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Novel Pharmacologic Approaches to the Management of Sepsis: Targeting the Host Inflammatory Response

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Abstract

Sepsis is currently the 10th leading cause of death overall and accounts for significant healthcare expenditures in the developed world. There are now more deaths attributable to sepsis than coronary artery disease, stroke, or cancer, and it is widely believed that the incidence of sepsis and sepsis-related mortality will continue to rise. Based on these sobering statistics, there is great interest in identifying novel treatments for managing critically ill children and adults with sepsis. Unfortunately, to date, there have been very few successful therapeutic agents employed in the clinical setting. Despite these disappointing results, new therapeutic agents continue to be identified, and there is reason for optimism and hope for the future. Herein, we will briefly review several novel therapeutic adjuncts for the management of critically ill patients with sepsis. We will largely focus on those therapies that directly target the host inflammatory response, specifically those that result in activation of the transcription factor, nuclear factor (NF)- κ B. We will also reference some of the patents recently filed that pertain to the host innate immune response and sepsis.

Keywords

Sepsis; Critical illness; Septic shock; Genomics; Gene polymorphisms; LPS; NF- κ B; Toll-like receptors; danger signals; heat shock proteins; inflammation; Pediatric; Adult

Introduction

The early recognition, diagnosis, and management of sepsis remains one of the greatest challenges in the field of critical care medicine today. Part of this challenge historically has been the lack of an adequate, standardized definition of sepsis, prompting an international panel of experts from the Society of Critical Care Medicine (SCCM) and the American College of Chest Physicians (ACCP) to propose the now familiar consensus definitions for the systemic inflammatory response syndrome (SIRS), sepsis, severe sepsis, and septic shock (Table 1) [1]. These definitions have been subsequently modified for use in critically ill children with sepsis (Table 2). However, these definitions are far from perfect [2–4], and as a result, several experts from SCCM and ACCP re-convened in December, 2001 and proposed a new staging system for sepsis [5]. The “PIRO” staging system for sepsis is modeled after the TNM (Tumor, Nodes, Metastasis) system [6] for staging malignancies and stratifies patients on the basis of

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their Predisposing conditions, the nature and extent of the insult (Infection), the nature and magnitude of the host Response, and the degree of concomitant Organ dysfunction. The PIRO staging system has many favorable attributes, but will require thorough validation and testing before it is widely adopted and applied in clinical practice [7].

According to the National Center for Health Statistics and the Centers for Disease Control and Prevention, sepsis was the 10th leading cause of death overall in 2004 [8]. Recent estimates suggest that there are between 77 to 240 new cases of sepsis per 100,000 population each year [9,10]. The incidence of sepsis is expected to further increase by 1.5% every year, resulting in an additional 1 million cases per year by 2020 [9,11,12]. Similarly, the incidence of sepsis and its complications continues to increase worldwide [10,13–18]. Sepsis accounts for nearly \$17 billion and €5.8–7.6 billion in annual health care expenditures in the U.S. and Europe, respectively [9,11,19]. Sepsis remains a significant health problem in children as well, accounting for nearly 4,500 deaths and close to \$2 billion per year in healthcare expenditures nationwide [20]. These statistics do not take into account the additional hidden costs attributed to the loss of productivity related to years of life lost for both critically ill children and adults who succumb to sepsis. Based on these sobering statistics, there is great interest in identifying novel treatments for managing critically ill children and adults with sepsis [21–23].

Unfortunately, promising therapies in pre-clinical models of sepsis have universally failed to live up to initial expectations in subsequent clinical trials in both critically ill adults [23–62] and children [24–26] (Table 3). In fact, to date there have been only three positive clinical trials in critically ill adults with sepsis – early goal-directed therapy (EGDT) [27], activated protein C (drotrecogin alfa, Xigris®, Eli Lilly and Co, Indianapolis, IN) [28], and afelimomab, a monoclonal antibody F(ab')₂ fragment directed against tumor necrosis factor (TNF)- α . [29]. EGDT, which emphasizes aggressive, early reversal of shock via titration of intravenous fluid therapy, optimization of cardiac output with inotropic support, and blood transfusion to predefined resuscitation endpoints (e.g., central venous pressure, blood pressure, and central venous oxygen saturation) was associated with a significant reduction in in-hospital mortality (46.5% vs. 30.5%, standard therapy vs. EGDT, respectively; $p=0.009$). Recent and controversial questions on the clinical design, research vigor, and conduct of this study have raised several concerns regarding the validity of these findings [30–34], and a five-year, multi-center, randomized trial of early, protocolized management of septic shock – Protocolized Care for Early Septic Shock (ProCESS) (ClinicalTrials.gov NCT00510835) with a planned enrollment of 1,935 patients recently started to further address these concerns. However, preliminary studies suggest that this therapy may be beneficial in selected groups of critically ill children with sepsis as well and provide further support for this type of management strategy in critically ill patients with sepsis [35,36].

The PROWESS study, a prospective, multi-center, randomized, placebo-controlled trial of activated protein C in 1,690 critically ill adults with severe sepsis was able to demonstrate an absolute reduction in mortality of 6.1% ($p=0.005$) [28]. However, a recent trial of aPC in critically ill children with sepsis was terminated prematurely following an interim analysis showing lack of therapeutic benefit and a trend toward increased complications in the group receiving aPC [37]. Moreover, due to persistent questions regarding the risk:benefit ratio of aPC in less critically ill patients, European pharmaceutical regulatory agencies have mandated an additional phase III clinical trial prior to approval of the drug for clinical use, which is currently in the final planning stages [23,38].

Finally, in the MONARCS study [29], 2,634 critically ill patients with severe sepsis were stratified by interleukin (IL)-6 levels into low- and high-risk groups. While the overall results of the trial were negative (35.9% versus 32.2% 28-day mortality in the placebo and afelimomab groups, respectively), there was a significant reduction in mortality in high-risk patients treated

with afelimomab (47.6% versus 43.6%, placebo vs. afelimomab, respectively; $p=0.041$). However, anti-TNF strategies in septic shock have not been adopted because of the inability to replicate the relatively small treatment effect demonstrated in the MONARCS study. Two additional therapies – adrenal corticosteroids [39,40] and intravenous immunoglobulin (IVIG) [41] have shown promise, though the results on mortality reduction have been inconsistent at best. The use of corticosteroids is discussed in greater detail below.

Herein, we will briefly review several novel therapeutic adjuncts for the management of critically ill patients with sepsis. We will largely focus on those therapies that directly target the host inflammatory response, specifically those that target the transcription factor, nuclear factor (NF)- κ B. The interested reader is also directed to several additional reviews of novel therapies directed at the coagulation cascade [42–44], apoptosis [45–49], oxidative stress [50–54], and nitric oxide [22,55–57]. Recent advances in antibiotic therapy, fluid resuscitation, and inotropic support will not be reviewed due to space limitations.

