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## Immunological Features Underlying Viral Hemorrhagic Fevers

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### Abstract

Several enveloped RNA viruses of the arenavirus, bunyavirus, filovirus and flavivirus families are associated with a syndrome known as viral hemorrhagic fever (VHF). VHF is characterized by fever, vascular leakage, coagulation defects and multi organ system failure. VHF is currently viewed as a disease precipitated by viral suppression of innate immunity, which promotes systemic virus replication and excessive proinflammatory cytokine responses that trigger the manifestations of severe disease. However, the mechanisms by which immune dysregulation contributes to disease remain poorly understood. Infection of nonhuman primates closely recapitulates human VHF, notably Ebola and yellow fever, thereby providing excellent models to better define the immunological basis for this syndrome. Here we review the current state of our knowledge and suggest future directions that will better define the immunological mechanisms underlying VHF.

### Introduction

Among the more well-known causes of VHF are the filoviruses Ebola virus (EBOV) and Marburg virus (MARV), the arenavirus Lassa virus, and the flaviviruses yellow fever (YFV) and dengue (DENV) virus. How diverse virus families with different replication strategies cause a similar clinical syndrome is incompletely understood, but several features typify these infections. The viruses effectively suppress innate antiviral defenses and replicate systemically to high titers; monocytes, macrophages and dendritic cells are targets of infection; a systemic cytokine storm occurs; and vascular leakage and hemorrhage may be seen. Nevertheless, specific details of the immunological underpinnings of VHF are lacking, and a unified view as to how the virus, the innate immune response and the adaptive immune response interact in the setting of VHF is also absent. Here, we argue that the availability of well-established nonhuman primate models of EBOV and YFV disease provide the necessary tools to define the immunological features common to VHFs, leading to a greater understanding of the syndrome and the suggestion of novel therapeutic approaches.

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## Detailed look at EBOV

The ebolaviruses and marburgviruses are enveloped viruses with non-segmented negative-sense single-stranded RNA genomes that belong to the family *Filoviridae*. There are 5 species of ebolavirus: Zaire ebolavirus (EBOV), Sudan ebolavirus (SUDV), Bundibugyo ebolavirus (BDBV), Tai Forrest ebolavirus (TAFV) and Reston ebolavirus (RESTV) and a single species of marburgvirus, Marburg marburgvirus (MARV). Only EBOV, SUDV, BDBV and MARV have been associated with outbreaks of severe disease and high mortality in humans. The most detailed descriptions of filovirus disease come from studies of EBOV and will form the main basis for our discussion of filovirus hemorrhagic fever.

Filovirus genomes possess 7 genes that encode: nucleoprotein (NP), viral protein of 35 kDa (VP35), VP40, glycoprotein (GP; mediates viral attachment and entry), VP30, VP24 and Large protein (L; the enzymatic component of the viral RNA-dependent RNA polymerase). The EBOV replication cycle takes place in the cytoplasm. Virus release occurs by budding from the plasma membrane in a process directed by the matrix protein VP40 and enhanced by other viral proteins, including GP.

## Pathophysiology

Infections occur due to direct contact with infectious material, such as bodily fluids containing infectious virus. Airborne transmission is not thought to be a significant route of human infection, but aerosolized virus does cause rapidly lethal disease in experimentally-infected non-human primates (reviewed in [1]). Following exposure, an incubation period of 2–21 days is followed by an abrupt but non-specific viral syndrome characterized by fever, chills and myalgia. As infection progresses, prostration, nausea, vomiting, abdominal pain and diarrhea appear. The final stages of disease are characterized by coagulopathy and vascular leakage resulting in hemorrhage and shock as reviewed in [2].

