

Tissue Damage Control in Disease Tolerance

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ABSTRACT

Immune driven resistance mechanisms are the prevailing host defense strategy against infection. In contrast, disease tolerance mechanisms limit disease severity by preventing tissue damage or ameliorating tissue function without interfering with pathogen load. Here we propose that tissue damage control underlies many of the protective effects of disease tolerance. We explore the mechanisms of cellular adaptation that underlie tissue damage control in response to infection as well as sterile inflammation, integrating both stress and damage responses. Finally, we discuss the potential impact of targeting these mechanisms in the treatment of disease.

INTRODUCTION

Immunity refers to the inherent ability of any given organism to protect itself from disease and more specifically from infectious diseases. The immune system is part of an evolutionarily conserved host defense strategy against infection that recognizes, destroys and/or expels invading pathogens. Host resistance to infection refers to this immune-driven defense strategy, which carries a negative impact on pathogens. This is distinct from antimicrobial resistance, which refers to the pathogen's capacity to evolve towards becoming refractory to the detrimental effects imposed by host resistance mechanisms or by antimicrobial agents.

It is widely accepted that immune-driven resistance mechanisms are the prevailing, if not the only, host defense strategy against infections. This notion is strongly supported by the overwhelming success of medical interventions targeting resistance mechanisms, in terms of reducing the global burden imposed by infectious diseases on mankind¹. This is illustrated by vaccination, where pre-emptive induction of immune-driven host resistance mechanisms provides robust and often long-lasting protection against

infectious diseases. Another related and highly successful therapeutic approach consists in the use of antimicrobial drugs, e.g. antibiotics, which can be perceived as providing pharmacologic-driven resistance as the means to limit the severity of infectious diseases.

In some instances however, immune- and/or pharmacologic-driven resistance mechanisms are not sufficient *per se* to prevent morbidity and/or mortality associated with infectious diseases, regardless of their capacity to exert a negative impact on pathogens. Moreover, microorganisms can evolve resistance mechanisms against host immunity² as well as against antimicrobial drugs and produce compounds³ that increase their virulence². These factors may in part explain why in some cases therapeutic approaches targeting resistance mechanisms fail to overcome the morbidity and mortality of infectious diseases such as: i) severe forms of malaria associated with *Plasmodium* infection, i.e. 600,000 deaths/year⁴, ii) severe sepsis associated with polymicrobial infections, i.e. 750,000 cases/year in the US alone⁵ or iii) respiratory infections such as pneumonia, associated with *influenza* virus infections, i.e. 500,000 deaths/year⁶, among others. We will argue that in these and probably other cases, a second host defense strategy may play a major role in limiting disease severity, namely, disease tolerance⁷⁻⁹.

Immune-driven resistance mechanisms likely co-evolved with disease tolerance mechanisms as genetically distinct defense strategies required to limit the severity of infectious diseases. In contrast to host resistance, disease tolerance mechanisms limit disease severity without affecting the host's pathogen load⁷⁻⁹, by protecting the infected host from tissue damage ([Box 1&2](#)). Here we propose that tissue damage control is a prevailing mechanism underlying the protective effects of disease tolerance. We explore the mechanisms underlying tissue damage control, and discuss the potential impact of targeting such mechanisms in the treatment of infectious diseases and possibly other immune mediated inflammatory conditions as well.

TISSUE DAMAGE CONTROL AND DISEASE TOLERANCE

We will refer to cells and/or soluble molecules contributing to host resistance mechanisms as the host's immune system ([Fig.1](#)). Cells and/or soluble molecules involved in maintaining the integrity of epithelial barriers have a dual protective effect against pathogens, i.e. to provide a physical barrier that prevents pathogen systemic access and to modulate microbial communities at the epithelial interface via the

production of anti-microbial peptides, among other molecules¹⁰ (*Fig. 1*). All other host cells and/or soluble molecules that do not exert a negative impact on pathogens will be referred hereby as the host's parenchyma (*Fig. 1*). While parenchyma cells, tissues and organs do not contribute directly to resistance mechanisms, they are a critical component in maintenance of homeostasis, i.e. health^{11,12}. Thus, impaired parenchyma function likely underlies the disruption of homeostasis associated with the pathogenesis of infectious diseases.

