungs, or liver pathology. Once again, these conflicting results emphasized the diversity of the immune response to malaria infection in different animal models [65].

3.2. TLR-Independent Signaling. In the erythrocytic stage, AT-rich motifs in the P. falciparum genome can also induce secretion of IFN-I, TNF-a, IL-6, and IL-15 via a TLRindependent pathway. This ligand engages in a distinct signaling pathway that involves cytoplasmic nucleic sensor STING, downstream kinase TBK1, and interferon regulatory factor (IRF) 3/7 [61]. Besides, PfTyrRS [111] and PfHMGB [112] are two other malarial ligands that were shown to induce proinflammatory activity. However, more studies are needed to identify the specific receptors that recognize these two ligands. Other cytoplasmic signaling molecules, such as the member of RLR family and its adaptor molecule, melanoma differentiation-associated protein 5/mitochondrial antiviral signaling protein (MDA5/MAVS), were also associated with IFN-I signaling during acute phase of nonlethal P. yoelii nigeriensis N67 (PyN N67) infection in C57BL/6 mice [85]. On the contrary, STING and MAVS were found to be redundant in early P. chabaudi infection [110] and P. yoelii liver-stage infection [126].

Host innate immune response does not only exist in the erythrocytic stage of the parasite life cycle. In fact, control of parasitic growth starts as early as in the asymptomatic liver stage [173, 174]. Liver resident cells of C57BL/6 and BALB/c mice were shown to induce IFN-I production upon infection with PbA or *Py*17XNL sporozoite, independent of TLR-MyD88 pathway [92]. The *Plasmodium* RNA was found to be identified by MDA5, which typically recognizes double stranded DNA. This triggers the assembly of MAVS, which mediates downstream production of IFN-I. Liver-stage specific IFN-I mobilizes leukocytes into the vicinity of infected hepatocytes to limit parasite load in the liver and consequently influences the induction of erythrocytic stage infection. Besides MDA5, there are other unknown malarial

ligands that signal through Mavs as evident by the differential IFN-I response in $MDA5^{-/-}$ and $MAVS^{-/-}$ mice [92].

4. Interferons

Recognition of PAMPs by PRRs triggers a cascade of downstream signaling pathways which stimulates production of IFN-I, IFN- γ , and many other proinflammatory mediators. The IFN compartment comprises 3 classes, namely, IFN-I, IFN-II, and IFN-III. IFN are renowned for their antiviral properties and share common secondary structure. Yet each class of IFN binds to distinct multichain receptor complexes. They engage in different JAK-STAT molecules, drive the expression of different interferon stimulated response elements (ISRE) and/or interferon-gamma activated sequences (GAS) elements [175], and induce various interferon stimulated genes (ISGs), which in turn regulate development, host defense, and signaling [176]. In humans and mice, the IFN-I family comprises 13 types of IFN- α and 1 IFN- β [177]. IFN-II consists of solely interferon gamma (IFN- γ), while there are 3 types of IFN-III, namely, IFN λ 1, IFN λ 2, and IFN λ 3 [175].

4.1. Type II Interferon (IFN-y). IFN-y is the only form of type II IFN. It regulates several components of the immune system such as antigen presentation [178-181], antimicrobial mechanism [182-184], leukocyte development [185], and immune cells trafficking [186, 187]. It is the most widely studied interferon in malaria infection since it is primarily involved in host defense against intracellular pathogens. Its protective role as an immune mediator emerged as early as in the liver stage [126, 188-193]. In vitro study of human recombinant IFN-y treatment on P. berghei sporozoites-infected murine hepatocytes [190] or human hepatoma cells [189] identified an inhibitory effect of IFN- γ on parasite multiplication. Further *in vivo* study validated the importance of IFN- γ in protective immunity as it inhibits intracellular development of parasite within hepatocytes following challenge with P. berghei [194], P. yoelii [191], or P. vivax sporozoites [188] in mice and chimpanzee, respectively. Recently, Miller et al. demonstrated that IFN-y secreted in primary P. yoelii sporozoite infection is the key innate mediator that controls liver-stage parasite growth in a secondary infection [126]. Above all, this inhibitory effect of IFN- γ on parasite development in liver stage extends and influences the initiation of blood stage parasite growth [126].

IFN- γ also plays a crucial protective role during bloodstage infection of various parasite strains. Administration of exogenous recombinant IFN- γ leads to control of parasite growth in *P. chabaudi adami* 556KA-infected CBA/CaH mice. After infection has been resolved, continuous IFN- γ treatment fully protected these mice from subsequent infection [96]. Lower level of parasitemia was also observed in IFN- γ treated SW mice that were infected with lethal strain of *P. yoelii*. In addition, these treated mice also exhibited better survival outcome [94]. *P. chabaudi* AS-infected mice treated with monoclonal antibody against IFN- γ had less control of parasite multiplication [195], once again suggesting that IFN- γ is essential for limiting parasite growth. Similar findings were observed in *P. chabaudi* AS-infected mice that were deficient in IFN- γ receptor. However, these mice had lower survival rates as compared to the WT controls [91]. This suggests that IFN- γ production at different period during infection could alter survival outcome. In *P. berghei* infection, IFN- γ also plays a protective role by mediating parasite clearance [196]. Population study of children in Papua New Guinea showed that high and early IFN- γ responses seem to protect from symptomatic malaria [197].

However, production of high level of IFN- γ during parasite blood stage development is associated with predisposition to severe malaria, such as CM. Studies in animal model of ECM corroborated findings from human study that IFN- γ is essential for the development of CM [66]. IFN- γ signaling in the brain regulates expression of adhesion molecules which influence parasites and leukocytes sequestration in the brain microvessels [97]. At the same time, there is also evidence that IFN- γ promotes trafficking of leukocytes, including pathogenic CD8⁺ T cells, to the brain [81, 83]. IFN- γ is essential in both protective immunity and pathogenesis of severe diseases [198]. Whether it protects or harms the host depends on when and where it is produced [67].

4.2. *Type I Interferon (IFN-\alpha/\beta)*. Unlike IFN- γ , IFN-I is only starting to gain more attention with increasing evidence that supports its role in protection [87, 199, 200]. This cytokine regulates various immune mechanisms such as MHC expression [201], antigen presentation [201], and T cell expansion [202, 203]. Furthermore, IFN-I can also modulate production of IFN- γ [204] and prime IFN- γ -mediated immune responses [205]. The earliest report which revealed its significance in malaria demonstrated that exogenous administration of unpurified mouse serum IFN was able to protect CF-1 mice from PbA sporozoite infection [206]. Although the experiment suggested a role for IFN-I, this unpurified mouse serum contains mediators other than IFN-I [207], such as IL-6, which have activity against Plasmodium liver stages [208]. Following that, a study of treatment with recombinant human IFN- α , which cross-reacts with mouse cells, did not show any effect on near matured (42 h) liver stage after a challenge with P. yoelii sporozoite [87]. However, recent analysis of liver transcriptome obtained from PbA [92] or Py [92, 126] sporozoite-infected C57BL/6 or BALB/c mice revealed an upregulation of genes expressions that are linked to IFN signaling. IFN-I was found to act during the very late phase of the liver stage and this liver specific IFN-I production partially limits parasite growth in the liver and influences initiation of erythrocytic stage infection [92]. In mice, P. yoelii and P. berghei liver stages last a minimum of 48 h and 51 h, respectively [209], and the effect of IFN-I was only apparent after 48 h but not 42 h after sporozoite infection. Interestingly, the IFN-I effect was indirect and mainly mediates the recruitment of leukocytes around liverstage parasites. IFN- γ -secreting immune cells, in particular CD1d-restricted NKT cells, are the main players responsible for the innate elimination of liver stage [126]. Leukocytemediated inhibition of liver-stage parasite further leads to a reduced development of parasitemia [92]. More importantly, this innate immune response can facilitate parasite elimination in subsequent liver-stage infection [126, 191]. In fact, early production of IFN-I prior to infection can impair parasite establishment [92].

Compared to liver-stage infection, IFN-I has a more striking role against blood stage parasites. Previous work shows that treatment of C57BL/6 mice with pure recombinant IFN- α inhibits *P. yoelii* or *P. berghei* blood stage development [87]. This effect was indirect and mediated by IFN- γ [210]. During early stage of *P. chabaudi* infection, IFN-I induced by the infection plays a pathogenic role by suppressing IFN- γ producing CD4⁺ T cells that control parasite load in C57BL/6 [77] but not in 129 Sv/Ev mice [98]. These results are not contradictory but suggest different levels of IFN-I and the duration of action is essential for proper immune response to control parasite growth.

In human, polymorphism in the receptor of IFN-I, IFNAR, has been shown to be robustly associated with progression of CM [79, 200]. It was further revealed that peripheral blood mononuclear cells from Malawian children recovering from severe malaria had higher expression of genes involved in interferon pathway [211]. In murine model, recombinant IFN- α [210] or IFN- β [68] treatment protected mice from ECM death. When PbA-infected C57BL/6J mice were administered with recombinant human IFN α , increased level of IFN- γ in treated mice was observed, which was linked to improved control of parasitemia and survival [210]. On the other hand, IFN- β treatment prevented ECM death by suppressing the expression of chemokine receptor CXCR3, the production of IFN-y, and chemokine ligand CXCL9. Consequently, decreased T cells migrate and sequester in the brain thereby preserving a better vascular integrity of blood brain barrier as compared to nontreated WT controls [68]. However, IFN-I induced endogenously during Plasmodium infection plays a pathogenic role in ECM development. Absence of IFN-I signaling, in mice deficient in IFNAR, either delayed [82] or fully protected [77, 79] the mice from ECM. Haque et al. [77] attributed this protection to a restrained parasite growth in the absence of IFN-I pathway whereas Ball et al. [79] and Palomo et al. [82] concluded that deficiency in IFN-I signaling reduced sequestration of pathogenic T cells in the brain. All these conflicting data suggest that effects of IFN-I might rely on precise level and timing of expression of systemic IFN-I.

5. Interferon Regulatory Factors

Both IFN-I and IFN- γ are essential in the immune response against malaria infection. Production of IFNs is triggered upon recognition of malaria antigen by receptors as discussed above. Although an array of receptors and downstream signaling molecules have been implicated, all signaling pathways ultimately converge to a few downstream transcription factors, such as IRFs, which regulate gene expression of IFNs. The family of IRFs comprised 9 members, namely, IRF1-9. Each IRF binds to a unique set of ISRE to stimulate transcription of diverse genes that are translated into functional proteins [212, 213]. The diverse roles of a few IRFs in malaria infection have been uncovered recently (Table 4).

5.1. Interferon Regulatory Factor 1. The first member of the IRF family identified that binds to the promoter region of IFN- β gene is IRF-1. This transcription factor is expressed in many cells types. It mediates signaling of both IFN-I and particularly IFN- γ , a strong inducer of IRF-1 expression. IRF-1 regulates antigen presentation, monocyte/macrophage differentiation, T cell development, and B cell growth [214] and promotes Th1 response [215]. In humans, the IRF-1 gene is located in chromosome 5q31-33 region and variation in 5q31-33 region was associated with variations in parasite density during P. falciparum erythrocytic infection [216]. A subsequent study in West African ethnic groups identified that polymorphisms in IRF-1 gene could lead to differential abilities to control P. falciparum infection [123]. Despite the fact that Mangano et al. discovered a correlation between IRF-1 and control of *P. falciparum* infection [123], they found no association of this transcription factor in the development of severe malaria pathology amongst African children [124]. Using mice deficient in IRF-1, Tan et al. showed that IRF-1 is essential in limiting parasite growth and survival outcome of PbA infection [125]. Further animal studies also demonstrated that IRF-1 regulates antigen presentation [214] and is indispensable in the pathogenesis of ECM. When infected with PbA, mice deficient in IRF1 were partially protected from ECM with a lesser control in parasite growth in the circulation [69]. Microarray analysis of brains from ECMsusceptible C57BL/6 mice as compared to ECM-resistant BALB/c mice revealed an increase of IRF-1 gene expression [70]. Similarly, IRF-1 gene expression was higher in brain from CBA/T6 mice infected with ECM-causing PbA parasite than with non-ECM causing *P. berghei* K173 parasite [95]. With this evidence, there is a need to further investigate the exact implication of IRF-1 in these different immune mechanisms which are essential for ECM pathogenesis [27].