Many of the details of EBOV pathogenesis are derived from nonhuman primate studies, as they closely parallel severe human infections and are considered the “gold-standard” model of EBOV disease (EVD). The hallmarks of EVD are high levels of systemic virus replication, cytokine production, liver damage, coagulopathy and lymphopenia [2]. Although filoviruses productively infect a variety of cell types, dendritic cells (DCs), macrophages and monocytes appear to be the preferential targets [2–5]. This may be due to 1) viral GP interaction with lectins, such as dendritic-cell-specific ICAM-3-grabbing non-integrin (DC-SIGN) on the surface of these cells [6–10], or 2) phosphatidylserine on the surface of virus particles interacting, either directly or through an intermediate, with molecules such as TIM-1, TAM or  $\alpha V\beta 3$  and  $\alpha V\beta 5$  integrins [11–18]. Because these immune cells support productive viral infection and are capable of trafficking *in vivo*, their infection likely facilitates dissemination of the virus to lymph nodes and systemically [2,4,5,19].

The dissemination of EBOV to hepatocytes, adrenal cortical cells and endothelial cells likely contributes to coagulopathy, which can result in hemorrhage and shock [4]. Virus-induced liver damage reduces production of coagulation factors, while infection of the adrenal gland reduces production of hormones that regulate blood pressure [4]. In addition, infected

monocytes and macrophages produce proinflammatory mediators (IL-1 $\beta$ , IL-6, IL-8, IL-10, MIP-1 $\beta$  and TNF $\alpha$ ), reactive oxygen species, nitric oxide, and tissue factor (TF) [20–27], which promote endothelial leakage and hypovolemia [28–31]. The cellular sensors and signaling pathways by which EBOV infection promotes production of cytokines and chemokines by monocytes are incompletely defined. *In vitro* studies demonstrate that extensive EBOV replication is not required to elicit cytokine production, but likely sustains the cytokine response.

### Immune evasion

In contrast to monocytes/macrophages, EBOV infection of DCs is characterized by an inhibition of IFN- $\alpha/\beta$  and cytokine production, down-regulation of co-stimulatory molecules, and reduced ability to activate T cells [32–36]. The VP35 proteins target multiple innate immune signaling pathways to suppress IFN- $\alpha/\beta$  production and its antiviral effects [37–47]. X-ray crystal structures demonstrate that the EBOV and MARV VP35s bind the phosphodiester backbone of dsRNA and that EBOV VP35 also “caps” the ends of dsRNAs in a manner that could mask 5'-triphosphates [38,40–43,48,49]. EBOV VP35 can also interact with cellular protein PACT to prevent PACT-mediated activation of RIG-I. Mutations in VP35 that disrupt interactions with dsRNA and PACT abrogate VP35 inhibition of IFN responses [36,38,40–43,48–54]. Furthermore, mutations in VP35 impair virus replication in IFN- $\alpha/\beta$  competent cells and attenuate the virus *in vivo*, demonstrating a critical role for innate immune suppression for pathogenesis [52–54].

In addition, EBOV and MARV block the Jak-STAT signaling pathways triggered when IFNs are added to cells, thereby disrupting the antiviral effects of these cytokines. EBOV VP24 blocks the nuclear accumulation of tyrosine phosphorylated STAT1 by binding to the NPI-1 subfamily of karyopherin alpha (KPNA) proteins [55–58], whereas MARV VP40 blocks signaling by tyrosine kinase Jak1, preventing all the tyrosine phosphorylation events that typically occur after IFN addition to cells [59,60].

The impact of DC suppression on the adaptive immunity *in vivo* remains to be determined, as virus-specific T cell responses develop in both EBOV-infected mice and people who survive infection [61,62]. Moreover, lymphopenia is another common feature of EBOV infection, with loss of CD4 T cells, CD8 T cells and NK cells in mouse and nonhuman primate models [63,64] as well as human patients [65]. Cell loss occurs primarily via apoptosis and although the basis for this phenomenon is not yet clear, it is believed to be mediated by pro-inflammatory cytokines, NO and soluble FAS ligand produced by monocytes/macrophages [22,25,66–68].