Pathophysiology of Sepsis

The pathophysiology of sepsis is inherently complex and will only be reviewed briefly here [58,59]. Traditionally, research efforts in the field of sepsis have largely focused on the innate immune system and conceptually viewed sepsis as a syndrome of *hyperinflammation*. Under this paradigm, overzealous activation of the host inflammatory response, ostensibly intended for pathogen eradication, becomes dysregulated and consequently causes auto-injury to the host, leading to multiple organ dysfunction syndrome (MODS) and death [60,61]. Many of the aforementioned studies (Table 3) were directed at this host inflammatory response, particularly the innate immune system, and were largely based upon pre-clinical data showing:

- i. Increased circulating levels of pro-inflammatory mediators in animals following infectious challenge with either LPS or live bacteria
- ii. Increased circulating levels of these same pro-inflammatory mediators in critically ill subjects with the sepsis syndrome
- iii. Recapitulation of the sepsis syndrome in animals or healthy humans following administration of these same pro-inflammatory mediators (e.g. TNF- α , IL-1 β , etc)
- iv. Improved survival following neutralization of these pro-inflammatory mediators in animal models of sepsis.

The astute reader will note that these are essentially Koch's postulates for determining causality for disease [62]. As an example of this kind of approach, several studies have shown that TNF- α levels are increased in both animals and humans with sepsis, TNF- α recapitulates the sepsis syndrome in both animals and healthy humans, and neutralization of TNF- α results in improved survival in several pre-clinical models of sepsis [63,64]. Based on these data, several so-called mediator-specific agents targeting TNF- α or other similar pro-inflammatory cytokines (e.g. IL-1 β) have been proposed and studied in critically ill patients with sepsis. For example, McKenna et al [65] recently filed a patent on the use of specific compounds that inhibit TNF- α . Unfortunately, as mentioned earlier, few, if any of these mediator-specific agents have been shown to improve outcome in subsequent prospective clinical trials [23,66], leading to speculation that the sepsis phenotype was more complex than originally believed.

A global view of the inherent complexity of the host inflammatory response has been provided by several genome-level expression studies using cDNA microarrays in various models of sepsis. For example, lipopolysaccharide (LPS) treatment results in the variable expression of 226 genes at 2 h in rats, many of which are involved in the acute phase response, inflammation, cell adhesion, and oxidative respiration [67]. Between 500–1,400 genes were differentially expressed at the 2 h time-point following either burn injury, trauma/hemorrhage, or LPS

administration in mice compared to sham animals. More importantly, thirteen of the differentially expressed genes were up- or down-regulated in common among all three models of injury, suggesting an early, highly conserved transcriptional response to injury and inflammation [68]. Low-dose LPS administration to healthy human volunteers resulted in the differential expression of over 1,500 genes, many of which are crucial to the host inflammatory response [69]. Based on these data, it would appear that the sepsis phenotype is inherently more complex than previously believed and provides further rationale to the reasons why clinical trials of therapeutic agents targeted against a single pathway or cytokine have been largely unsuccessful.

Our group recently reported the first genome-level expression data involving children with septic shock during the first 24 h after admission to the pediatric intensive care unit (PICU) [70]. A global view of the data reaffirmed, at a genomic level, that widespread regulation of inflammation- and innate immunity-related genes are fundamental components of septic shock. Perhaps the most intriguing finding generated from this initial study involves the large number of genes that were downregulated in this cohort of children with septic shock. Of interest, approximately 12% of the >1,000 gene probes that were significantly repressed in children with septic shock corresponded to functional annotations and gene ontology terms related to zinc and metal binding [70]. These data suggest that pediatric septic shock is characterized by large scale repression of genes that either depend on zinc homeostasis for normal function or directly participate in zinc homeostasis. In keeping with this assertion, functional validation data demonstrated that children with septic shock who died had significantly lower serum zinc levels compared to children with septic shock who survived [70].

A follow-up study focused on longitudinal expression profiles (i.e. over the initial 3 days of illness) [71]. This study again highlighted the ubiquitous regulation of inflammation- and innate immunity-related genes, and documented expression of genes corresponding to canonical signaling pathways and gene networks in a time-dependent manner. In addition, these longitudinal studies validated the previous observations regarding zinc-related biology and documented the persistence of this particular gene repression pattern during the initial three days of illness. The most intriguing data derived from these longitudinal studies involves the coordinated repression of genes corresponding to lymphocyte function [71]. A large number of genes that were repressed throughout the initial three days of illness corresponded to canonical signaling pathways and gene networks involving T cell receptor signaling, the antigen presentation pathway, and natural killer cell function. These data are consistent with persistent dysfunction of the adaptive immune system in children with septic shock and fit well with evolving paradigms in the field [61,72].

Consistent with these data, the currently available evidence supports the concept that sepsis results from a dysregulated host response, such that the balance between the pro-inflammatory mechanisms that are largely responsible for sepsis and the compensatory, anti-inflammatory mechanisms that counteract, “fine-tune”, and regulate these mechanisms largely determines the nature of the host response. There are two prevailing theories to explain this dysregulated response – namely, the serial theory and the parallel theory of sepsis [73] Fig (1). While it is recognized that these two theories may be overly simplistic, they adequately convey the concept that the sepsis phenotype is quite heterogeneous and that a “one-size fits all” approach to treatment is not likely to be successful. For example, a shift in the homeostatic balance to a predominantly anti-inflammatory phenotype leads to a state of relative immune suppression or *immunoparalysis*, resulting in an inability to clear the pathogen and hence, an increased risk of nosocomial infection [74,75]. These patients would benefit from therapies that are designed to augment or stimulate the host immune response, e.g. interferon- γ [76–78] and/or granulocyte-macrophage colony-stimulating factor (GM-CSF) [79–83]. Conversely, a shift in balance toward a predominantly pro-inflammatory phenotype results in further cellular injury,

multiple organ failure, and death. These patients, on the other hand, would benefit from therapies that are designed to suppress or attenuate the host immune response. It is the nature of the host response, then, that largely determines the type of therapy required – either stimulation or attenuation of the host response to infection [84,85].

An Individualized Approach to the Management of Sepsis

What then determines the nature of the host response to infection? Certainly, age (increased mortality at the extremes of age – both young and old) [11,20], gender (increased severity of illness and mortality in males compared to females) [86,87], nutritional status (increased morbidity and mortality with malnutrition or obesity) [88–91], and the presence or absence of co-morbid conditions (e.g., immunosuppression secondary to chemotherapy, solid organ transplantation, or bone marrow transplantation) [11,20] significantly impacts the host response to infection, but these factors clearly are not all that determines this response. Critical care physicians have all been frustrated by the common scenario in which two patients of similar age and having similar co-morbidities are treated in an identical manner, yet only one of the two patients survives, while the other patient progresses to multiple organ system failure and death. The answer to why the one patient survives and the other patient does not may be found in their genetic make-up. In other words, our genes may affect the way we respond to infection. While no clear “sepsis gene” has yet been identified, genetic factors undoubtedly play an important role in the pathophysiology of sepsis [92]. Perhaps the best evidence of the importance of genetics in determining the nature of the response to infection provided to date is the landmark study published by Sorensen and associates [93] in 1988. These investigators conducted a longitudinal cohort study involving over 900 adopted children born between 1924 and 1926. The adopted children and both their biologic and adoptive parents were followed until 1982. The death of a biologic parent before age 50 years resulted in a significantly increased risk of death in the adopted children (R.R. 1.71, 95% C.I. 1.14 to 2.57) for all causes. Of greater interest, if a biologic parent died of infection before the age of 50 years, the relative risk of death from infectious causes in the child was highly significant, with a relative risk of 5.81 (95% C.I. 2.47 to 13.7). In contrast, the death of an adoptive parent from infectious causes did not confer a greater risk of death in the adopted child.