Recently, Wu et al. also demonstrated that higher expression of IRF-1 gene and production of IFN-I enabled better control of parasitemia in nonlethal *P. yoelii* N67-infected mice than in lethal *P. yoelii* N67C-infected mice [85]. However, the role of IRF-1 in IFN- β signaling remains controversial as stimulation of splenocytes from IRF-1 deficient mice with malarial genome-alike AT-rich oligonucleotides did not abrogate IFN- β production [61]. This discrepancy could be due to the use of different malaria ligand to induce IFN-I production comforting previous speculation of multiple signaling pathway to produce IFN-I [217].

5.2. Interferon Regulatory Factor 3/7. Among the 9 IRFs, IRF-3 and IRF-7 are the master regulators of IFN-I. They are responsible for driving the initial transcription of IFN-I during early stage of infection. Induction of IFN-I is generated through a biphasic mechanism which warrants transcriptional efficiency and diversity of targeted genes. IRF-3 is constitutively expressed in the cytoplasm of all cells and resides as an inactive form. Upon phosphorylation, activated IRF-3 translocates into the nucleus and forms enhanceosome

Mediators of Inflammation

	Host /model	Infection	Functions	Ref.
	Human	P. falciparum	Controls parasitemia	[123]
	Tuman	1. jau param	Not involved in development of severe malaria	[124]
		Py nigeriensis N67 iRBCs	Plays a role in IFN-I signaling	[85]
IRF-1			Involved in ECM development Controls parasitemia	[69]
	Mice	PbA iRBCs	Involved in ECM development Promotes parasitemia	[125]
			Regulates production of IFN- γ and IL12p4 Controls CD8 ⁺ T cells numbers	[72]
			Plays a role in ECM development	[70, 95]
	Ex vivo	AT-rich oligonucleotides	No effect on IFN- β production by splenocytes	[61]
IRF-3	Mice	P. yoelii sporozoite	Mediates IFN-I-induced innate response during liver-stage infection	[126]
		P. chabaudi iRBCs	Mediates splenic IFN- α , but not IFN- β , transcription in red pulp macrophages	[90]
			Not involved in IFN-I production	[110]
IRF-5	Ex vivo	AT-rich oligonucleotides	Not involved in IFN- β production by splenocytes	[61]
		Py nigeriensis N67 iRBCs	Plays a role in IFN-I signaling	[85]
IRF-7	Mice	PbA iRBCs	Plays a role in ECM development	[70, 71]
110 -7		P.chabaudi iRBCs	Mediates splenic IFN-I transcription in red pulp macrophages	[90]
			Involved in IFN-I production	[110]
	Mice	PbA sporozoite	Mediate IFN-I response in liver-stage infection Control parasite load in the liver	[92]
IRF-3 and IRF-7		PbA iRBCs	Involved in ECM development	
	Ex vivo	AT-rich oligonucleotides	Mediate IFN- β production by splenocytes	[61]
		<i>Pf</i> iRBCs	Mediate IFN- β production by macrophages	
			Plays a role in ECM development	[95]
IRF-8	Mice	PbA iRBCs	Regulates production of proinflammatory cytokines Mediates IFN-I production Controls antigen processing and presentation and chemotaxis	[72]
		Py nigeriensis N67 iRBCs	Plays a role in IFN-I signaling	[85]
IRF-9	Mice	PbA iRBCs	Plays a role in ECM development	[72]

with other transcription factors, namely, NF-kB and AP-1 [218], which will lead to IFN- β transcription [219–221]. On the other hand, IRF-7 is expressed at very low levels in the cytoplasm of most cells. Positive feedback of IFN- β increases IRF-7 expression. Like IRF-3, it undergoes nuclear translocation and forms heterodimer with IRF-3 to bind with ISRE. Unlike IRF3, IRF-7 induces maximal transcription of both IFN- α and IFN- β [222]. The role of IRF-3 and IRF-7 in malaria infection remains poorly defined.

When mice deficient in either IRF-3 or IRF-7 were infected with PbA sporozoite, significant impairment in IFN-I response was observed. Consequently, these deficient mice had higher parasite load in the liver and peripheral circulation as compared to their WT counterparts. Initiation of blood-stage infection was also found to be 1-day earlier in the KO as compared to WT mice [92]. On the other hand, only mice deficient in IRF-3 displayed marked impairment in the control of parasite burden in the liver upon secondary *P. yoelii* sporozoite infection [126]. Such disparity could be attributed to the strain of parasite or the time point measured in each study. Since IRF-3 stimulates IFN- β production [219–221] and IRF-7 induces both IFN- α and IFN- β production [222], the significance of IRFs in each infection model could possibly hint on the importance of IFN- α and/or IFN- β at different window of the liverstage infection. When stimulated with infected red blood cells or AT-rich motif derived from genome of *P. falciparum*, splenocytes obtained from mice deficient in both IRF-3 and IRF-7 had attenuated IFN- β production, demonstrating a role for one or both of these factors in IFN- β production [61].

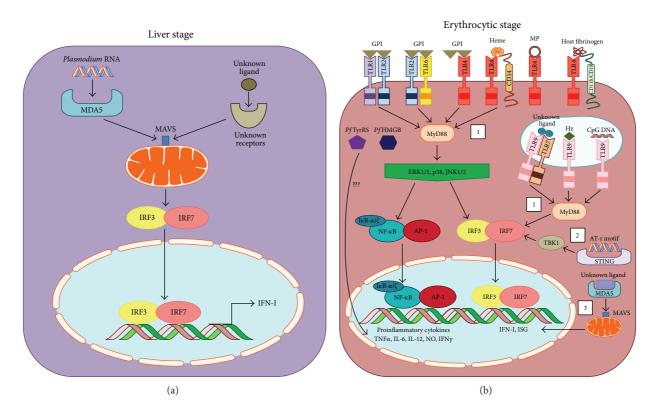


FIGURE 1: (a) Signaling pathway induced by malarial ligand during liver-stage infection. Plasmodium RNA is recognized by MDA5 (melanoma differentiation-association protein 5) present in the cytoplasm. Ligand-receptor interaction triggers assembly of MAVS (mitochondrial antiviral signaling protein) that aggregate on the surface of mitochondria. This eventually leads to the activation of both IRF-3 and IRF-7 which regulate transcription of IFN-I. Besides MDA5, activation of other receptors can also trigger aggregation of MAVS. However, this specific receptor and its corresponding malarial ligand have yet to be identified. (b) Signaling pathway induced by malarial ligand during erythrocyticstage infection. Surface TLR4 recognizes a number of malarial ligands such as GPI (glycosylphosphatidylinositol membrane anchor) and MP (microparticles). Together with CD14 or CD11b/CD18 integrin, it can recognize heme and host fibrinogen, respectively. Both TLR heterodimer TLR1/TLR2 and TLR2/TLR6 recognize GPI. Within the endosomal compartment, Hz (Hemozoin) and CpG DNA are recognized by TLR9. In addition, TLR7/TLR9 heterodimer has been proposed to recognize an unknown malarial ligand. These ligand-receptor interactions trigger 3 proposed pathways. (1) TLR-dependent pathway involves the recruitment of MyD88 (myeloid differentiation primary gene 88) to TLR, which phosphorylates downstream MAPKs (mitogen-activating protein kinases), such as ERK1/2 (extracellular-signal-regulated kinases 1/2), p38 MAPK, and JNK1/2 (c-Jun N-terminal kinases 1/2). Subsequently, NF- κ B (nuclear factor kappa-light-chain-enhancer of activated B cells) and AP-1 (activating protein-1) translocate into the nucleus and stimulate production of proinflammatory cytokines. At the same time, phosphorylated MAPKs or MyD88 can induce activation of IRF-3 and IRF-7 to transcribe IFN-I and ISGs (interferon stimulated genes). (2) Activation of TLR-independent pathway triggered by AT-rich motif present in the plasmodial genome engages STING, TBK, IRF-3, and IRF-7. (3) Another TLR-independent pathway involves MDA5 and MAVS. Pf TyrRS (P. falciparum tyrosyl-tRNA synthetase) and Pf HMGB (P. falciparum high mobility group box protein) were shown to induce proinflammatory responses but the exact signaling pathways have yet to be identified.

In mice infected with *P. chabaudi*, early IFN- α production by red pulp macrophages is dependent on both IRF-3 and IRF-7. Intriguingly, contrary to what is observed with viruses [223– 226], IFN- β production was independent of IRF-3 [90, 110], suggesting an alternate pathway of activation for malaria parasite. Microarray analysis of brain from ECM-susceptible mice showed a higher transcriptional activity of IRF-7 than ECM-resistant [70] and uninfected control mice [71]. Double IRF-3/IRF-7 deficient mice infected with PbA were resistant to ECM upon infection [61] confirming a role for IFN-I in ECM. However, the precise functions of IRF-3 and IRF-7 in CM remained to be determined.

5.3. Interferon Regulatory Factor 8. IRF-8 is one of the unique IRFs that is only expressed in immune cells [227]. Unlike

IRF-3 and IRF-7, expression of IRF-8 is induced by IFN- γ instead of IFN-I. This transcription factor coordinates growth and differentiation of myeloid cells, such as macrophages and dendritic cells, and production of proinflammatory cytokines, such as IFN-I and IL-12p40 [227]. Together with IRF-1 [228], IRF-8 directs transcription programs in immune cells towards a Th1-dominated response [229]. Since ECM is a Th1-mediated pathology [230–232], it is not surprising that amplification in IRF-8 gene expression was observed in the brains of ECM-susceptible PbA-infected CBA/T6 mice [95]. Mice with dysfunctional IRF-8 are protected from ECM due to downregulated transcriptional activity of many IRF-8-dependent genes which are essential in various aspects of the immune response during PbA infection. These modulated genes are involved in antigen processing and presentation,

chemotaxis, maturation of phagosomes, and production of proinflammatory cytokines [72]. Though both reports concurred that IRF-8 is involved in ECM development, further research is mandatory to ascertain its role in human CM.

5.4. Other Interferon Regulatory Factors. Apart from IRF-1, IRF-3, IRF-7, and IRF-8, some studies have also briefly explored the role of IRF-5 and IRF-9 in malaria infection. IRF-5 is expressed in B cells and dendritic cells. Like IRF-7, it is mainly regulated by IFN-I. This transcription factor interacts with IRF-1, IRF-3, and IRF-7 to induce expression of proinflammatory cytokines [233, 234]. The only report on IRF-5 in malaria infection revealed that it is dispensable in the production of IFN- β by splenocytes in response to stimulation by AT-rich oligonucleotides that resemble those in the malarial genome [61]. Another member, IRF-9, is expressed constitutively in many cell types and unlike the rest of the IRFs, it functions only when it dimerizes with STAT1 and STAT2 to form an active trimeric complex, known as ISGF3. This complex binds to ISRE and activates ISGs [235, 236]. During nonlethal PyNN67 infection, IRF-9 participates in the production of IFN-I to control parasite growth [85]. A robust IRF-8-dependent amplification of IRF-9 was detected in brain of mice infected with PbA [72]. These separate studies seem to hint on the possibility of more IRFs involvement in the immune response during malaria infection.