## Detailed look at YFV

### Virus epidemiology, genetics and replication

YFV is endemic in central Africa and South America where it results in approximately 200,000 cases and 30,000 deaths annually [69]. YFV is an arbovirus that is spread via mosquitoes belonging to the genera *Haemagogus* and *Aedes*. YFV is maintained through two life cycles: in the urban cycle, YFV is transmitted between humans via *Aedes aegypti*; and in the jungle cycle, YFV transmission occurs between non-human primates via

*Hemagogus* mosquitos in South America and *Aedes africanus* in Africa while humans can be infected by mosquitos that previously fed on an infected monkey [70,71].

Like other members of the *Flaviviridae* family, YFV is a single positive stranded RNA virus with an 11Kb genome composed of a 5' non-coding region, a single open-reading frame (ORF), and a 3' non-coding region. The ORF encodes 3 structural proteins (capsid (C), membrane (prM), and envelope (E)) and 7 nonstructural proteins (NS1, NS2a, NS2b, NS3, NS4a, NS4b, and NS5) [72]. Virus proteins are processed after translation of the entire polyprotein within the rough endoplasmic reticulum (ER). The main structural protein is envelope, which is anchored in the lipid bilayer of the viral envelope and plays an important role in viral entry [73]. Nonstructural proteins are mainly involved in RNA replication and post-translational cleavage of the virus polyprotein [74].

YFV cell entry is mediated by the surface E protein and is internalized via clathrin-dependent endocytosis. The low-pH environment of endosomes induces un-coating of the virus, and the viral RNA genome is released into the cytoplasm, where replication can occur [73,75]. The positive sense RNA is translated to either synthesize complementary negative RNA strands, which serve as templates for progeny positive strands, or encode structural proteins for virion assembly and viral enzymes required for replication and post-translational processing [72].

### Pathophysiology

YFV elicits two patterns of injury, viscerotropism and neurotropism. YFV primarily causes a viscerotropic disease in humans and nonhuman primates with lesions observed in multiple organs such as liver, spleen, heart and kidneys [76–78]. Golden hamsters and immunodeficient mice (AG129 mice) have been developed to study YFV infection [79–82]. However, there are limitations to these models. The hamster model requires a hamster-adapted strain of YFV. Infection of immunodeficient mice with the vaccine strain YFV-17D results in encephalitis but not viscerotropic disease as observed in nonhuman primates and humans and hampers studies of host immune response to YFV [82]. In contrast, non-human primates are a robust model for studying YFV since they are a natural reservoir during the jungle cycle of transmission and the clinical manifestations following YFV challenge of rhesus macaques mimic human viscerotropic disease [83].

Approximately 10<sup>3</sup> YFV is first introduced into the epidermis via saliva from a blood-feeding mosquito [84]. Previous studies suggest that dendritic cells residing in the epidermis are important early targets for flavivirus replication [85–87]. The virus then spreads via infected DCs through lymphatic channels to draining lymph nodes and subsequently into the bloodstream, eventually disseminating to the liver, spleen, additional lymph nodes, heart, and kidneys [84]. Yellow fever presents in three distinct stages: infection, remission and intoxication. Infection lasts 3–6 days after the initial mosquito bite and is characterized with the onset of fever, headache, malaise, photophobia, backache, myalgia, irritability and nausea with viremia peaking on 3 days after onset of symptoms [74,88]. During remission, which lasts between 12 to 48 hours, fever and symptoms subside [74]. Most patients recover, but approximately 15% of patients will become severely ill and enter the period of intoxication in which patients develop jaundice, oliguria or anuria, cardiovascular instability,

hemorrhagic fever and multi-organ dysfunction [74,89]. Case-fatality rates of patients that develop visceral disease with jaundice range from 20% to 50% [89].

Hepatic dysfunction is the hallmark of YFV and is characterized by eosinophilic degeneration of hepatocytes (known as Councilman bodies [90]) and Kupffer cells, Fas mediated midzonal hepatocellular apoptosis, absence of inflammation, and steatosis [91–94]. The predominance of apoptotic versus necrotic liver injury may explain the minimal inflammation and infiltration [91,92,94]. Renal pathology is characterized by eosinophilic degeneration and fatty change of the renal tubular epithelium without inflammation [83].