The host's immune system drives resistance to infection via a series of mechanisms that rely initially on pathogen sensing via cognate binding of pathogen associated molecular patterns (PAMP) by host pattern recognition receptors (PRR)¹³. In addition, other classes of sensors may recognize molecular patterns associated with pathogen's effector activities rather than the pathogen itself, i.e. the guard hypothesis¹⁴ (*Fig. 1*). This hypothesis was raised initially in the context of host-pathogen interactions in plants, in which resistance genes were found to protect the infected host from disease caused by virulence genes encoded by pathogens. The initial assumption was that the products of resistance genes would interact directly and neutralize virulence factors. It became apparent however, that resistance genes also act as a PRR, recognizing virulence factors and activating immune-driven resistance mechanisms^{14,15}. An alternative explanation, i.e. the guard hypothesis, proposes that the products of host resistance genes interact physically with host proteins, once these are targeted by virulence factors^{14,15}. This hypothesis is supported by the finding that host resistance genes encode a family of proteins containing leucine-rich repeats (LRR), which are typically involved in protein-protein interactions. Moreover, these were shown to interact physically with host proteins modified posttranslationally by virulence factors to prevent disease severity^{14,15}. The evolutionary conserved nature of these resistance genes suggests that a similar defense mechanism may be operational in animals^{14,16}

Pathogen sensors are essential to activate innate and adaptive immune responses^{17,18}, driving the effector phase of host resistance to infection¹³. Host resistance mechanisms act in a pathogen-class specific manner destroying certain classes of pathogens, i.e. bacteria, viruses, fungi and protozoan parasites while expelling others, i.e. helminthes.

Pathogens also express toxins that can elicit varying levels of stress and dysfunction to host cells, tissues and organs, eventually leading to programmed cell death, tissue damage and organ dysfunction. These include pore-forming toxins that can compromise

the integrity of plasma membranes as well as intracellular membranes, disrupting cellular homeostasis¹⁹. Toxins and other virulence factors are perceived as a central mechanism of pathogenicity associated with infectious diseases (*Fig. 1*). This pathogenic effect is countered essentially via host resistance mechanisms that reduce pathogen load and limit the damaging effects of the associated toxins and virulence factors (*Fig. 1*). However, resistance mechanisms *per se* can impose varying levels of stress, dysfunction and eventually damage to the host parenchyma. This phenomenon referred as immunopathology, plays a central role in the pathogenesis of many infectious diseases (*Fig. 1*)⁷⁻⁹. Of note, not all resistance mechanisms are potentially damaging to the host, with some having low if any associated toxicity, e.g. anti-microbial peptides, while others are potentially highly damaging, e.g. hypochlorous acid produced by activated polymorphonuclear (PMN) cells.

Depending on the extent of damage imposed to host cells and tissues by microbial toxins and/or host resistance mechanisms, desequstration of intracellular damage-associated molecular patterns, e.g. heat shock proteins (HSP), adenosine triphosphate (ATP), high mobility group box 1 protein (HMGB1), mitochondrial DNA, hemoglobin or heme, can occur and engage host PRR²⁰. This phenomenon, referred as sterile inflammation can reinforce resistance mechanisms but also immunopathology^{20,21}.

While host resistance mechanisms are central to clear invading pathogens, controlling the severity of infectious diseases requires an additional host defense strategy that limits the extent of tissue damage imposed during infection, a protective mechanism referred as disease tolerance (*Box 1&2; Fig. 1*)⁷⁻⁹. This requirement for a tight coupling of host resistance mechanisms to an additional protective strategy enforcing disease tolerance is well illustrated for the regulation of host iron metabolism during infection (*Box 3*). It is worth noting that disease tolerance describes a biological phenomenon quite distinct from immunological tolerance, which has as a hallmark the protection of self tissues from immune attack. While the two may be linked functionally, for example in their ability to limit tissue damage, they act via distinct effector mechanisms.