6. Future Perspectives

In Figure 1, we illustrate the different malarial ligands and the various signaling pathways triggered to produce IFN-I and proinflammatory cytokines in the liver and erythrocytic stages. Though controversial, these studies demonstrated that IFN-I [77] and IFN- γ [94] produced during infection may modulate the course of disease progression. However, the same immune response that initially protects the host could inevitably contribute to the pathogenesis of severe malaria [66, 82, 94].

Thus far, the most effective malaria treatment is administration of antimalarial drugs, Chloroquine (CQ) or Artemisinin (ART) and its derivatives, which solely targets the parasite. But the emergence of CQ/ART-resistance parasite species rendered these treatments increasingly ineffective [237, 238]. In the recent years, increased knowledge of the host immune response uncovers a potential to employ host-directed therapy in malaria infection. In fact, immunotherapy has emerged as a hot topic for both research and treatment against a diverse array of disease over the last few centuries [239–241]. Specifically, interferon therapy has been widely reported to treat cancer [242-246] and viral infections [247-249]. Recently, a synthetic innate defense regulator-1018 (IDR-1018) adjunctive treatment, in combination with antimalarial drug, demonstrated efficacy against ECM [250]. Taken together, these data offer the possibility of interferon treatment as an immunotherapy for malaria infection. Thus, dissecting the innate signaling pathways and their corresponding cytokine responses would

provide further insights into the induction of adaptive immune response and offer some directions on vaccine or drug developments.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

Authors' Contribution

Sin Yee Gun, Carla Claser, Kevin Shyong Wei Tan, and Laurent Rénia contributed equally to the paper.

Acknowledgments

This work was supported by an intramural grant from Singapore's Agency for Science, Technology and Research (A*STAR). Sin Yee Gun is supported by a postgraduate scholarship from the Yong Loo Lin School of Medicine, National University of Singapore, Singapore.

References

- WHO, "World malaria report 2013 shows major progress in fight against malaria, calls for sustained financing," Tech. Rep., 2013.
- [2] A. F. Cowman and S. H. I. Kappe, "Malaria's stealth shuttle," *Science*, vol. 313, no. 5791, pp. 1245–1246, 2006.
- [3] M. Giboda, J. Gutvirth, M. Maloveská, F. Kosina, M. Hocmanová, and V. Struncová, "Imported malaria diagnostic and clinical features," *Bratislavske Lekarske Listy*, vol. 88, no. 1, pp. 104–111, 1987.
- [4] D. J. Perkins, T. Were, G. C. Davenport, P. Kempaiah, J. B. Hittner, and J. M. Ong'echa, "Severe malarial anemia: innate immunity and pathogenesis," *International Journal of Biological Sciences*, vol. 7, no. 9, pp. 1427–1442, 2011.
- [5] W. R. J. Taylor, J. Hanson, G. D. H. Turner, N. J. White, and A. M. Dondorp, "Respiratory manifestations of malaria," *Chest*, vol. 142, no. 2, pp. 492–505, 2012.
- [6] R. Idro, N. E. Jenkins, and C. R. J. Newton, "Pathogenesis, clinical features, and neurological outcome of cerebral malaria," *The Lancet Neurology*, vol. 4, no. 12, pp. 827–840, 2005.
- [7] L. Rénia, M. S. Marussig, D. Grillot et al., "In vitro activity of CD4⁺ and CD8⁺ T lymphocytes from mice immunized with a synthetic malaria peptide," *Proceedings of the National Academy* of Sciences of the United States of America, vol. 88, no. 18, pp. 7963–7967, 1991.
- [8] L. Schofield and G. E. Grau, "Immunological processes in malaria pathogenesis," *Nature Reviews Immunology*, vol. 5, no. 9, pp. 722–735, 2005.
- [9] J. M. Horne-Debets, R. Faleiro, D. S. Karunarathne et al., "PD-1 dependent exhaustion of CD8+ T cells drives chronic malaria," *Cell Reports*, vol. 5, no. 5, pp. 1204–1213, 2013.
- [10] K. J. Ewer, G. A. O'Hara, C. J. A. Duncan et al., "Protective CD8⁺ T-cell immunity to human malaria induced by chimpanzee adenovirus-MVA immunisation," *Nature Communications*, vol. 4, article 2836, 2013.
- [11] K. Artavanis-Tsakonas and E. M. Riley, "Innate immune response to malaria: rapid induction of $IFN-\gamma$ from human NK

cells by live Plasmodium falciparum-infected erythrocytes," *The Journal of Immunology*, vol. 169, no. 6, pp. 2956–2963, 2002.

- [12] J. Santhanam, L. Råberg, and N. Jon Savill, "Immune-mediated competition in rodent Malaria is most likely caused by induced changes in innate immune clearance of merozoites," *PLoS Computional Biology*, vol. 10, no. 1, Article ID e1003416, 2014.
- [13] L. Molineaux, M. Träuble, W. E. Collins, G. M. Jeffery, and K. Dietz, "Malaria therapy reinculation data suggest individual variation of an innate immune response and independent acquisition of antiparasitic and antitoxic immunities," *Transactions of the Royal Society of Tropical Medicine and Hygiene*, vol. 96, no. 2, pp. 205–209, 2002.
- [14] I. G. Scragg, "Early cytokine induction by *Plasmodium fal-ciparum* is not a classical endotoxin-like process," *European Journal of Immunology*, vol. 29, no. 8, pp. 2636–2644, 1999.
- [15] H. Brown, G. Turner, S. Rogerson et al., "Cytokine expression in the brain in human cerebral malaria," *Journal of Infectious Diseases*, vol. 180, no. 5, pp. 1742–1746, 1999.
- [16] I. Angulo and M. Fresno, "Cytokines in the pathogenesis of and protection against malaria," *Clinical and Diagnostic Laboratory Immunology*, vol. 9, no. 6, pp. 1145–1152, 2002.
- [17] E. Tjitra, N. M. Anstey, P. Sugiarto et al., "Multidrug-resistant Plasmodium vivax associated with severe and fatal malaria: a prospective study in Papua, Indonesia," *PLoS Medicine*, vol. 5, no. 6, pp. 0890–0899, 2008.
- [18] S. Ahamada, M. Wery, and R. Hamers, "Rodent malaria parasites: molecular karyotypes characterize species, subspecies and lines," *Parasite*, vol. 1, no. 1, pp. 31–38, 1994.
- [19] S. L. Perkins, I. N. Sarkar, and R. Carter, "The phylogeny of rodent malaria parasites: simultaneous analysis across three genomes," *Infection, Genetics and Evolution*, vol. 7, no. 1, pp. 74– 83, 2007.
- [20] F. H. Amante, A. Haque, A. C. Stanley et al., "Immunemediated mechanisms of parasite tissue sequestration during experimental cerebral malaria," *Journal of Immunology*, vol. 185, no. 6, pp. 3632–3642, 2010.
- [21] C. Claser, B. Malleret, S. Y. Gun et al., "Cd8⁺ T cells and IFN- γ mediate the time-dependent accumulation of infected red blood cells in deep organs during experimental cerebral malaria," *PLoS ONE*, vol. 6, no. 4, Article ID e18720, 2011.
- [22] J. A. McQuillan, A. J. Mitchell, Y. F. Ho et al., "Coincident parasite and CD8 T cell sequestration is required for development of experimental cerebral malaria," *International Journal for Parasitology*, vol. 41, no. 2, pp. 155–163, 2011.
- [23] F. El-Assaad, J. Whewaya, A. J. Mitchell, and et al, "Cytoadherence of *Plasmodium* berghei-infected red blood cells to murine brain and lung microvascular endothelial cells *in vitro*," *Infection and Immunity*, vol. 81, no. 11, pp. 3984–91, 2013.
- [24] C. R. J. C. Newton, T. T. Hien, and N. White, "Cerebral malaria," *Journal of Neurology Neurosurgery & Psychiatry*, vol. 69, no. 4, pp. 433–441, 2000.
- [25] S. C. Wassmer, V. Combes, and G. E. Grau, "Pathophysiology of cerebral malaria: Role of host cells in the modulation of cytoadhesion," *Annals of the New York Academy of Sciences*, vol. 992, pp. 30–38, 2003.
- [26] E. Belnoue, M. Kayibanda, A. M. Vigario et al., "On the pathogenic role of brain-sequestered alphabeta CD8+ T cells in experimental cerebral malaria," *Journal of Immunology*, vol. 169, no. 11, pp. 6369–6375, 2002.
- [27] S. W. Howland, C. M. Poh, S. Y. Gun et al., "Brain microvessel cross-presentation is a hallmark of experimental cerebral

malaria," *EMBO Molecular Medicine*, vol. 5, no. 7, pp. 984–999, 2013.

- [28] R. Medzhitov and J. Janeway C., "Advances in immunology: innate immunity," *The New England Journal of Medicine*, vol. 343, no. 5, pp. 338–344, 2000.
- [29] R. Medzhitov and C. Janeway Jr., "Innate immune recognition: Mechanisms and pathways," *Immunological Reviews*, vol. 173, pp. 89–97, 2000.
- [30] S. Akira, S. Uematsu, and O. Takeuchi, "Pathogen recognition and innate immunity," *Cell*, vol. 124, no. 4, pp. 783–801, 2006.
- [31] T. Vasselon and P. A. Detmers, "Toll receptors: a central element in innate immune responses," *Infection and Immunity*, vol. 70, no. 3, pp. 1033–1041, 2002.
- [32] T. Kawai and S. Akira, "Toll-like receptor and RIG-1-like receptor signaling," *Annals of the New York Academy of Sciences*, vol. 1143, pp. 1–20, 2008.
- [33] S. Chtarbanova and J. Imler, "Microbial sensing by toll receptors: a historical perspective," *Arteriosclerosis, Thrombosis, and Vascular Biology*, vol. 31, no. 8, pp. 1734–1738, 2011.
- [34] A. Cambi and C. G. Figdor, "Dual function of C-type lectinlike receptors in the immune system," *Current Opinion in Cell Biology*, vol. 15, no. 5, pp. 539–546, 2003.
- [35] E. Pyz, A. S. J. Marshall, S. Gordon, and G. D. Brown, "C-type lectin-like receptors on myeloid cells," *Annals of Medicine*, vol. 38, no. 4, pp. 242–251, 2006.
- [36] T. B. H. Geijtenbeek and S. I. Gringhuis, "Signalling through C-type lectin receptors: shaping immune responses," *Nature Reviews Immunology*, vol. 9, no. 7, pp. 465–479, 2009.
- [37] T.-D. Kanneganti, M. Lamkanfi, and G. Núñez, "Intracellular NOD-like receptors in host defense and disease," *Immunity*, vol. 27, no. 4, pp. 549–559, 2007.
- [38] M. Proell, S. J. Riedl, J. H. Fritz, A. M. Rojas, and R. Schwarzenbacher, "The Nod-Like Receptor (NLR) family: a tale of similarities and differences," *PLoS ONE*, vol. 3, no. 4, Article ID e2119, 2008.
- [39] K. Geddes, J. G. Magalhães, and S. E. Girardin, "Unleashing the therapeutic potential of NOD-like receptors," *Nature Reviews Drug Discovery*, vol. 8, no. 6, pp. 465–479, 2009.
- [40] Y. M. Loo and M. Gale Jr., "Immune Signaling by RIG-I-like Receptors," *Immunity*, vol. 34, no. 5, pp. 680–692, 2011.
- [41] M. Muzio, D. Bosisio, N. Polentarutti et al., "Differential expression and regulation of toll-like receptors (TLR) in human leukocytes: selective expression of TLR3 in dendritic cells," *Journal of Immunology*, vol. 164, no. 11, pp. 5998–6004, 2000.
- [42] V. Hornung, S. Rothenfusser, S. Britsch et al., "Quantitative expression of toll-like receptor 1-10 mRNA in cellular subsets of human peripheral blood mononuclear cells and sensitivity to CpG oligodeoxynucleotides," *Journal of Immunology*, vol. 168, no. 9, pp. 4531–4537, 2002.
- [43] D. Jarrossay, G. Napolitani, M. Colonna, F. Sallusto, and A. Lanzavecchia, "Specialization and complementarity in microbial molecule recognition by human myeloid and plasmacytoid dendritic cells," *European Journal of Immunology*, vol. 31, no. 11, pp. 3388–3393, 2001.
- [44] T. Ito, R. Amakawa, T. Kaisho et al., "Interferon- α and interleukin-12 are induced differentially by toll-like receptor 7 ligands in human blood dendritic cell subsets," *Journal of Experimental Medicine*, vol. 195, no. 11, pp. 1507–1512, 2002.
- [45] T. B. H. Geijtenbeek, R. Torensma, S. J. Van Vliet et al., "Identification of DC-SIGN, a novel dendritic cell-specific ICAM-3 receptor that supports primary immune responses," *Cell*, vol. 100, no. 5, pp. 575–585, 2000.