Similar to Ebola hemorrhagic fever, cytokine dysregulation is thought to mediate endothelial damage, disseminated intravascular coagulation and circulatory shock observed in the terminal stage of YFV. Thrombocytopenia, prolonged clotting and prothrombin times have been observed in human patients and nonhuman primates due to diminished liver production of fibrinogen and clotting factors [74,95].

### Immune evasion

Yellow Fever Virus employs strategies to evade host innate immunity by inhibiting type I interferon response. NS4B, whose function is conserved among flaviviruses, can block STAT1 activation and interferon stimulated gene expression in Vero cells after addition of IFN $\beta$  [96]. A recent study that characterized gene expression within peripheral blood mononuclear cells from rhesus macaques 3 days post YFV infection reported the down-regulation of 43 genes associated with innate immunity, including interferon gamma receptor (IFNGR1), CD83 (a marker of DC maturation), and TNFSF11 (hypothesized to induce DCs to stimulate naïve T cell proliferation) [97,98]. The importance of evasion of innate immunity to the pathogenesis of YFV is highlighted by the reduced mortality in rhesus macaques treated with polyriboinosinicpolyribocytidylic acid, poly-L-lysine and carboxymethylcellulose, which are inducers of IFN $\alpha$  [99]. Similarly, administration of IFN $\gamma$  reduced viremia and hepatitis severity in squirrel monkeys while prolonging survival time in rhesus macaques [100].

Similar to EBOV, YFV infection also results in profound lymphopenia. Depletion of lymphocytes in germinal centers of spleen, lymph nodes, tonsils and Peyer's patches are observed [83,101,102]. In rhesus macaques infected with YFV strain DakH1279, circulating lymphocytes declined by 71% in animals that required euthanasia compared to a 23% decrease in animals that survived challenge, with a significant negative correlation between viral load and extent of lymphocyte loss [97]. The loss of lymphocytes is most likely due to the cytokine storm that accompanies YFV infection. Levels of pro-inflammatory modulators such as IL-6, MCP-1, IP-10, TNF $\alpha$  and anti-inflammatory cytokine IL-1RA were significantly higher in patients with fatal Yellow Fever compared to patients who survived [103]. Similarly, levels of IL-6, IFN $\gamma$ , MCP-1 and IL-15 were elevated in rhesus macaques infected with Yellow Fever strain DakH1279 [97].

## Remaining questions and future directions

The host response to infection plays prominent roles in EVD and YFV viscerotropic disease, but a direct demonstration of how specific interactions between virus and host immune response contribute to VHF *in vivo* is largely lacking. The availability of well-developed animal models provides the opportunity to address these gaps in knowledge and to use this information to develop new therapeutic approaches.

### How does viral suppression of the IFN response influence viral pathogenesis?

Although we know a great deal about how filoviral VP35s regulate viral replication and suppress IFN response *in vitro*, the contribution of these functions to the pathogenesis of VHF *in vivo* remains poorly defined [32–36]. Recombinant EBOVs with point mutations in VP35 are attenuated in rodent models [52,53], however these models do not fully recapitulate human VHF [104]. Therefore to address the role of VP35 in VHF, primates must be infected with VP35 mutant viruses. Because the role of VP35 in innate immune evasion and viral replication are not easily separable, very early time points should be examined to uncover changes in DC and monocyte activation in draining lymph nodes.

A VP24 mutant EBOV was found to modestly impact DC maturation phenotypes *in vitro* [33]. However, this mutation may not completely inactivate VP24 IFN-antagonist function [105]. Recent structural and functional studies have defined new amino acid residues on EBOV VP24 critical for suppression of IFN signaling that should be investigated *in vivo* [58]. Finally, additional studies are required before we can define the contribution of MARV VP40 and to identify additional YFV proteins that contribute to suppression of innate immunity and impact pathogenesis *in vivo*.