A gene polymorphism is defined as the regular occurrence, in a population, of two or more alleles at a particular chromosome location. The most frequent type of gene polymorphism is called a single nucleotide polymorphism (SNP). A SNP is a substitution, deletion, or insertion of a single nucleotide that occurs in approximately 1 per every 200–300 base pairs of human DNA, which may or may not result in a biologically significant alteration in protein. It is believed that approximately 10% of all SNPs found in the human genome result in either a change in expression or function of a protein [94]. Pertinent to the present discussion, several SNPs in candidate proteins involved in the host immune response to sepsis have been described [84]. These SNPs may have a profound impact on the nature of the host response to infection and may determine the type of treatment that is necessary for a particular patient. Hopefully, further research in this area will lead to a more individualized approach to the management of critically ill patients with sepsis and septic shock, taking into account both the genetic make-up of the host, as well as the characteristics of the immune response, i.e. predominantly pro-inflammatory or predominantly anti-inflammatory. We believe that a strategy based upon “the right therapy, at the right time, in the right patient” will achieve the best possible outcome.

Why Previous Treatments Have Failed

Several experts have speculated on the reasons as to why the vast majority of therapeutic trials in sepsis have failed [23,95–97]. One commonly cited reason is the sheer complexity of the sepsis phenotype. How could a single therapeutic agent targeted at just one particular mediator

be expected to impact outcome when viewed in context of the fact that several hundred genes are differentially expressed in sepsis [68–71,98,99], many of which involved in redundant and overlapping pathways. Upon closer inspection, however, there appears to be some room for optimism. For most of the aforementioned studies, there is a consistent, albeit small, absolute reduction in mortality of about 2–4% Fig (2). Unfortunately, in most, if not all of these studies, this reduction in mortality is not statistically significant. A landmark study by Eichacker and colleagues [100] suggested that the efficacy of anti-inflammatory or mediator-directed therapeutic agents in critically ill patients with sepsis may depend to a greater extent on the individual's severity of illness. In other words, there may be some level of risk to these agents, such that the risk of harm is unacceptably increased in patients with a decreased severity of illness and correspondingly low risk of mortality. Conversely, if the severity of illness in a particular patient corresponds to a high risk of mortality, therapy directed at the host response may, in fact, be beneficial. Early studies using a human monoclonal antibody (HA-1A) directed against endotoxin [101], the p55 TNF receptor fusion protein (Ienercept) [102], and recombinant IL-1Ra [103] were able to demonstrate either a trend towards or statistically significant reduction in mortality when patients were stratified by severity of illness. This concept is further supported by the findings of the MONARCS study [29], in which mortality was significantly improved when afelimomab was administered to critically ill patients stratified to a high risk of mortality, defined as a serum IL-6 concentration above 1,000 pg/mL.

In further support of the above concept put forth by Eichacker and colleagues, our group recently measured serum levels of IL-8 in a cohort of critically ill children with septic shock [104]. A serum IL-8 \leq 220 pg/mL obtained within 24 h of admission to the pediatric intensive care unit (PICU) had a 95% negative predictive value for 28-day mortality. In other words, the vast majority of children with IL-8 levels less than 220 pg/mL will survive with conventional therapy alone. We suggest that a serum IL-8 level \leq 220 pg/mL could be used to exclude critically ill children with sepsis from interventional trials, as these children would be expected to survive with conventional therapy alone. A similar approach with IL-8 or other relevant biomarkers could be used in studies performed in critically ill adults with sepsis.

The Host Innate Immune Response

The host response to an infectious challenge may be broadly classified into the innate immune system and the acquired, or adaptive immune system. The innate immune system is the first line of defense against pathogens, while the adaptive immune system relies upon the proliferation of T and B lymphocytes specific to a particular pathogen. Importantly, the innate immune response is present prior to pathogen exposure and is generally not further enhanced by pathogen exposure. In contrast, the adaptive immune response is specifically stimulated by exposure to pathogens (and other foreign antigens), is highly pathogen-specific, and increases in magnitude, potency, and efficiency with repeated exposure to a given pathogen. Thus, whereas the innate immune response can be thought as a first line of relatively non-specific defense, the adaptive immune response can be thought of as a long term and highly specific mechanism of defense.

The innate immune response begins with the recognition of a repertoire of molecular motifs found on pathogens, known as pathogen-associated molecular patterns (PAMPs) by a surprisingly limited number of highly conserved pattern recognition receptors (PRRs). The family of PRR, which include the Toll-like receptors (TLRs) and nucleotide-binding oligomerization domain (NOD) receptors are crucial to the recognition of pathogens by the cells of the innate immune system. These PRR recognize both endogenous and exogenous “danger signals” [105], which include PAMPs such as lipopolysaccharide (LPS), lipoteichoic

acid, and peptidoglycan [106,107], as well as endogenous danger signals [108], including uric acid [109] and extracellular heat shock proteins [110].

At present, ten human TLRs have been identified [111–116]. These TLRs recognize a wide array of molecular patterns from bacteria, fungi, yeast, and viruses (Table 4) and undoubtedly play a major role in the pathophysiology of sepsis. The Toll-like receptors are members of the Toll/IL-1 receptor (TIR) superfamily of receptors (which include the Toll-like receptors, IL-1 receptor, and IL-18) which all share to the highly conserved TIR homology domain [117, 118]. The TIR domain is necessary for propagating the pro-inflammatory signal from the cell membrane to additional intracellular signaling domains via interaction with the TIR domain on other adaptor proteins. These adaptor proteins include, MyD88 (necessary for MyD88-dependent signaling in all TLR, with the exception of TLR-3), TIRAP/Mal (TLR-2 and TLR-4 signaling), TICAM-1 (TLR-3 and MyD88-independent TLR-4 signaling), and TRAM (MyD88-independent TLR-4 signaling) [108].

The signal transduction pathways that result in LPS-mediated pro-inflammatory gene expression are perhaps the best characterized of the innate immune response [119–121]. Recognition of LPS or endotoxin, a component of the outer cell membrane of gram-negative bacteria by TLR-4 results in a massive cytokine release responsible for most of the signs and symptoms of gram-negative septic shock. Conversely, mice that carry an inherited mutation in the TLR-4 receptor are resistant to these effects [122,123]. As mentioned briefly above, two major pathways of LPS signal transduction have been characterized – the MyD88-dependent pathway Fig (3) and the MyD88-independent pathway Fig (4). The MyD88-dependent pathway culminates in activation of the transcription factor, NF- κ B. While other transcription factors (e.g. activating protein-1, AP-1) are certainly involved in LPS-mediated pro-inflammatory signaling, NF- κ B appears to act as a master control switch for the activation of several pro-inflammatory genes that play a major pathophysiologic role in sepsis (Table 5) [124]. Conversely, the MyD88-independent pathway culminates in the activation of interferon (IFN)-inducible genes, such as IP10 and glucocorticoid-attenuated response gene 16 (GARG16) via the transcription factor, IFN regulatory factor 3 (IRF-3). The MyD88-independent activation also results in a delayed, late activation of NF- κ B-dependent pro-inflammatory gene expression.