- [46] L. F. Poulin, Y. Reyal, H. Uronen-Hansson et al., "DNGR-1 is a specific and universal marker of mouse and human Batf3-dependent dendritic cells in lymphoid and nonlymphoid tissues," *Blood*, vol. 119, no. 25, pp. 6052–6062, 2012.
- [47] H. H. Smits, A. Engering, D. Van Der Kleij et al., "Selective probiotic bacteria induce IL-10-producing regulatory T cells in vitro by modulating dendritic cell function through dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin," *Journal of Allergy and Clinical Immunology*, vol. 115, no. 6, pp. 1260–1267, 2005.
- [48] T. B. Geijtenbeek, S. J. van Vliet, E. A. Koppel et al., "Mycobacteria target DC-SIGN to suppress dendritic cell function," *Journal* of Experimental Medicine, vol. 197, no. 1, pp. 7–17, 2003.
- [49] M. P. Bergman, A. Engering, H. H. Smits et al., "Helicobacter pylori modulates the T helper cell 1/T helper cell 2 balance through phase-variable interaction between lipopolysaccharide and DC-SIGN," *Journal of Experimental Medicine*, vol. 200, no. 8, pp. 979–990, 2004.
- [50] J. Li, Z. Ma, Z. Tang, T. Stevens, B. Pitt, and S. Li, "CpG DNA-mediated immune response in pulmonary endothelial cells," *The American Journal of Physiology—Lung Cellular and Molecular Physiology*, vol. 287, no. 3, pp. L552–L558, 2004.
- [51] L. Guillott, S. Medjane, K. Le-Barillec et al., "Response of human pulmonary epithelial cells to lipopolysaccharide involves tolllike receptor 4 (TLR4)-dependent signaling pathways: Evidence for an intracellular compartmentalization of TLR4," *The Journal* of *Biological Chemistry*, vol. 279, no. 4, pp. 2712–2718, 2004.
- [52] D. Droemann, T. Goldmann, D. Branscheid et al., "Toll-like receptor 2 is expressed by alveolar epithelial cells type II and macrophages in the human lung," *Histochemistry and Cell Biology*, vol. 119, no. 2, pp. 103–108, 2003.
- [53] S. Claeys, T. de Belder, G. Holtappels et al., "Human β-defensins and toll-like receptors in the upper airway," *Allergy*, vol. 58, no. 8, pp. 748–753, 2003.
- [54] C. Maaser, J. Heidemann, C. Von Eiff et al., "Human intestinal microvascular endothelial cells express Toll-like receptor 5: a binding partner for bacterial flagellin," *Journal of Immunology*, vol. 172, no. 8, pp. 5056–5062, 2004.
- [55] E. Cario and D. K. Podolsky, "Differential alteration in intestinal epithelial cell expression of Toll-like receptor 3 (TLR3) and TLR4 in inflammatory bowel disease," *Infection and Immunity*, vol. 68, no. 12, pp. 7010–7017, 2000.
- [56] A. T. Gewirtz, T. A. Navas, S. Lyons, P. J. Godowski, and J. L. Madara, "Cutting edge: bacterial flagellin activates basolaterally expressed TLR5 to induce epithelial proinflammatory gene expression," *Journal of Immunology*, vol. 167, no. 4, pp. 1882– 1885, 2001.
- [57] S. Frantz, L. Kobzik, Y. Kim et al., "Toll4 (TLR4) expression in cardiac myocytes in normal and failing myocardium," *Journal* of *Clinical Investigation*, vol. 104, no. 3, pp. 271–280, 1999.
- [58] Y. Bulut, E. Faure, L. Thomas et al., "Chlamydial heat shock protein 60 activates macrophages and endothelial cells through toll-like receptor 4 and MD2 in a MyD88-dependent pathway," *The Journal of Immunology*, vol. 168, no. 3, pp. 1435–1440, 2002.
- [59] T. Imaizumi, S. Aratani, T. Nakajima et al., "Retinoic acidinducible gene-I is induced in endothelial cells by LPS and regulates expression of COX-2," *Biochemical and Biophysical Research Communications*, vol. 292, no. 1, pp. 274–279, 2002.
- [60] B. Opitz, S. Förster, A. C. Hocke et al., "Nod1-mediated endothelial cell activation by Chlamydophila pneumoniae," *Circulation Research*, vol. 96, no. 3, pp. 319–326, 2005.

- [61] S. Sharma, R. B. DeOliveira, P. Kalantari et al., "Innate immune recognition of an AT-rich stem-loop DNA motif in the Plasmodium falciparum genome," *Immunity*, vol. 35, no. 2, pp. 194– 207, 2011.
- [62] Z. Lu, L. Serghides, S. N. Patel et al., "Disruption of JNK2 decreases the cytokine response to *Plasmodium falciparum* glycosylphosphatidylinositol in vitro and confers protection in a cerebral malaria model," *Journal of Immunology*, vol. 177, no. 9, pp. 6344–6352, 2006.
- [63] C. Coban, S. Uematsu, N. Arisue et al., "Pathological role of Toll-like receptor signaling in cerebral malaria," *International Immunology*, vol. 19, no. 1, pp. 67–79, 2007.
- [64] B. Lepenies, J. P. Cramer, G. D. Burchard, H. Wagner, C. J. Kirschning, and T. Jacobs, "Induction of experimental cerebral malaria is independent of TLR2/4/9," *Medical Microbiology and Immunology*, vol. 197, no. 1, pp. 39–44, 2008.
- [65] J. W. Griffith, C. O'Connor, K. Bernard, T. Town, D. R. Goldstein, and R. Bucala, "Toll-like receptor modulation of murine cerebral malaria is dependent on the genetic background of the host," *Journal of Infectious Diseases*, vol. 196, no. 10, pp. 1553– 1564, 2007.
- [66] W. Rudin, N. Favre, G. Bordmann, and B. Ryffel, "Interferon-γ is essential for the development of cerebral malaria," *European Journal of Immunology*, vol. 27, no. 4, pp. 810–815, 1997.
- [67] A. J. Mitchell, A. M. Hansen, L. Hee et al., "Early cytokine production is associated with protection from murine cerebral malaria," *Infection and Immunity*, vol. 73, no. 9, pp. 5645–5653, 2005.
- [68] C. N. Morrell, K. Srivastava, A. Swaim et al., "Beta interferon suppresses the development of experimental cerebral malaria," *Infection and Immunity*, vol. 79, no. 4, pp. 1750–1758, 2011.
- [69] G. Senaldi, C. L. Shaklee, J. Guo et al., "Protection against the mortality associated with disease models mediated by TNF and IFN-γ in mice lacking IFN regulatory factor-1," *Journal of Immunology*, vol. 163, no. 12, pp. 6820–6826, 1999.
- [70] F. E. Lovegrove, S. A. Gharib, S. N. Patel, C. A. Hawkes, K. C. Kain, and W. C. Liles, "Expression microarray analysis implicates apoptosis and interferon-responsive mechanisms in susceptibility to experimental cerebral malaria," *The American Journal of Pathology*, vol. 171, no. 6, pp. 1894–1903, 2007.
- [71] A. C. Sexton, R. T. Good, D. S. Hansen et al., "Transcriptional profiling reveals suppressed erythropoiesis, up-regulated glycolysis, and interferon-associated responses in murine malaria," *Journal of Infectious Diseases*, vol. 189, no. 7, pp. 1245–1256, 2004.
- [72] J. Berghout, D. Langlais, and P. Gros, "Irf8-regulated genomic responses drive pathological inflammation during cerebral Malaria," *PLoS Pathogens*, vol. 9, no. 7, p. 11, 2013.
- [73] J. C. R. Hafalla, J. Burgold, A. Dorhoi et al., "Experimental cerebral malaria develops independently of caspase recruitment domain-containing protein 9 signaling," *Infection and Immunity*, vol. 80, no. 3, pp. 1274–1279, 2012.
- [74] F. E. Lovegrove, L. Peña-Castillo, N. Mohammad, W. C. Liles, T. R. Hughes, and K. C. Kain, "Simultaneous host and parasite expression profiling identifies tissue-specific transcriptional programs associated with susceptibility or resistance to experimental cerebral malaria," *BMC Genomics*, vol. 7, article 295, 2006.
- [75] N. F. Delahaye, N. Coltel, D. Puthier et al., "Gene expression analysis reveals early changes in several molecular pathways in cerebral malaria-susceptible mice versus cerebral malariaresistant mice," *BMC Genomics*, vol. 8, article 452, 2007.