### What inflammatory pathways are activated by infection and in which cell types?

Excessive pro-inflammatory cytokine production is thought to be a major factor in pathogenesis of VHF [20,22]. Although the responses of infected monocytes and macrophages *in vitro* suggest these cells as a source of inflammatory cytokines, the cell types most relevant to the inflammatory response *in vivo*, the signaling pathways that contribute to this response, and the role of virus infection in triggering these responses remain to be defined. Depletion of specific immune cell subsets together with transcriptome and phenotype analysis of monocytes isolated from infected humans and nonhuman primates during acute infection would help address these questions.

### What is the contribution of the immune responses in the vascular leakage and coagulopathy?

*In vitro* studies attribute EBOV-induced endothelial leakage to cytokines, TF and soluble GP, and *in vivo* studies suggest mechanisms other than destruction of the endothelium by virus replication [5,28,30]. Although complicated to address in NHPs, the use of cytokine-neutralizing antibodies or specific inhibitors in EBOV or YFV-infected animals, could clarify disease mechanisms and suggest therapeutic approaches. Further, the contribution of liver damage or damage to the adrenal gland to coagulopathy or low blood pressure also need further examination [2].



## What is the status of the adaptive immune response?

The suppression of DC maturation *in vitro* suggests that EBOV may impair development of T cell responses. Fatal infections are associated with the absence of specific antibody responses and with the apoptotic loss of lymphocytes [25,63,64,106]. These findings suggest defects in adaptive immunity during the course of infection; however, survivors develop specific T cell responses [61,62]. Therefore, it is important to further characterize the status of the adaptive immune response *in vivo*. Important questions to be answered include mechanisms of lymphocyte apoptosis and dysregulation of lymphocyte activation and proliferation using careful examination of lymphocyte transcriptome and phenotype *ex vivo* using clinical samples and nonhuman primate models.

## Tools to address these questions

The availability of well-developed animal models for both EBOV and YFV affords the opportunity to address these gaps in knowledge and to use this information to develop new therapeutic approaches. It should be possible to take advantage of different viruses from within the same family with different degrees of virulence. For example, whereas intramuscular injection of Zaire EBOV is nearly 100 percent lethal in macaques, a comparable injection of Bundibugyo EBOV is only 66 percent lethal [107]. Examination of host responses in survivors versus lethal infections with either virus could highlight those features that most determine the outcome of infection. Moreover, the similar pathogenic mechanisms employed by EBOV and YFV, suggest that YFV may serve as a model for Ebola hemorrhagic fever. One major advantage of YFV is the ability to study it under biosafety level 3 (BSL-3) conditions. In contrast, study of EBOV and other filoviruses requires biosafety level 4 (BSL-4) containment facilities, which are available to only a handful of researchers worldwide.

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**Highlights**

Several families of RNA viruses cause viral hemorrhagic fever in humans

Viral hemorrhagic fever (VHF) is characterized by fever, vascular leak and bleeding