NF- κ B belongs to the Rel family of transcription factors, which share common structural motifs for dimerization and DNA binding. Five known subunits belong to the mammalian NF- κ B/Rel family: c-Rel, NF- κ B1 (p50/p105), NF- κ B2 (p52/p100), rel A (p65), and rel B. “NF- κ B” consists of two such subunits arranged as either homodimers (e.g. p50/p50) or heterodimers (e.g. p65/p50). The most common form of activated NF- κ B consists of a p65 (Rel A) and p50 heterodimer [125–127]. Other subunit combinations, however, are known to exist and appear to have different DNA binding characteristics that can impart an additional level of gene regulation by the NF- κ B pathway [125].

NF- κ B is predominantly localized to the cytoplasm compartment of the cell in an inactive state, bound to a related inhibitory protein known as I κ B. Several forms of I κ B exist, all characterized by the presence of five to seven conserved domains known as ankyrin repeats. By way of these ankyrin repeats, I κ B physically masks the nuclear translocation sequence (NLS) of the p65 subunit of NF- κ B, though the NLS of the p50 subunit remains exposed. Nuclear export sequences on I κ B, coupled with the NLS on p50 lead to constant shuttling of the I κ B/NF- κ B complex between the nucleus and cytoplasm, although the localization of this complex under steady-state conditions appears to be predominantly in the cytoplasm [126,128]. The canonical pathway for activation of NF- κ B occurs when I κ B is phosphorylated by I κ B kinase (IKK). Activation of IKK occurs in response to a variety of proinflammatory signals such as LPS, TNF- α , interleukin-1 β , oxidants, bacteria, and viruses. Phosphorylated I κ B is targeted for rapid

ubiquitination, which results in degradation by the 26S proteasome. Degradation of I κ B unmask the NLS of NF- κ B, favoring nuclear localization of NF- κ B. Once in the nucleus, NF- κ B is free to direct the transcription of target genes [125,126].

Targeting the Host Innate Immune Response

Corticosteroids

As mentioned in the preceding paragraphs above, corticosteroids have been used in the management of critically ill patients with sepsis [129]. The approach until the early 1980's focused on administering very high, supraphysiologic doses of corticosteroids in an attempt to block the host inflammatory response – consistent with the prevailing theory of the pathophysiology of sepsis at the time (above). Unfortunately, large, multicenter, randomized, placebo-controlled trials failed to show any benefits to this practice [130,131]. Two subsequent meta-analyses [132,133] failed to demonstrate any benefit to high-dose corticosteroid administration in this patient population, and the practice was largely abandoned [134].

Recently, there has been a resurgence of interest in the use of corticosteroids in the management of critically ill patients with septic shock. Following the promising results of smaller studies that suggested a benefit to moderate-dose corticosteroids [135,136], Annane and co-workers [39] conducted a multicenter, randomized, placebo-controlled, double-blind trial comparing the use of stress-dose hydrocortisone (50 mg i.v. every 6 hours) and fludrocortisone (50 μ g once daily) or placebo in critically ill adults with septic shock and relative adrenal insufficiency (as determined by an inadequate response to ACTH). While the trial suffered from some methodologic concerns [129], there was a significant reduction in the duration of vasopressor therapy and 28-day mortality in patients with relative adrenal insufficiency who were randomized to the treatment group.

The results of the Corticosteroid Therapy of Septic Shock (CORTICUS) trial [40] were recently reported, in which hydrocortisone treatment shortened the duration of time to shock reversal in patients with an inadequate cortisol response to ACTH, as well as those patients who did respond with an adequate cortisol response to ACTH. However, there was no difference in 28-day mortality in either the responder group or non-responder group in patients randomized to hydrocortisone treatment versus placebo. Unfortunately, the trial was underpowered to detect a difference in mortality, as the trial was prematurely terminated after only 500 of the planned 800 subjects were enrolled due to slow enrollment. It appears then that the jury is still out on this type of therapy, and further studies are warranted.

Endogenous immunomodulatory and anti-microbial peptides

On-going translational research efforts are focused on the TLR-4 pathway, as well as additional [137–139] mammalian Toll-like receptor pathways and their activation by pathogen ligands in the hopes of identifying potential therapeutic targets for the treatment of sepsis. Several endogenous compounds that negatively modulate LPS-TLR-4 signal transduction exist and impart an additional level of regulation to pro-inflammatory gene expression (Table 6) [140–154]. These compounds would appear to be attractive therapeutic targets for critically ill patients with sepsis. In addition, there is growing interest in anti-microbial peptides, endogenous compounds such as lysozymes, lactoferrin, defensins, and cathelicidins that play a major role in innate immunity [155–157]. Similarly, anti-microbial peptides derived from amphibians have been tested in pre-clinical models and appear to directly inhibit the effects of LPS [158–160].

LPS, LBP, and sCD14

Several novel therapeutic agents directed at the LPS-TLR-4 signal transduction pathway have been tested in pre-clinical models of sepsis. One attractive strategy is to target the LPS molecule and neutralize it before it activates the host innate immune response [161,162]. For example, analogs of lipid-binding protein (LBP), which shuttles LPS to the TLR-4 complex, have been shown to block LPS-LBP interactions and effectively inhibit LPS-mediated pro-inflammatory gene expression [163]. Similarly, treatment with recombinant soluble CD14 (sCD14) improves outcome in a murine model of endotoxic shock [164], and a monoclonal antibody directed at CD14 (membrane-bound) has been tested in phase I clinical trials [165]. Leturcq et al recently filed a patent on the use of monoclonal antibodies directed against CD14 [166]. Recently, studies have shown that high-density lipoprotein (HDL) can act as a “sink” for LPS and prevent LPS-mediated pro-inflammatory gene expression both *in vitro* and *in vivo* [19,167]. HDL may have other immunomodulatory effects aside from direct LPS binding. Collectively, these studies have opened up an entire line of investigation into the role of lipoproteins and pharmacologic agents that target lipoproteins (e.g. HMG-CoA reductase inhibitors) in the management of patients with sepsis [167,168].

Endogenous danger signals

The fact that LPS is not readily measured or detectable in the majority of patients who present to the ICU with sepsis casts some doubt on therapeutic strategies targeting this molecule. In many cases, the early surge in pro-inflammatory cytokines has already abated by the time these critically ill patients are diagnosed with sepsis and treatment is initiated. However, as mentioned earlier, recent studies suggest that endogenous danger signals, including several members of the family of proteins known as heat shock proteins (Hsp10, Hsp60, Hsp72, and Hsp90) and high mobility group box-1 (HMGB-1), also activate the host innate immune response via TLR-4 [169,170]. HMGB-1 appears to be a relatively late mediator of sepsis and would appear to be an attractive therapeutic target [171,172].