- [76] P. E. van den Steen, N. Geurts, K. Deroost et al., "Immunopathology and dexamethasone therapy in a new model for malaria-associated acute respiratory distress syndrome," *American Journal of Respiratory and Critical Care Medicine*, vol. 181, no. 9, pp. 957–968, 2010.
- [77] A. Haque, S. E. Best, A. Ammerdorffer et al., "Type I interferons suppress CD4 + T-cell-dependent parasite control during blood-stage Plasmodium infection," *European Journal of Immunology*, vol. 41, no. 9, pp. 2688–2698, 2011.
- [78] D. Togbe, L. Schofield, G. E. Grau et al., "Murine cerebral malaria development is independent of toll-like receptor signaling," *The American Journal of Pathology*, vol. 170, no. 5, pp. 1640–1648, 2007.
- [79] E. A. Ball, M. R. Sambo, M. Martins et al., "IFNAR1 controls progression to cerebral malaria in children and CD8 + T cell brain pathology in plasmodium berghei-infected mice," *Journal* of *Immunology*, vol. 190, no. 10, pp. 5118–5127, 2013.
- [80] M. Kordes, K. Matuschewski, and J. C. R. Hafalla, "Caspase-1 activation of interleukin-1ß (IL-1ß) and IL-18 Is dispensable for induction of experimental cerebral malaria," *Infection and Immunity*, vol. 79, no. 9, pp. 3633–3641, 2011.
- [81] A. Villegas-Mendez, R. Greig, T. N. Shaw et al., "IFN-γproducing CD4⁺ T cells promote experimental cerebral malaria by modulating CD8⁺ T cell accumulation within the brain," *The Journal of Immunology*, vol. 189, no. 2, pp. 968–979, 2012.
- [82] J. Palomo, M. Fauconnier, L. Coquard et al., "Type I interferons contribute to experimental cerebral malaria development in response to sporozoite or blood-stage *Plasmodium berghei* ANKA," *European Journal of Immunology*, vol. 43, no. 10, pp. 2683–2695, 2013.
- [83] E. Belnoue, S. M. Potter, D. S. Rosa et al., "Control of pathogenic CD8⁺ T cell migration to the brain by IFN-γ during experimental cerebral malaria," *Parasite Immunology*, vol. 30, no. 10, pp. 544–553, 2008.
- [84] S. Epiphanio, M. G. Campos, A. Pamplona et al., "VEGF promotes malaria-associated acute lung injury in mice," *PLoS Pathogens*, vol. 6, no. 5, Article ID e1000916, 2010.
- [85] J. Wu, L. Tian, X. Yu et al., "Strain-specific innate immune signaling pathways determine malaria parasitemia dynamics and host mortality," *Proceedings of the National Academy of Sciences*, vol. 111, no. 4, pp. E511–E520, 2014.
- [86] N. M. Gowda, X. Wu, and D. C. Gowda, "TLR9 and MyD88 are crucial for the development of protective immunity to malaria," *The Journal of Immunology*, vol. 188, no. 10, pp. 5073–5085, 2012.
- [87] A. M. Vigário, E. Belnoue, A. Cumano et al., "Inhibition of Plasmodium yoelii blood-stage malaria by interferon α through the inhibition of the production of its target cell, the reticulocyte," *Blood*, vol. 97, no. 12, pp. 3966–3971, 2001.
- [88] K. Adachi, H. Tsutsui, S. I. Kashiwamura et al., "Plasmodium berghei infection in mice induces liver injury by an IL-12- and toll-like receptor/myeloid differentiation factor 88-dependent mechanism," *Journal of Immunology*, vol. 167, no. 10, pp. 5928– 5934, 2001.
- [89] R. Barboza, A. S. Reis, L. G. da Silva et al., "MyD88 signaling is directly involved in the development of murine placental malaria," *Infection and Immunity*, 2013.
- [90] C. C. Kim, C. S. Nelson, E. B. Wilson, B. Hou, A. L. DeFranco, and J. L. DeRisi, "Splenic red pulp macrophages produce type I interferons as early sentinels of malaria infection but are dispensable for control," *PLoS ONE*, vol. 7, no. 10, Article ID e48126, 2012.

- [91] Z. Su and M. M. Stevenson, "Central role of endogenous gamma interferon in protective immunity against blood-stage Plasmodium chabaudi AS infection," *Infection and Immunity*, vol. 68, no. 8, pp. 4399–4406, 2000.
- [92] P. Liehl, V. Zuzarte-Luís, J. Chan et al., "Host-cell sensors for Plasmodium activate innate immunity against liver-stage infection," *Nature Medicine*, vol. 20, no. 1, pp. 47–53, 2014.
- [93] L. A. Gonçalves, L. Rodrigues-Duarte, J. Rodo, L. Vieira de Moraes, I. Marques, and C. Penha-Gonçalves, "TREM2 governs Kupffer cell activation and explains belr1 genetic resistance to malaria liver stage infection," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 110, pp. 19531–19536, 2013.
- [94] H. L. Shear, R. Srinivasan, T. Nolan, and C. Ng, "Role of IFN-γ in lethal and nonlethal malaria in susceptible and resistant murine hosts," *Journal of Immunology*, vol. 143, no. 6, pp. 2038–2044, 1989.
- [95] J. Miu, N. H. Hunt, and H. J. Ball, "Predominance of interferonrelated responses in the brain during murine malaria, as identified by microarray analysis," *Infection and Immunity*, vol. 76, no. 5, pp. 1812–1824, 2008.
- [96] I. A. Clark, N. H. Hunt, G. A. Butcher, and W. B. Cowden, "Inhibition of murine malaria (Plasmodium chabaudi) in vivo by recombinant interferon-γ or tumor necrosis factor, and its enhancement by butylated hydroxyanisole," *The Journal of Immunology*, vol. 139, no. 10, pp. 3493–3496, 1987.
- [97] V. Amani, A. M. Vigário, E. Belnoue et al., "Involvement of IFN-γ receptor-mediated signaling in pathology and antimalarial immunity induced by Plasmodium berghei infection," *European Journal of Immunology*, vol. 30, no. 6, pp. 1646–1655, 2000.
- [98] C. Voisine, B. Mastelic, A. Sponaas, and J. Langhorne, "Classical CD11c⁺ dendritic cells, not plasmacytoid dendritic cells, induce T cell responses to *Plasmodium chabaudi* malaria," *International Journal for Parasitology*, vol. 40, no. 6, pp. 711–719, 2010.
- [99] J. Zhu, G. Krishnegowda, G. Li, and D. Channe Gowda, "Proinflammatory responses by glycosylphosphatidylinositols (GPIs) of Plasmodium falciparum are mainly mediated through the recognition of TLR2/TLR1," *Experimental Parasitology*, vol. 128, no. 3, pp. 205–211, 2011.
- [100] J. Zhu, G. Krishnegowda, and D. C. Gowda, "Induction of proinflammatory responses in macrophages by the glycosylphosphatidylinositols of Plasmodium falciparum: The requirement of extracellular signal-regulated kinase, p38, c-Jun N-terminal kinase and NF-κB pathways for the expression of proinflammatory cytokines and nitric oxide," *Journal of Biological Chemistry*, vol. 280, no. 9, pp. 8617–8627, 2005.
- [101] G. Krishnegowda, A. M. Hajjar, J. Zhu et al., "Induction of proinflammatory responses in macrophages by the glycosylphosphatidylinositols of Plasmodium falciparum: cell signaling receptors, glycosylphosphatidylinositol (GPI) structural requirement, and regulation of GPI activity," *Journal of Biological Chemistry*, vol. 280, no. 9, pp. 8606–8616, 2005.
- [102] J. Zhu, X. Wu, S. Goel et al., "MAPK-activated protein kinase 2 differentially regulates plasmodium falciparum glycosylphosphatidylinositol-induced production of tumor necrosis Factor- α and interleukin-12 in macrophages," *The Journal of Biological Chemistry*, vol. 284, no. 23, pp. 15756– 15761, 2009.

- [103] J. Zhu, R. Weinberg, X. Wu, N. M. Gowda, T. Muta, and D. C. Gowda, "Ikappab-zeta plays an important role in the ERK-dependent dysregulation of malaria parasite GPI-induced IL-12 expression," *IUBMB Life*, vol. 64, no. 2, pp. 187–193, 2012.
- [104] C. Coban, K. J. Ishii, T. Kawai et al., "Toll-like receptor 9 mediates innate immune activation by the malaria pigment hemozoin," *The Journal of Experimental Medicine*, vol. 201, no. 1, pp. 19–25, 2005.
- [105] P. Parroche, F. N. Lauw, N. Goutagny et al., "Malaria hemozoin is immunologically inert but radically enhances innate responses by presenting malaria DNA to Toll-like receptor 9," *Proceedings* of the National Academy of Sciences of the United States of America, vol. 104, no. 6, pp. 1919–1924, 2007.
- [106] V. Barrera, O. A. Skorokhod, D. Baci, G. Gremo, P. Arese, and E. Schwarzer, "Host fibrinogen stably bound to hemozoin rapidly activates monocytes via TLR-4 and CD11b/CD18-integrin: A new paradigm of hemozoin action," *Blood*, vol. 117, no. 21, pp. 5674–5682, 2011.
- [107] B. B. Andrade, T. Araújo-Santos, N. F. Luz et al., "Heme impairs prostaglandin E2 and TGF- β production by human mononuclear cells via Cu/Zn superoxide dismutase: insight into the pathogenesis of severe malaria," *The Journal of Immunology*, vol. 185, no. 2, pp. 1196–1204, 2010.
- [108] R. T. Figueiredo, P. L. Fernandez, D. S. Mourao-Sa et al., "Characterization of heme as activator of toll-like receptor 4," *The Journal of Biological Chemistry*, vol. 282, no. 28, pp. 20221– 20229, 2007.
- [109] K. N. Couper, T. Barnes, J. C. R. Hafalla et al., "Parasite-derived plasma microparticles contribute significantly to malaria infection-induced inflammation through potent macrophage stimulation," *PLoS Pathogens*, vol. 6, no. 1, Article ID e1000744, 2010.
- [110] A. Baccarella, M. F. Fontana, E. Chen, and C. C. Kim, "Toll-like receptor 7 mediates early innate immune responses to malaria," *Infection and Immunity*, vol. 81, no. 12, pp. 4431–4442, 2013.
- [111] T. K. Bhatt, A. Sharma, S. Khan et al., "Malaria parasite tyrosyl-tRNA synthetase secretion triggers pro-inflammatory responses," *Nature Communications*, vol. 2, no. 1, article 530, 2011.
- [112] K. Kumar, A. Singal, M. M. A. Rizvi, and V. S. Chauhan, "High mobility group box (HMGB) proteins of Plasmodium falciparum: DNA binding proteins with pro-inflammatory activity," *Parasitology International*, vol. 57, no. 2, pp. 150–157, 2008.
- [113] L. Hamann, G. Bedu-Addo, T. A. Eggelte, R. R. Schumann, and F. P. Mockenhaupt, "The toll-like receptor 1 variant S248N influences placental malaria," *Infection, Genetics and Evolution*, vol. 10, no. 6, pp. 785–789, 2010.
- [114] F. M. S. Leoratti, L. Farias, F. P. Alves et al., "Variants in the toll-like receptor signaling pathway and clinical outcomes of malaria," *The Journal of Infectious Diseases*, vol. 198, no. 5, pp. 772–780, 2008.
- [115] J. A. Greene, N. Sam-Agudu, C. C. John, R. O. Opoka, P. A. Zimmerman, and J. W. Kazura, "Toll-like receptor polymorphisms and cerebral malaria: TLR2 Δ22 polymorphism is associated with protection from cerebral malaria in a case control study," *Malaria Journal*, vol. 11, no. 47, pp. 1475–2875, 2012.
- [116] S. Zakeri, S. Pirahmadi, A. A. Mehrizi, and N. D. Djadid, "Genetic variation of *TLR-4*, *TLR-9* and *TIRAP* genes in Iranian malaria patients," *Malaria Journal*, vol. 10, article 77, 2011.
- [117] S. Esposito, C. G. Molteni, A. Zampiero et al., "Role of polymorphisms of toll-like receptor (TLR) 4, TLR9, toll-interleukin

1 receptor domain containing adaptor protein (TIRAP) and FCGR2A genes in malaria susceptibility and severity in Burundian children," *Malaria Journal*, vol. 11, article 196, 2012.