Immunological mechanisms are thought to underlie the symptoms of VHF

Ebola virus and Yellow Fever virus provide two excellent models to study VHF

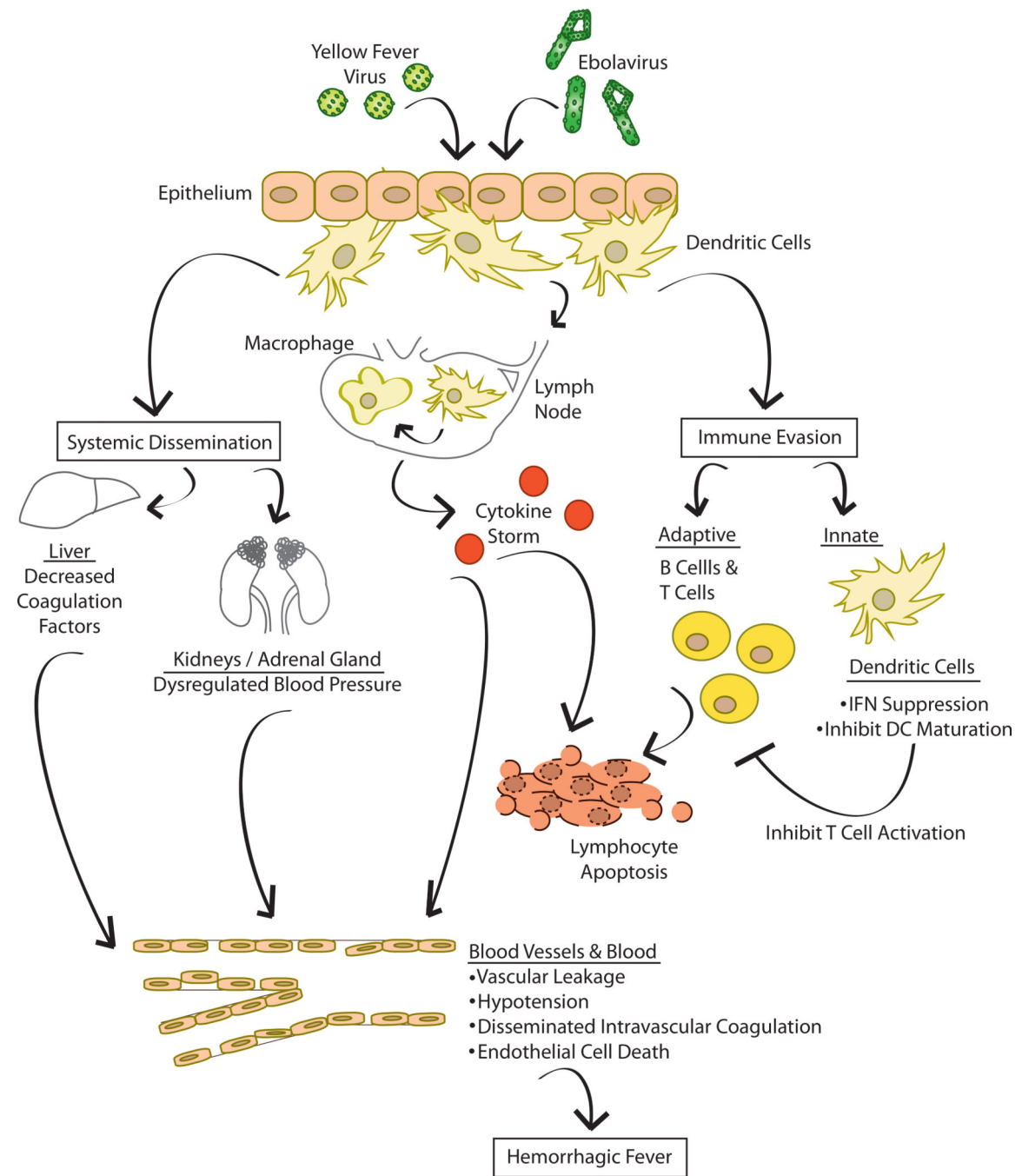
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**Figure.** Infection with EBOV or YFV occurs when virus breaches epithelial/mucosal barriers. This may occur following exposure of EBOV to breaks in skin or to the mucosal epithelium. For YFV, this occurs via mosquito bite. Macrophages and dendritic cells are important early targets of infection. These cells not only support productive replication but can also traffic to local lymph nodes and to other tissues and organs, thereby promoting systemic dissemination. Infection of and damage to different organs promotes the indicated pathologic processes. Infection of macrophages also results in prolific production of

cytokines, commonly referred to as cytokine storm. This can promote vascular leakage and hypotension and can activate coagulation pathways that ultimately lead to disseminated intravascular coagulation. Also, cytokines likely contribute to apoptosis of lymphocytes. Infection of dendritic cells leads to a dysregulated phenotype where interferon (IFN) responses are suppressed and maturation of the dendritic cells is impaired. This likely inhibits activation of T cells, further preventing control of the infection.

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