Several clinical studies have recently been published in which extracellular heat shock proteins are directly targeted for therapy. For example, a human recombinant antibody directed against yeast-derived Hsp90 (Mycograb, Neutec-Pharma, Manchester, UK) derived [173] has been used to treat critically ill patients with invasive candidiasis [174,175]. In this study, recombinant antibody to Hsp90 plus lipid-associated amphotericin B produced significant clinical and culture-confirmed improvement in outcome for patients with invasive candidiasis. Phase I studies of 17-allylaminogeldanamycin (17-AAG), an inhibitor of tumor-derived Hsp90 have been recently completed in both children [176,177] and adults [178] with solid tumors. Chaperonin 10 (Hsp10) was recently used to treat 23 adults with moderate to severe active rheumatoid arthritis in a randomized, double-blind, multicenter clinical trial. Biweekly administration of chaperonin 10 was well tolerated and effective in reducing the symptoms of rheumatoid arthritis, at least in the short term [179]. DiaPep277, a peptide derived from Hsp60, has been found to slow the deterioration of beta-cell function after the clinical onset of diabetes in preclinical studies and several small clinical trials [180]. Collectively, these studies support the overall concept of targeting endogenous danger signals in critically ill patients with sepsis.

TLR-4

Given the importance of the TLR-4 in initiating and propagating the host innate immune response, there is growing interest in targeting TLR-4 and other Toll receptors in patients with sepsis. As an example, E5564 (Eritoran), a structural analog of the lipid A portion of the LPS molecule has been shown to inhibit TLR-4-mediated proinflammatory gene expression *in vitro* and *in vivo* [181–183]. A recent phase II trial of eritoran in patients undergoing cardiopulmonary bypass (CPB) did not appear to prevent the inflammatory response and attendant organ dysfunction and injury following CPB, though the drug was shown to be safe

and without overt toxicity [184]. Further studies will be required to establish both the safety and efficacy of this therapeutic approach in critically ill patients with severe sepsis and septic shock. To this end, a phase III, randomized, placebo-controlled trial of eritoran in critically ill adults with severe sepsis (ACCESS – “A controlled comparison of eritoran tetrasodium and placebo in patients with severe sepsis”) is currently enrolling patients with an estimated completion date of June, 2010 (NCT00334828). The future of this kind of therapeutic strategy, in which pharmacologic agents are directed at the TLR-4 receptor or other similar PRR will depend to a great extent on the success or failure of this trial.

NF- κ B

It is clear that the NF- κ B pathway is linked to the dysregulated inflammation that is characteristic of sepsis. Many of the genes that comprise the complex network contributing to this dysregulated inflammation, both on the pro-inflammatory and anti-inflammatory side, are regulated at the transcriptional level by NF- κ B [58,124,185,186]. The NF- κ B pathway would then appear to be a logical therapeutic target for the treatment of critically ill patients with sepsis [185]. Several compounds appear to inhibit NF- κ B *in vitro* and *in vivo* [185,187], most notably the salicylates, non-steroidal anti-inflammatory drugs (NSAIDs), corticosteroids, and anti-oxidants. In addition, several natural compounds, including curcumin [188,189], sesquiterpene lactones [190–192], and tea polyphenols [193], such as epigallocatechin-3-gallate (EGCG) [194–196] and theaflavin [197] have been shown to inhibit NF- κ B activation. However, several recent studies have led to questions surrounding this kind of therapeutic strategy [198]. For example, given its critical role in the innate and adaptive immune responses to infection, inhibition of NF- κ B may worsen pathogen clearance and increase the risk of mortality from overwhelming infection. Alternatively, NF- κ B plays an important anti-apoptotic role (see below) – inhibition may then have unintended and untoward effects on cell survival and function. Finally, other studies suggest that NF- κ B has a critical anti-inflammatory function in preventing an overwhelming host inflammatory response to infectious challenge [199–202]. Obviously, further studies, both in the pre-clinical and clinical setting will be necessary to further validate this therapeutic approach.

Current and Future Developments

While the majority of clinical studies of so-called mediator-directed therapy in critically ill patients with sepsis have been unsuccessful, there is continued optimism and support for this kind of therapeutic strategy. However, the “one size fits all” approach that has been utilized in the clinical design of these studies will not work in the future. We need to address the role of host factors, such as age, gender, presence of co-morbid conditions, and genetic predisposition in determining the individual response to therapy. When designing clinical trials, critically ill patients should be stratified according to severity of illness in order to maximize the signal-to-noise ratio of new therapeutic agents. Ideally, those patients who would generally survive with standard therapy alone should not be included in such studies [104]. Further, we need to recognize that immunomodulation as a therapeutic strategy encompasses both augmentation of the immune response in critically ill patients with the immunoparalysis phenotype, as well as suppression of the immune response in those patients with a predominantly pro-inflammatory phenotype. Ideally, new diagnostic tools and biomarkers will be developed, such that these two diametrically opposing phenotypes can be easily and quickly identified at the bedside. Finally, it is likely that one particular therapeutic agent directed against any one mediator is not likely to be successful. Given the inherent complexity and redundancy of the host inflammatory response, future management strategies will likely encompass the use of multiple, synergistic agents acting upon different steps in the mediator cascade [23,96]. Regardless of these challenges, this kind of management approach seems both reasonable and feasible

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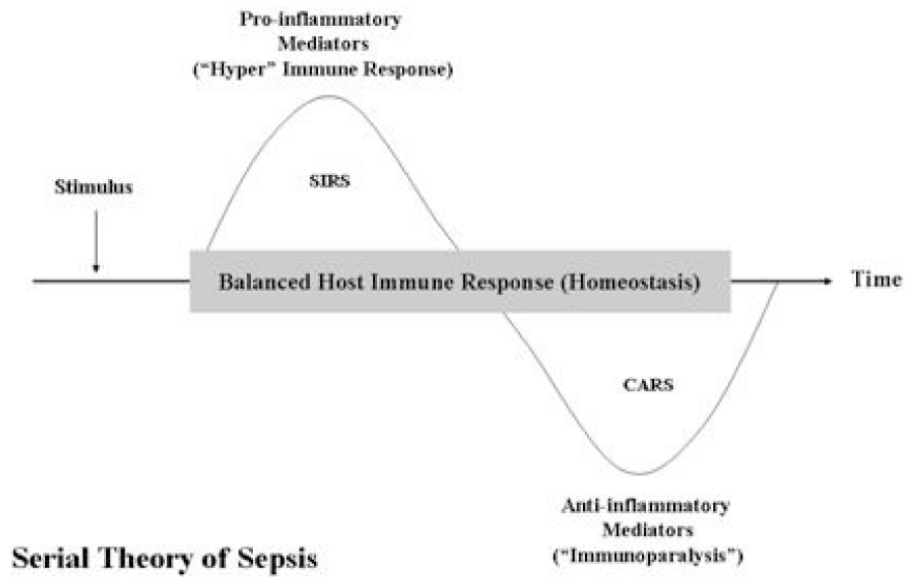
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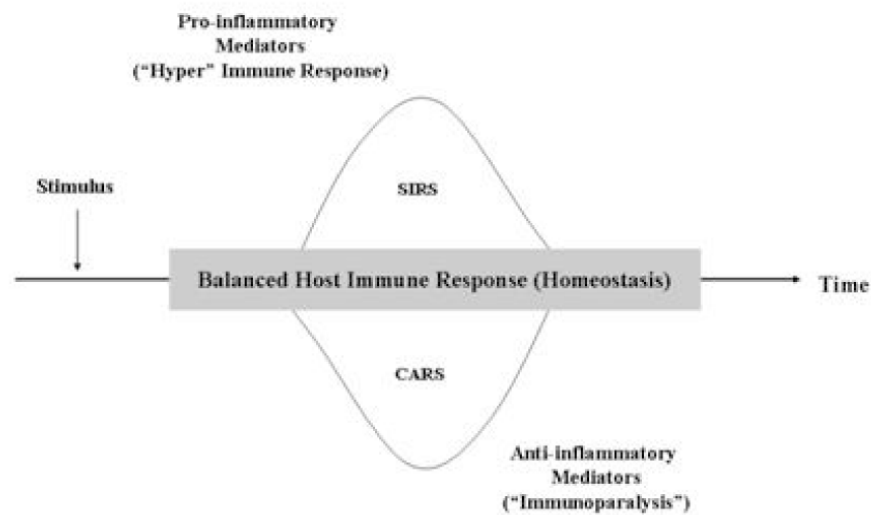
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Serial Theory of Sepsis