- [118] F. P. Mockenhaupt, L. Hamann, C. Von Gaertner et al., "Common polymorphisms of toll-like receptors 4 and 9 are associated with the clinical manifestation of malaria during pregnancy," *Journal of Infectious Diseases*, vol. 194, no. 2, pp. 184–188, 2006.
- [119] F. P. Mockenhaupt, J. P. Cramer, L. Hamann et al., "Toll-like receptor (TLR) polymorphisms in African children: common TLR-4 variants predispose to severe malaria," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 103, no. 1, pp. 177–182, 2006.
- [120] A. H. Omar, M. Yasunami, A. Yamazaki et al., "Toll-like receptor 9 (TLR9) polymorphism associated with symptomatic malaria: a cohort study," *Malaria Journal*, vol. 11, article 168, pp. 1475– 2875, 2012.
- [121] N. A. Sam-Agudu, J. A. Greene, R. O. Opoka et al., "TLR9 polymorphisms are associated with altered IFN-ylevels in children with cerebral malaria," *The American Journal of Tropical Medicine and Hygiene*, vol. 82, no. 4, pp. 548–555, 2010.
- [122] C. C. Khor, S. J. Chapman, F. O. Vannberg et al., "A Mal functional variant is associated with protection against invasive pneumococcal disease, bacteremia, malaria and tuberculosis," *Nature Genetics*, vol. 39, no. 4, pp. 523–528, 2007.
- [123] V. D. Mangano, G. Luoni, K. A. Rockett et al., "Interferon regulatory factor-1 polymorphisms are associated with the control of *Plasmodium falciparum* infection," *Genes & Immunity*, vol. 9, no. 2, pp. 122–129, 2008.
- [124] V. D. Mangano, T. G. Clark, S. Auburn et al., "Lack of association of *interferon regulatory factor 1* with severe malaria in affected child-parental trio studies across three African populations," *PLoS ONE*, vol. 4, no. 1, Article ID e4206, 2009.
- [125] R. S. Tan, C. Feng, Y. Asano, and A. U. Kara, "Altered immune response of interferon regulatory factor 1-deficient mice against Plasmodium berghei blood-stage malaria infection," *Infection and Immunity*, vol. 67, no. 5, pp. 2277–2283, 1999.
- [126] J. L. Miller, B. K. Sack, M. Baldwin, A. M. Vaughan, and S. H. Kappe, "Interferon-mediated innate immune responses against malaria parasite liver stages," *Cell Reports*, vol. 7, no. 2, pp. 436– 447, 2014.
- [127] N. J. Gay and M. Gangloff, "Structure and function of toll receptors and their ligands," *Annual Review of Biochemistry*, vol. 76, pp. 141–145, 2007.
- [128] O. Takeuchi and S. Akira, "Pattern recognition receptors and inflammation," *Cell*, vol. 140, no. 6, pp. 805–820, 2010.
- [129] E. M. Pietras, S. K. Saha, and G. Cheng, "The interferon response to bacterial and viral infections," *Journal of Endotoxin Research*, vol. 12, no. 4, pp. 246–250, 2006.
- [130] A. K. Perry, G. Chen, D. Zheng, H. Tang, and G. Cheng, "The host type I interferon response to viral and bacterial infections," *Cell Research*, vol. 15, no. 6, pp. 407–422, 2005.
- [131] J. Currier, H. Beck, B. Currie, and M. F. Good, "Antigens released at schizont burst stimulate Plasmodium falciparumspecific CD4+ T cells from non-exposed donors: Potential for cross-reactive memory T cells to cause disease," *International Immunology*, vol. 7, no. 5, pp. 821–833, 1995.
- [132] K. P. O'Dea and G. Pasvol, "Optimal tumor necrosis factor induction by Plasmodium falciparum requires the highly localized release of parasite products," *Infection and Immunity*, vol. 71, no. 6, pp. 3155–3164, 2003.

- [133] D. Kwiatkowski, J. G. Cannon, K. R. Manogue, A. Cerami, C. A. Dinarello, and B. M. Greenwood, "Tumour necrosis factor production in Falciparum malaria and its association with schizont rupture," *Clinical and Experimental Immunology*, vol. 77, no. 3, pp. 361–366, 1989.
- [134] S. F. Kitchen, "Symptomology: general considerations," in Malariology: A Comprehensive Survey of all Aspects of this Group of Diseases from a Global Standpoint, Saunders, Philadelphia, Pa, USA, 1949.
- [135] P. Gerold, L. Schofield, M. J. Blackman, A. A. Holder, and R. T. Schwarz, "Structural analysis of the glycosylphosphatidylinositol membrane anchor of the merozoite surface proteins-1 and -2 of *Plasmodium falciparum*," *Molecular and Biochemical Parasitology*, vol. 75, no. 2, pp. 131–143, 1996.
- [136] V. K. Goel, X. Li, H. Chen, S. C. Liu, A. H. Chishti, and S. S. Oh, "Band 3 is a host receptor binding merozoite surface protein 1 during the *Plasmodium falciparum* invasion of erythrocytes," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 100, no. 9, pp. 5164–5169, 2003.
- [137] D. T. Riglar, D. Richard, D. W. Wilson et al., "Super-resolution dissection of coordinated events during malaria parasite invasion of the human erythrocyte," *Cell Host and Microbe*, vol. 9, no. 1, pp. 9–20, 2011.
- [138] J. A. Dvorak, L. H. Miller, W. C. Whitehouse, and T. Shiroishi, "Invasion of erythrocytes by malaria merozoites," *Science*, vol. 187, no. 4178, pp. 748–750, 1975.
- [139] M. J. Boyle, C. Langer, J. A. Chan et al., "Sequential processing of merozoite surface proteins during and after erythrocyte invasion by *Plasmodium falciparum*," *Infection and Immunity*, vol. 82, no. 3, pp. 924–936, 2014.
- [140] M. Aikawa, L. H. Miller, J. Johnson, and J. Rabbege, "Erythrocyte entry by malarial parasites. A moving junction between erythrocyte and parasite," *Journal of Cell Biology*, vol. 77, no. 1, pp. 72–82, 1978.
- [141] M. Chugh, V. Sundararaman, S. Kumar et al., "Protein complex directs hemoglobin-to-hemozoin formation in *Plasmodium falciparum*," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 110, no. 14, pp. 5392–5397, 2013.
- [142] S. Kapishnikov, A. Weiner, E. Shimoni et al., "Oriented nucleation of hemozoin at the digestive vacuole membrane in Plasmodium falciparum," *Proceedings of the National Academy* of Sciences of the United States of America, vol. 109, no. 28, pp. 11188–11193, 2012.
- [143] S. Kapishnikov, A. Weiner, E. Shimoni, G. Schneider, M. Elbaum, and L. Leiserowitz, "Digestive vacuole membrane in *Plasmodium falciparum* infected erythrocytes: relevance to templated nucleation of hemozoin," *Langmuir*, vol. 29, no. 47, pp. 14595–14602, 2013.
- [144] M. Abkarian, G. Massiera, L. Berry, M. Roques, and C. Braun-Breton, "A novel mechanism for egress of malarial parasites from red blood cells," *Blood*, vol. 117, no. 15, pp. 4118–4124, 2011.
- [145] C. Coban, Y. Igari, M. Yagi et al., "Immunogenicity of wholeparasite vaccines against *Plasmodium falciparum* involves malarial hemozoin and host TLR9," *Cell Host and Microbe*, vol. 7, no. 1, pp. 50–61, 2010.
- [146] C. Hashimoto, K. L. Hudson, and K. V. Anderson, "The Toll gene of drosophila, required for dorsal-ventral embryonic polarity, appears to encode a transmembrane protein," *Cell*, vol. 52, no. 2, pp. 269–279, 1988.
- [147] R. Medzhitov, P. Preston-Hurlburt, and C. A. Janeway Jr., "A human homologue of the Drosophila toll protein signals

activation of adaptive immunity," *Nature*, vol. 388, no. 6640, pp. 394–397, 1997.

- [148] S. Pandey and D. K. Agrawal, "Immunobiology of Toll-like receptors: emerging trends," *Immunology and Cell Biology*, vol. 84, no. 4, pp. 333–341, 2006.
- [149] T. Chuang and R. J. Ulevitch, "Identification of hTLR10: a novel human Toll-like receptor preferentially expressed in immune cells," *Biochimica et Biophysica Acta: Gene Structure* and Expression, vol. 1518, no. 1-2, pp. 157–161, 2001.
- [150] F. Yarovinsky, "Innate immunity to Toxoplasma gondii infection," *Nature Reviews Immunology*, vol. 14, no. 2, pp. 109–121, 2014.
- [151] T. Kawai and S. Akira, "Pathogen recognition with Toll-like receptors," *Current Opinion in Immunology*, vol. 17, no. 4, pp. 338–344, 2005.
- [152] T. Kawai and S. Akira, "TLR signaling," Cell Death and Differentiation, vol. 13, no. 5, pp. 816–825, 2006.
- [153] L. Schofield and F. Hackett, "Signal transduction in host cells by a glycosylphosphatidylinositol toxin of malaria parasites," *Journal of Experimental Medicine*, vol. 177, no. 1, pp. 145–153, 1993.
- [154] S. D. Tachado, P. Gerold, M. J. McConville et al., "Glycosylphosphatidylinositol toxin of Plasmodium induces nitric oxide synthase expression in macrophages and vascular endothelial cells by a protein tyrosine kinase-dependent and protein kinase C-dependent signaling pathway," *Journal of Immunology*, vol. 156, no. 5, pp. 1897–1907, 1996.
- [155] X. Wu, N. M. Gowda, S. Kumar, and D. C. Gowda, "Protein-DNA complex is the exclusive malaria parasite component that activates dendritic cells and triggers innate immune responses," *The Journal of Immunology*, vol. 184, no. 8, pp. 4338–4348, 2010.
- [156] S. Pichyangkul, K. Yongvanitchit, U. Kum-Arb et al., "Malaria blood stage parasites activate human plasmacytoid dendritic cells and murine dendritic cells through a toll-like receptor 9dependent pathway," *Journal of Immunology*, vol. 172, no. 8, pp. 4926–4933, 2004.
- [157] E. Hempelmann and T. J. Egan, "Pigment biocrystallization in Plasmodium falciparum," *Trends in Parasitology*, vol. 18, no. 1, article 11, 2002.
- [158] B. S. Franklin, P. Parroche, M. A. Ataíde et al., "Malaria primes the innate immune response due to interferon- γ induced enhancement of toll-like receptor expression and function," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 106, no. 14, pp. 5789–5794, 2009.
- [159] V. Jeney, J. Balla, A. Yachie et al., "Pro-oxidant and cytotoxic effects of circulating heme," *Blood*, vol. 100, no. 3, pp. 879–887, 2002.
- [160] J. Balla, G. Balla, V. Jeney, G. Kakuk, H. S. Jacob, and G. M. Vercellotti, "Ferriporphyrins and endothelium: a 2-edged sword—promotion of oxidation and induction of cytoprotectants," *Blood*, vol. 95, no. 11, pp. 3442–3450, 2000.
- [161] J. Balla, H. S. Jacob, G. Balla, K. Nath, J. W. Eaton, and G. M. Vercellotti, "Endothelial-cell heme uptake from heme proteins: induction of sensitization and desensitization to oxidant damage," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 90, no. 20, pp. 9285–9289, 1993.
- [162] E. Seixas, R. Gozzelino, Â. Chora et al., "Heme oxygenase-1 affords protection against noncerebral forms of severe malaria," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 106, no. 37, pp. 15837–15842, 2009.

- [163] M. A. Arruda, A. G. Rossi, M. S. De Freitas, C. Barja-Fidalgo, and A. V. Graça-Souza, "Heme inhibits human neutrophil apoptosis: involvement of phosphoinositide 3-kinase, MAPK, and NF-κB," *Journal of Immunology*, vol. 173, no. 3, pp. 2023– 2030, 2004.
- [164] A. V. Graça-Souza, M. A. B. Arruda, M. S. de Freitas, C. Barja-Fidalgo, and P. L. Oliveira, "Neutrophil activation by heme: implications for inflammatory processes," *Blood*, vol. 99, no. 11, pp. 4160–4165, 2002.
- [165] B. N. Porto, L. S. Alves, P. L. Fernández et al., "Heme induces neutrophil migration and reactive oxygen species generation through signaling pathways characteristic of chemotactic receptors," *Journal of Biological Chemistry*, vol. 282, no. 33, pp. 24430–24436, 2007.
- [166] S. Nomura, N. N. Tandon, T. Nakamura, J. Cone, S. Fukuhara, and J. Kambayashi, "High-shear-stress-induced activation of platelets and microparticles enhances expression of cell adhesion molecules in THP-1 and endothelial cells," *Atherosclerosis*, vol. 158, no. 2, pp. 277–287, 2001.
- [167] S. F. Mause, P. von Hundelshausen, A. Zernecke, R. R. Koenen, and C. Weber, "Platelet microparticles: a transcellular delivery system for RANTES promoting monocyte recruitment on endothelium," *Arteriosclerosis, Thrombosis, and Vascular Biology*, vol. 25, no. 7, pp. 1512–1518, 2005.
- [168] N. Amabile, A. P. Guérin, A. Leroyer et al., "Circulating endothelial microparticles are associated with vascular dysfunction in patients with end-stage renal failure," *Journal of the American Society of Nephrology*, vol. 16, no. 11, pp. 3381–3388, 2005.
- [169] C. M. Boulanger, A. Scoazec, T. Ebrahimian et al., "Circulating microparticles from patients with myocardial infarction cause endothelial dysfunction," *Circulation*, vol. 104, no. 22, pp. 2649– 2652, 2001.
- [170] B. Fritzsching, B. Schwer, J. Kartenbeck, A. Pedal, V. Horejsi, and M. Ott, "Release and intercellular transfer of cell surface CD81 via microparticles," *Journal of Immunology*, vol. 169, no. 10, pp. 5531–5537, 2002.
- [171] M. Baj-Krzyworzeka, R. Szatanek, K. Węglarczyk et al., "Tumour-derived microvesicles carry several surface determinants and mRNA of tumour cells and transfer some of these determinants to monocytes," *Cancer Immunology, Immunotherapy*, vol. 55, no. 7, pp. 808–818, 2006.
- [172] V. Combes, N. Coltel, M. Alibert et al., "ABCA1 gene deletion protects against cerebral malaria: potential pathogenic role of microparticles in neuropathology," *The American Journal of Pathology*, vol. 166, no. 1, pp. 295–302, 2005.
- [173] Z. M. Khan, C. Ng, and J. P. Vanderberg, "Early hepatic stages of *Plasmodium berghei*: release of circumsporozoite protein and host cellular inflammatory response," *Infection and Immunity*, vol. 60, no. 1, pp. 264–270, 1992.
- [174] S. Epiphanio, S. A. Mikolajczak, L. A. Gonçalves et al., "Heme oxygenase-1 is an anti-inflammatory host factor that promotes murine plasmodium liver Infection," *Cell Host and Microbe*, vol. 3, no. 5, pp. 331–338, 2008.
- [175] N. A. De Weerd and T. Nguyen, "The interferons and their receptors—distribution and regulation," *Immunology and Cell Biology*, vol. 90, no. 5, pp. 483–491, 2012.
- [176] M. J. de Veer, M. Holko, M. Frevel et al., "Functional classification of interferon-stimulated genes identified using microarrays," *Journal of Leukocyte Biology*, vol. 69, no. 6, pp. 912–920, 2001.

- [177] G. Trinchieri, "Type I interferon: friend or foe?" Journal of Experimental Medicine, vol. 207, no. 10, pp. 2053–2063, 2010.
- [178] H. Hisamatsu, N. Shimbara, Y. Saito et al., "Newly identified pair of proteasomal subunits regulated reciprocally by interferon *y*," *Journal of Experimental Medicine*, vol. 183, no. 4, pp. 1807–1816, 1996.
- [179] B. Boes, H. Hengel, T. Ruppert, G. Multhaup, U. H. Koszinowski, and P. Kloetzel, "Interferon *y* stimulation modulates the proteolytic activity and cleavage site preference of 20S mouse proteasomes," *The Journal of Experimental Medicine*, vol. 179, no. 3, pp. 901–909, 1994.
- [180] L. A. Cramer, S. L. Nelson, and M. J. Klemsz, "Synergistic induction of the Tap-1 gene by IFN-γ and lipopolysaccharide in macrophages is regulated by STAT1," *The Journal of Immunology*, vol. 165, no. 6, pp. 3190–3197, 2000.
- [181] D. Wallach, M. Fellous, and M. Revel, "Preferential effect of γ interferon on the synthesis of HLA antigens and their mRNAs in human cells," *Nature*, vol. 299, no. 5886, pp. 833–836, 1982.
- [182] D. V. Erbe, J. E. Collins, L. Shen, R. F. Graziano, and M. W. Fanger, "The effect of cytokines on the expression and function of Fc receptors for IgG on human myeloid cells," *Molecular Immunology*, vol. 27, no. 1, pp. 57–67, 1990.
- [183] R. C. Strunk, F. S. Cole, D. H. Perlmutter, and H. R. Colten, " γ -Interferon increases expression of class III complement genes C2 and factor B in human monocytes and in murine fibroblasts transfected with human C2 and factor B genes," *Journal of Biological Chemistry*, vol. 260, no. 28, pp. 15280–15285, 1985.
- [184] D. A. Drevets, P. J. M. Leenen, and P. A. Campbell, "Complement receptor type 3 mediates phagocytosis and killing of Listeria monocytogenes by a TNF-α- and IFN-γ-stimulated macrophage precursor hybrid," *Cellular Immunology*, vol. 169, no. 1, pp. 1–6, 1996.
- [185] A. Yoshida, Y. Koide, M. Uchijima, and T. O. Yoshida, "IFN-γ induces IL-12 mRNA expression by a murine macrophage cell line, J774," *Biochemical and Biophysical Research Communications*, vol. 198, no. 3, pp. 857–861, 1994.
- [186] M. P. Gil, E. Bohn, A. K. O'Guin et al., "Biologic consequences of Stat1-independent IFN signaling," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 98, no. 12, pp. 6680–6685, 2001.
- [187] D. D. Taub, A. R. Lloyd, K. Conlon et al., "Recombinant human interferon-inducible protein 10 is a chemoattractant for human monocytes and T lymphocytes and promotes T cell adhesion to endothelial cells," *The Journal of Experimental Medicine*, vol. 177, no. 6, pp. 1809–1814, 1993.
- [188] A. Ferreira, L. Schofield, V. Enea et al., "Inhibition of development of exoerythrocytic froms of malaria parasites by γinterferon," *Science*, vol. 232, no. 4752, pp. 881–884, 1986.
- [189] L. Schofield, A. Ferreira, R. Altszuler, V. Nussenzweig, and R. S. Nussenzweig, "Interferon-γ inhibits the intrahepatocytic development of malaria parasites in vitro," *The Journal of Immunology*, vol. 139, no. 6, pp. 2020–2025, 1987.
- [190] S. Mellouk, S. J. Green, C. A. Nacy, and S. L. Hoffman, "IFN-γ inhibits development of Plasmodium berghei exoerythrocytic stages in hepatocytes by an L-arginine-dependent effector mechanism," *Journal of Immunology*, vol. 146, no. 11, pp. 3971– 3976, 1991.
- [191] A. K. Nussler, L. Renia, V. Pasquetto, F. Miltgen, H. Matile, and D. Mazier, "In vivo induction of the nitric oxide pathway in hepatocytes after injection with irradiated malaria sporozoites, malaria blood parasites or adjuvants," *European Journal of Immunology*, vol. 23, no. 4, pp. 882–887, 1993.

- [192] A. J. F. Luty, B. Lell, R. Schmidt-Ott et al., "Interferon-γ responses are associated with resistance to reinfection with Plasmodium falciparum in young African children," *Journal of Infectious Diseases*, vol. 179, no. 4, pp. 980–988, 1999.
- [193] B. Perlaza, J. Sauzet, K. Brahimi, L. Benmohamed, and P. Druilhe, "Interferon-γ, a valuable surrogate marker of Plasmodium falciparum pre-erythrocytic stages protective immunity," *Malaria Journal*, vol. 10, article 27, 2011.
- [194] L. Schofield, J. Villaquiran, A. Ferreira, H. Schellekens, R. Nussenzweig, and V. Nussenzweig, "Gamma Interferon, CD8+ T cells and antibodies required for immunity to malaria sporozoites," *Nature*, vol. 330, no. 6149, pp. 664–666, 1987.
- [195] M. M. Stevenson, M. F. Tam, M. Belosevic, P. H. van der Meide, and J. E. Podoba, "Role of endogenous gamma interferon in host response to infection with blood-stage Plasmodium chabaudi AS," *Infection and Immunity*, vol. 58, no. 10, pp. 3225–3232, 1990.
- [196] T. Yoneto, T. Yoshimoto, C. Wang et al., "Gamma interferon production is critical for protective immunity to infection with blood-stage Plasmodium berghei XAT but neither NO production nor NK cell activation is critical," *Infection and Immunity*, vol. 67, no. 5, pp. 2349–2356, 1999.
- [197] M. C. D'Ombrain, L. J. Robinson, D. I. Stanisic et al., "Association of early interferon-γ production with immunity to clinical malaria: a longitudinal study among Papua New Guinean children," *Clinical Infectious Diseases*, vol. 47, no. 11, pp. 1380– 1387, 2008.
- [198] S. Inoue, M. Niikura, S. Mineo, and F. Kobayashi, "Roles of IFNgamma and gammadelta T Cells in protective immunity against blood-stage malaria," *Frontiers in Immunology*, vol. 4, article 258, 2013.
- [199] A. J. F. Luty, D. J. Perkins, B. Lell et al., "Low interleukin-12 activity in severe Plasmodium falciparum malaria," *Infection* and Immunity, vol. 68, no. 7, pp. 3909–3915, 2000.
- [200] C. Aucan, A. J. Walley, B. J. W. Hennig et al., "Interferon-alpha receptor-1 (IFNAR1) variants are associated with protection against cerebral malaria in The Gambia," *Genes & Immunity*, vol. 4, no. 4, pp. 275–282, 2003.
- [201] D. P. Simmons, P. A. Wearsch, D. H. Canaday et al., "Type I IFN drives a distinctive dendritic cell maturation phenotype that allows continued class II MHC synthesis and antigen processing," *Journal of Immunology*, vol. 188, no. 7, pp. 3116– 3126, 2012.
- [202] J. M. Curtsinger, J. O. Valenzuela, P. Agarwal, D. Lins, and M. F. Mescher, "Cutting edge: type I IFNs provide a third signal to CD8 T cells to stimulate clonal expansion and differentiation," *Journal of Immunology*, vol. 174, no. 8, pp. 4465–4469, 2005.
- [203] P. Agarwal, A. Raghavan, S. L. Nandiwada et al., "Gene regulation and chromatin remodeling by IL-12 and type I IFN in programming for CD8 T cell effector function and memory," *Journal of Immunology*, vol. 183, no. 3, pp. 1695–1704, 2009.
- [204] C. A. Hunter, K. E. Gabriel, T. Radzanowski, L. E. Neyer, and J. S. Remington, "Type I interferons enhance production of IFN-γ by NK cells," *Immunology Letters*, vol. 59, no. 1, pp. 1–5, 1997.
- [205] D. J. Gough, N. L. Messina, L. Hii et al., "Functional crosstalk between type I and II interferon through the regulated expression of STAT1," *PLoS Biology*, vol. 8, no. 4, Article ID e1000361, 2010.
- [206] R. I. Jahiel, J. Vilcek, and R. S. Nussenzweig, "Exogenous interferon protects mice against Plasmodium berghei malaria," *Nature*, vol. 227, no. 5265, pp. 1350–1351, 1970.
- [207] J. Van Damme, M. R. Schaafsma, W. E. Fibbe, J. H. F. Falkenburg, G. Opdenakker, and A. Billiau, "Simultaneous production

of interleukin 6, interferon- β and colony-stimulating activity by fibroblasts after viral and bacterial infection," *European Journal of Immunology*, vol. 19, no. 1, pp. 163–168, 1989.