Parallel Theory of Sepsis

Figure 1. Current prevailing theories of the pathophysiology of sepsis. The serial theory of sepsis The initial response to an infectious (e.g. bacteria, virus, fungus) or non-infectious (e.g. acute pancreatitis, burns, trauma, etc) insult is characterized by a predominantly pro-inflammatory response (SIRS), which if severe enough leads to further cellular injury and subsequent organ dysfunction. This pro-inflammatory response is soon followed by a period of relative immune suppression or immunoparalysis (Compensatory Anti-inflammatory response syndrome, or CARS), characterized by the release of anti-inflammatory mediators. If severe, immunoparalysis leads to an increased risk of nosocomial infection (a “second hit”) and multiple organ dysfunction syndrome. **The parallel theory of sepsis.** The initial response to an infectious or non-infectious insult depends upon a multitude of factors and may lead to either

a balanced immune response, an overwhelmingly pro-inflammatory response (SIRS), or an overwhelmingly anti-inflammatory response (CARS). The nature of the host response is largely determined by the host's genetic background, gender, and the specific pathogen involved. Adapted from Ronco C, Tetta C, Mariano F, et al. Interpreting the mechanisms of continuous renal replacement therapy in sepsis: The peak concentration hypothesis. *Artif Organs* 2003; 27:792–801.

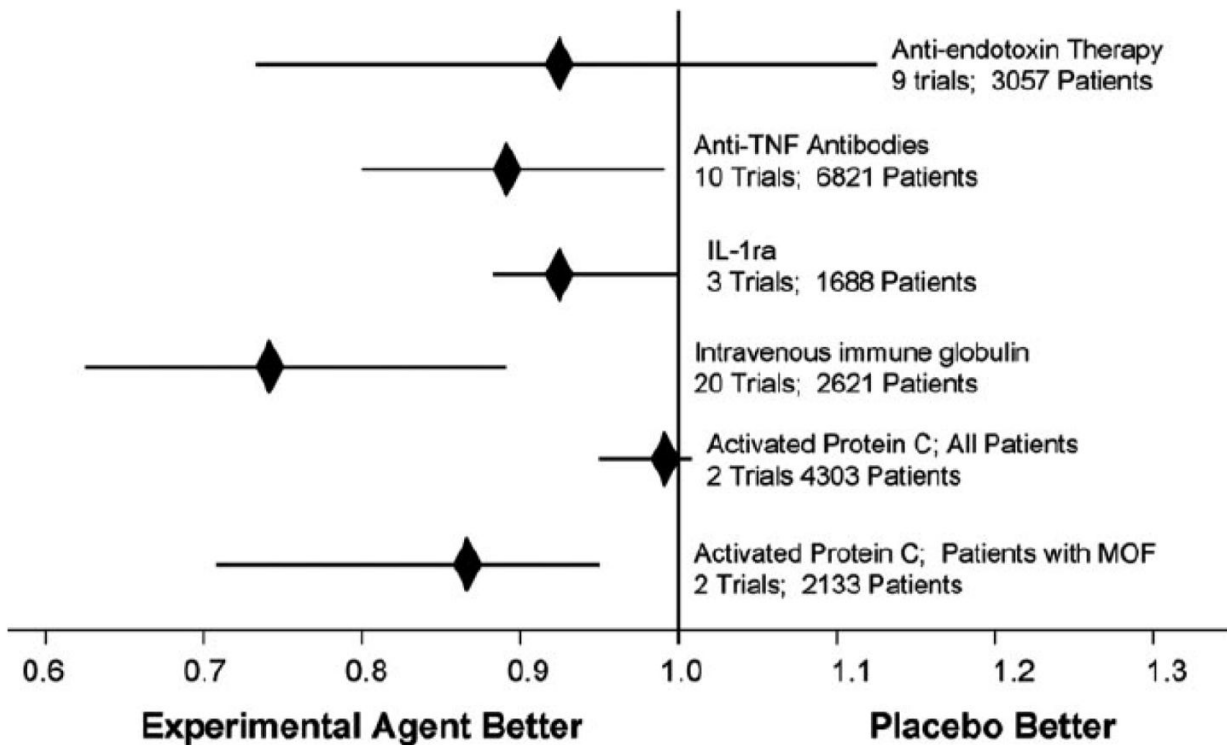


Figure 2. Pooling data from clinical trials of five different therapeutic strategies targeting microbial products or endogenous mediators of the host response reveal a consistent signal, suggesting clinical benefit. IL-1ra, IL-1R antagonist; MOF, multiple organ failure. Copied with permission from [23]