- [208] A. Nussler, J.-ac. Drapier, L. Renia et al., "L-Arginine-dependent destruction of intrahepatic malaria parasites in response to tumor necrosis factor and/or interleukin 6 stimulation," *European Journal of Immunology*, vol. 21, no. 1, pp. 227–230, 1991.
- [209] I. Landau and P. Gautret, "Animal models: rodents," in *Malaria: Parasite Biology, Pathogenesis, and Protection*, I. W. Sherman, Ed., pp. 401–417, ASM Press, Washington, DC, USA, 1998.
- [210] A. M. Vigário, E. Belnoue, A. C. Grüner et al., "Recombinant human IFN-α inhibits cerebral malaria and reduces parasite burden in mice," *Journal of Immunology*, vol. 178, no. 10, pp. 6416–6425, 2007.
- [211] M. Krupka, K. Seydel, C. M. Feintuch et al., "Mild Plasmodium falciparum malaria following an episode of severe malaria is associated with induction of the interferon pathway in Malawian children," *Infection and Immunity*, vol. 80, no. 3, pp. 1150–1155, 2012.
- [212] T. Taniguchi, K. Ogasawara, A. Takaoka, and N. Tanaka, "IRF family of transcription factors as regulators of host defense," *Annual Review of Immunology*, vol. 19, pp. 623–655, 2001.
- [213] K. Ozato, P. Tailor, and T. Kubota, "The interferon regulatory factor family in host defense: mechanism of action," *Journal of Biological Chemistry*, vol. 282, no. 28, pp. 20065–20069, 2007.
- [214] A. Kröger, M. Köster, K. Schroeder, H. Hauser, and P. P. Mueller, "Activities of IRF-1," *Journal of Interferon and Cytokine Research*, vol. 22, no. 1, pp. 5–14, 2002.
- [215] K. Honda, A. Takaoka, and T. Taniguchi, "Type I interferon [corrected] gene induction by the interferon regulatory factor family of transcription factors," *Immunity*, vol. 25, no. 3, pp. 349–360, 2006.
- [216] P. Rihet, Y. Traoré, L. Abel, C. Aucan, T. Traoré-Leroux, and F. Fumoux, "Malaria in humans: plasmodium falciparum blood infection levels are linked to chromosome 5q31-q33," *American Journal of Human Genetics*, vol. 63, no. 2, pp. 498–505, 1998.
- [217] K. Honda, H. Yanai, A. Takaoka, and T. Taniguchi, "Regulation of the type I IFN induction: a current view," *International Immunology*, vol. 17, no. 11, pp. 1367–1378, 2005.
- [218] Y. Liu, L. Zeng, A. T. Tian et al., "Endoplasmic reticulum stress regulates the innate immunity critical transcription factor IRF3," *Journal of Immunology*, vol. 189, no. 9, pp. 4630–4639, 2012.
- [219] M. Yoneyama, W. Suhara, Y. Fukuhara, M. Fukuda, E. Nishida, and T. Fujita, "Direct triggering of the type I interferon system by virus infection: activation of a transcription factor complex containing IRF-3 and CBP/p300," *EMBO Journal*, vol. 17, no. 4, pp. 1087–1095, 1998.
- [220] M. G. Wathelet, C. H. Lin, B. S. Parekh, L. V. Ronco, P. M. Howley, and T. Maniatis, "Virus infection induces the assembly of coordinately activated transcription factors on the IFN-β enhancer in vivo," *Molecular Cell*, vol. 1, no. 4, pp. 507–518, 1998.
- [221] J. Yie, K. Senger, and D. Thanos, "Mechanism by which the IFN-β enhanceosome activates transcription," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 96, no. 23, pp. 13108–13113, 1999.
- [222] M. Sato, N. Hata, M. Asagiri, T. Nakaya, T. Taniguchi, and N. Tanaka, "Positive feedback regulation of type I IFN genes by the IFN-inducible transcription factor IRF-7," *FEBS Letters*, vol. 441, no. 1, pp. 106–110, 1998.

- [223] D. L. Noah, M. A. Blum, and B. Sherry, "Interferon regulatory factor 3 is required for viral induction of beta interferon in primary cardiac myocyte cultures," *Journal of Virology*, vol. 73, no. 12, pp. 10208–10213, 1999.
- [224] C. F. Basler, A. Mikulasova, L. Martinez-Sobrido et al., "The Ebola virus VP35 protein inhibits activation of interferon regulatory factor 3," *Journal of Virology*, vol. 77, no. 14, pp. 7945– 7956, 2003.
- [225] J. Ye and T. Maniatis, "Negative regulation of interferon-β gene expression during acute and persistent virus infections," *PLoS ONE*, vol. 6, no. 6, Article ID e20681, 2011.
- [226] M. Sagong and C. Lee, "Porcine reproductive and respiratory syndrome virus nucleocapsid protein modulates interferonβ production by inhibiting IRF3 activation in immortalized porcine alveolar macrophages," *Archives of Virology*, vol. 156, no. 12, pp. 2187–2195, 2011.
- [227] T. Tamura and K. Ozato, "ICSBP/IRF-8: its regulatory roles in the development of myeloid cells," *Journal of Interferon and Cytokine Research*, vol. 22, no. 1, pp. 145–152, 2002.
- [228] M. Horiuchi, A. Itoh, D. Pleasure, K. Ozato, and T. Itoh, "Cooperative contributions of interferon regulatory factor 1 (IRF1) and IRF8 to interferon-γ-mediated cytotoxic effects on oligodendroglial progenitor cells," *Journal of Neuroinflammation*, vol. 8, article 8, pp. 1742–2094, 2011.
- [229] P. H. Driggers, D. L. Ennist, S. L. Gleason et al., "An interferon γregulated protein that binds the interferon- inducible enhancer element of major histocompatibility complex class I genes," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 87, no. 10, pp. 3743–3747, 1990.
- [230] J. Nitcheu, O. Bonduelle, C. Combadiere et al., "Perforindependent brain-infiltrating cytotoxic CD8⁺ T lymphocytes mediate experimental cerebral malaria pathogenesis," *Journal of Immunology*, vol. 170, no. 4, pp. 2221–2228, 2003.
- [231] G. L. Suidan, J. R. Mcdole, Y. Chen, I. Pirko, and A. J. Johnson, "Induction of blood brain barrier tight junction protein alterations by CD8 T cells," *PLoS ONE*, vol. 3, no. 8, Article ID e3037, 2008.
- [232] M. Fauconnier, J. Palomo, M. L. Bourigault et al., "IL-12Rβ2 is essential for the development of experimental cerebral malaria," *The Journal of Immunology*, vol. 188, no. 4, pp. 1905–1914, 2012.
- [233] B. J. Barnes, P. A. Moore, and P. M. Pitha, "Virus-specific activation of a novel Interferon regulatory factor, IRF-5, results in the induction of distinct interferon alpha genes," *The Journal* of *Biological Chemistry*, vol. 276, no. 26, pp. 23382–23390, 2001.
- [234] B. J. Barnes, M. J. Kellum, A. E. Field, and P. M. Pitha, "Multiple regulatory domains of IRF-5 control activation, cellular localization, and induction of chemokines that mediate recruitment of T lymphocytes," *Molecular and Cellular Biology*, vol. 22, no. 16, pp. 5721–5740, 2002.
- [235] X. Y. Fu, D. S. Kessler, S. A. Veals, D. E. Levy, and J. E. Darnell Jr., "ISGF3, the transcriptional activator induced by interferon α, consists of multiple interacting polypeptide chains," *Proceedings* of the National Academy of Sciences of the United States of America, vol. 87, no. 21, pp. 8555–8559, 1990.
- [236] S. A. Qureshi, M. Salditt-Georgieff, and J. E. Darnell Jr., "Tyrosine-phosphorylated Stat1 and Stat2 plus a 48-kDa protein all contact DNA in forming interferon-stimulated-gene factor 3," *Proceedings of the National Academy of Sciences of the United States of America*, vol. 92, no. 9, pp. 3829–3833, 1995.
- [237] C. J. Sutherland, A. Alloueche, J. Curtis et al., "Gambian children successfully treated with chloroquine can harbor and transmit

Plasmodium falciparum gametocytes carrying resistance genes," *The American Journal of Tropical Medicine and Hygiene*, vol. 67, no. 6, pp. 578–585, 2002.

- [238] K. Na-Bangchang, P. Muhamad, R. Ruaengweerayut, W. Chaijaroenkul, and J. Karbwang, "Identification of resistance of *Plasmodium falciparum* to artesunate-mefloquine combination in an area along the Thai-Myanmar border: integration of clinico-parasitological response, systemic drug exposure, and *in vitro* parasite sensitivity," *Malaria Journal*, vol. 12, no. 1, article 263, 2013.
- [239] J. Hadden, "Recent thoughts on the immunotherapy of infectious diseases including HIV infection," in *Microbial Infections*, H. Friedman, T. Klein, and H. Yamaguchi, Eds., pp. 13–22, Springer, 1992.
- [240] M. Jeffrey and M. Jacobson, "Immunotherapy for infectious diseases," in *Infectious Disease*, V. S. Georgiev, Ed., p. 331, Humana Press, New York, NY, USA, 2002.
- [241] V. Kak, V. Sundareshan, J. Modi, and N. M. Khardori, "Immunotherapies in infectious diseases," *Medical Clinics of North America*, vol. 96, no. 3, pp. 455–474, 2012.
- [242] M. Talpaz, H. M. Kantarjian, K. McCredie, J. M. Trujillo, M. J. Keating, and J. U. Gutterman, "Hematologic remission and cytogenetic improvement induced by recombinant human interferon alpha(A) in chronic myelogenous leukemia," *The New England Journal of Medicine*, vol. 314, no. 17, pp. 1065–1069, 1986.
- [243] D. Goldstein and J. Laszlo, "The role of interferon in cancer therapy: a current perspective," *Ca: A Cancer Journal for Clinicians*, vol. 38, no. 5, pp. 258–277, 1988.
- [244] J. M. Kirkwood, M. S. Ernstoff, C. A. Davis, M. Reiss, R. Ferraresi, and S. A. Rudnick, "Comparison of intramuscular and intravenous recombinant alpha-2 interferon in melanoma and other cancers," *Annals of Internal Medicine*, vol. 103, no. 1, pp. 32–36, 1985.
- [245] L. Repetto, P. G. Giannessi, E. Campora et al., "Tamoxifen and interferon-beta for the treatment of metastatic breast cancer," *Breast Cancer Research and Treatment*, vol. 39, no. 2, pp. 235– 238, 1996.
- [246] G. H. Windbichler, H. Hausmaninger, W. Stummvoll et al., "Interferon-gamma in the first-line therapy of ovarian cancer: a randomized phase III trial," *British Journal of Cancer*, vol. 82, no. 6, pp. 1138–1144, 2000.
- [247] M. L. Shiffman, "Pegylated interferons: what role will they play in the treatment of chronic hepatitis C?" *Current Gastroenterol*ogy Reports, vol. 3, no. 1, pp. 30–37, 2001.
- [248] G. Chander, M. S. Sulkowski, M. W. Jenckes et al., "Treatment of chronic hepatitis C: a systematic review," *Hepatology*, vol. 36, no. 5, supplement 1, pp. S135–S144, 2002.
- [249] J. Yang, Y. G. Pu, Z. M. Zeng et al., "Interferon for the treatment of genital warts: a systematic review," *BMC Infectious Diseases*, vol. 9, no. 156, pp. 1471–2334, 2009.
- [250] A. H. Achtman, S. Pilat, C. W. Law et al., "Effective adjunctive therapy by an innate defense regulatory peptide in a preclinical model of severe malaria," *Science Translational Medicine*, vol. 4, no. 135, Article ID 135ra64, 2012.