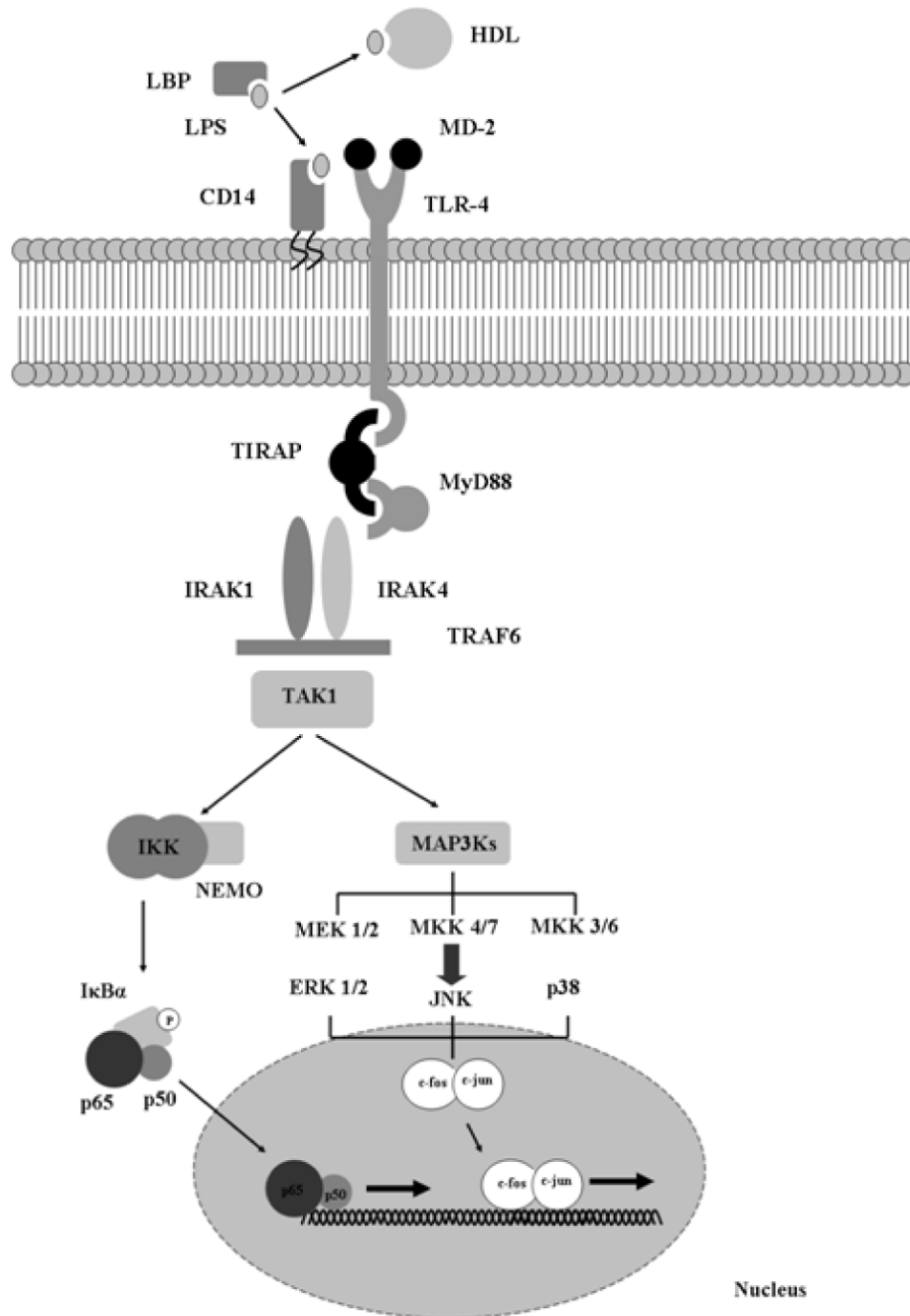


Figure 3. LPS signal transduction via the MyD88-dependent pathway.

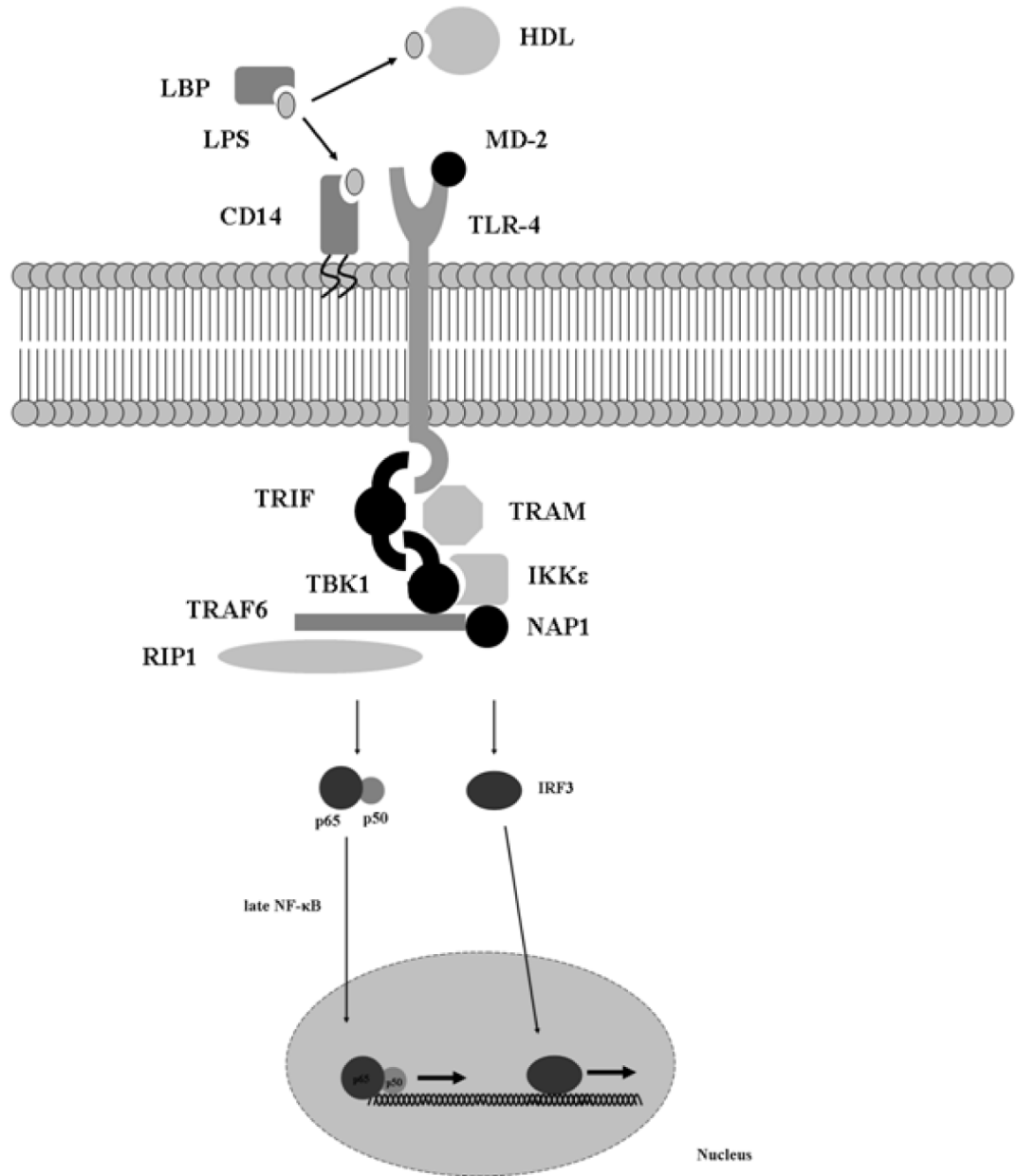


Figure 4.
LPS signal transduction via the MyD88-independent pathway.

Table 1
American College of Physicians (ACCP)/Society of Critical Care Medicine (SCCM) Consensus Definitions for SIRS, Infection, Sepsis, Severe Sepsis, and Septic Shock

Systemic Inflammatory Response Syndrome (SIRS)

The presence of at least two of the following four criteria, one of which must be abnormal temperature or leukocyte count:

- Core temperature > 38°C or <36°C (by rectal, bladder, oral or central catheter probe)
- Tachycardia, defined as heart rate > 90/min
- Tachypnea, defined as respiratory rate > 20/min or PaCO₂ < 32 mm Hg
- White blood cell count > 12,000 cells/μL or < 4,000 cells/μL

Infection

A suspected or proven (i.e. by positive culture, tissue stain, polymerase chain reaction, etc) infection caused by any pathogen OR a clinical syndrome associated with a high probability of infection (e.g. presence of white blood cells in a normally sterile body fluid, chest radiograph consistent with pneumonia, petechial or purpuric rash, etc)

Sepsis

SIRS + Infection

Severe Sepsis (Sepsis with Organ Dysfunction)

Sepsis plus either cardiovascular dysfunction or acute respiratory distress syndrome (ARDS) OR two or more other organ dysfunctions

Septic Shock

Severe Sepsis with arterial hypotension defined by a systolic blood pressure below 90 mm Hg, mean arterial pressure (MAP) < 60 mm Hg, or a reduction in systolic blood pressure >40 mm Hg from baseline, despite adequate volume resuscitation and in the absence of other causes for hypotension.

Adapted from [1]

Table 2
 Consensus Definitions for Pediatric SIRS, Infection, Sepsis, Severe Sepsis, and Septic Shock

Systemic Inflammatory Response Syndrome (SIRS)

The presence of at least two of the following four criteria, one of which must be abnormal temperature or leukocyte count:

- Core temperature > 38.5°C or <36°C (by rectal, bladder, oral or central catheter probe)
- Tachycardia, defined as mean heart rate >2 SD for age (in the absence pain, fever, drug therapy, etc) or otherwise persistent elevation over a 0.5–4 hour time period OR for children < 1 year of age: Bradycardia, defined as mean heart rate < 10th percentile for age (in the absence of drug therapy or presence of congenital heart disease) or otherwise persistent depression over a 0.5 hour time period
- Mean respiratory rate >2 SD above normal for age or mechanical ventilation (not for underlying neuromuscular disease or receipt of general anesthesia)
- Leukocyte count elevated or depressed for age (not due to chemotherapy-induced leucopenia) or >10% immature neutrophils

Infection

A suspected or proven (i.e. by positive culture, tissue stain, polymerase chain reaction, etc) infection caused by any pathogen OR a clinical syndrome associated with a high probability of infection (e.g. presence of white blood cells in a normally sterile body fluid, chest radiograph consistent with pneumonia, petechial or purpuric rash, etc)

Sepsis

SIRS + Infection

Severe Sepsis

Sepsis plus either cardiovascular dysfunction or acute respiratory distress syndrome (ARDS) OR two or more other organ dysfunctions (see Table 2)

Septic Shock

Sepsis and cardiovascular organ dysfunction

Adapted from Goldstein B, Giroir B, Randolph A, and the Members of the International Consensus Conference on Pediatric Sepsis. International pediatric sepsis consensus conference: Definitions for sepsis and organ dysfunction in pediatrics. *Pediatr Crit Care Med* 2005; 6:2–8.

Table 3
The “dustpile of failed sepsis trials”

anti-TNF monoclonal antibody (MAb) clinical trials [203,204]
NORAEPT I
NORASEPT II
INTERSEPT
p55 tumor necrosis factor receptor fusion protein [102,205–207]
Fc portion of IgG1 (TNFR:Fc) [205]
anti-TNF antibody fragment [208]
MAK 195F
anti-endotoxin MAb clinical trials [24,101,209–217]
HA-1A
E5
recombinant human interleukin-1 receptor antagonist [103,218]
NOS inhibitor 546C88 [219]
pentoxifylline [220]
Anti-thrombin III [221–228]
Tissue factor pathway inhibitor (TFPI) [229,230]
platelet-activating factor acetylhydrolase (PAF-AH) [231,232]
group IIA secretory phospholipase A [233]
Bactericidal/permeability-increasing protein (BPI) [25,26]
Ibuprofen [234,235]

Table 4

Toll-like receptors and their agonists

TOLL-LIKE RECEPTOR	LIGAND
TLR1	Triacyl lipopeptides (Bacteria)
TLR2	Peptidoglycan (Gram-positive bacteria) Lipoteichoic acid (Gram-positive bacteria) Lipopolysaccharide (<i>Leptospira interrogans</i>) Lipopolysaccharide (<i>Porphyromonas gingivalis</i>) Zymosan (Fungi) Heat shock protein (Hsp) 70 (Host origin)*
TLR3	Double-stranded RNA (Viruses)
TLR4	Lipopolysaccharide (Gram-negative bacteria) Taxol (Plants) Fusion protein (Respiratory syncytial virus) HMGB-1 (Host origin) Hsp 60 (<i>Chlamydia pneumoniae</i>)* Hsp70 (Host origin)* Hyaluronic acid (Host origin) Fibrinogen (Host origin) Fibronectin A domain (Host origin)
TLR5	Flagellin (Bacteria)
TLR6	Diacyl lipopeptides (<i>Mycoplasma</i>) Lipoteichoic acid (Gram-positive bacteria) Zymosan (Fungi)
TLR7	Imidazoquinoline (Synthetic compound) Single-stranded RNA (Viruses)
TLR8	Imidazoquinoline (Synthetic compound) Single-stranded RNA (Viruses)
TLR9	CpG-containing DNA (Bacteria and viruses)
TLR10	?

* Some of the reported effects of extracellular heat shock proteins may be due to endotoxin contamination of these recombinant proteins.

Table 5
Genes regulated by the transcription factor, NF- κ B

Cytokines and Chemokines

Tumor necrosis factor- α
Interleukins-1, -2, -3, -6, -8, and -12
RANTES
Eotaxin
Gro- α , - β , and - γ
Macrophage inhibitory protein 1 α (MIP-1 α)
Macrophage chemotactic protein 1 (MCP-1)

Cell Adhesion Molecules

Intracellular adhesion molecule 1 (ICAM-1)
Vascular cell adhesion molecule 1 (VCAM-1)
E-selectin

Growth Factors

Granulocyte-macrophage colony-stimulating factor (GM-CSF)
Granulocyte colony-stimulating factor (G-CSF)
Macrophage colony-stimulating factor (M-CSF)

Miscellaneous

Inducible Nitric oxide synthase
C reactive protein (CRP)
5-lipoxygenase
Inducible cyclo-oxygenase 2

Table 6

Selected endogenous modulators of the host innate immune response

MODULATOR	SITE OF ACTION	MECHANISM OF ACTION
sTLR-4 [142]	Extracellular	“sink” for LPS
sST2 [143]	Extracellular	? ↓ TLR-4 expression
sCD14 [144,164]	Extracellular	“sink” for LPS
RP105 [145]	Membrane	TLR-4 homolog
SIGIRR [146,147]	Membrane	Inhibition of MyD88, IRAK, TRAF6
TRAIL-R [148]	Membrane	Stabilization of I κ B α
A20 [137,149]	Intracellular	Removes ubiquitin from TRAF6
ABIN-3 [138]	Intracellular	Inhibition of NF- κ B
ATF-3 [139,150]	Intracellular	Alters chromatin structure
β -arrestin [141,151]	Intracellular	Inhibition of TRAF6
Dok-1/Dok-2 [152]	Intracellular	Inhibition of ERK
IRAK-M [153]	Intracellular	Inhibition of IRAK-4/IRAK-1
Monarch-1 [154]	Intracellular	Inhibition of IRAK-4/IRAK-1
MyD88s [140]	Intracellular	Inhibition of IRAK-4/IRAK-1

sTLR-4, soluble Toll-like receptor-4; sST2, ; sCD14, soluble CD14; SIGIRR, single Ig IL-1 receptor-related molecule; TRAIL-R, TRAIL receptor, ABIN-3, A20-binding inhibitor of NF- κ B activation; ATF-3, activating transcription factor-3; Dok-1/2, downstream of tyrosine kinase-1/2; IRAK, IL-1R-associated kinase