We posit that disease tolerance relies on a number of cellular and systemic adaptive responses that protect host parenchyma tissues from stress, dysfunction and/or damage, and will refer to these protective mechanisms as tissue damage control (*Fig. 1*). In contrast to host resistance mechanisms, tissue damage control limits host disease severity without interfering with pathogen load (*Fig. 1*)⁷⁻⁹. This countervailing protective

response should be required to limit the pathogenic effect associated not only with toxins expressed by pathogens but also with some potentially damaging host resistance mechanisms. Thus, tissue damage control acts as an inherent component of host defense against infection, required to decouple potentially deleterious immune-driven resistance mechanisms from disease severity.

One should consider that when tissue damage control mechanisms operate on cells of the host immune system, these can act in an immunoregulatory manner^{22,23} that impacts on host resistance mechanisms (*Fig. 1*)²⁴. Moreover, when exerted in epithelial cells, tissue damage control should enforce barrier function and thus prevent pathogen access to host tissues (*Fig. 1*)¹⁰. This is in keeping with the notion that tissue damage control is an integral component of host defense mechanisms against infection, which regulates not only disease tolerance but also resistance and barrier function mechanisms when acting on parenchyma, immune cells or barrier epithelial cells, respectively.

Tissue damage control can be enforced via different mechanisms including: i) neutralization of toxins and other virulence factors, ii) immunoregulatory mechanisms limiting the damaging effects of host resistance mechanisms and/or iii) cellular and systemic adaptive responses limiting the deleterious effects associated with different forms of stress and damage imposed by pathogens and/or host resistance mechanisms (*Fig. 1*). Failure of any of these regulatory mechanisms to prevent tissue damage is expected to exacerbate stress, dysfunction and/or tissue damage and as such the severity of infectious diseases, presumably without interfering with pathogen load (*Fig. 1*). We will focus in the next sections on the molecular basis of cellular and systemic adaptive responses limiting tissue damage imposed during infection, i.e. tissue damage control.

ADAPTIVE RESPONSES UNDERLYING TISSUE DAMAGE CONTROL

Tissue damage control is regulated by a number of evolutionary conserved adaptive responses acting in a cell autonomous and systemic level to preserve the functional integrity of the host tissues^{7,25}. We will discriminate two types of adaptive responses, namely stress-responses and damage-responses. This distinction is based on two criteria: 1) the sensors used to activate the corresponding adaptive responses, and 2) their biologic outputs. Stress-responses are triggered by sensors that respond to environmental cues such as those related to variations of oxygen tension, redox status,

osmolarity, metabolite concentration, toxins, etc (*Fig.2*). Stress-sensors and the ensuing responses can in principle be triggered in the absence of cellular damage. These aim essentially at maintaining cellular function, while preventing different forms of stress from causing cellular damage. This occurs via activation of specific stress-responsive programs, which provide metabolic adaptation to the environmental changes driving different forms of stress while reducing, whenever possible, those forms of stress. Damage-responses on the other hand are triggered by sensors that respond to different forms of cellular damage. These include damage to macromolecules, i.e. DNA, proteins or lipids and to organelles, i.e. mitochondria, endoplasmic reticulum (ER), Golgi apparatus or lysosomes. Damage-sensors and their issuing responses are triggered in the context of cellular stress - the underlying cause of damage - but in contrast to stress-responses, they aim essentially at maintaining cellular function and repairing ongoing macromolecular and/or organelle damage.

Assuming that different classes of pathogens, i.e. viruses, fungi, bacteria, protozoan and eukaryotic parasites, might elicit distinct forms of stress and damage, the sensors for those forms of stress and damage and their corresponding responses should report on those classes of pathogens, a concept originally proposed by Ruslan Medzhitov in discussions at scientific conferences. This suggests as well that stress- and damage-responses are functionally integrated within inflammatory responses, likely fine-tuning host immunity to specific classes of pathogens¹². In keeping with this notion, signal transduction pathways triggered by PRR or associated with immunoregulatory mechanisms exerted by specific immune cell types and/or involving interleukins can modulate different stress- and damage-responses, and *vice versa* and as such regulate tissue damage control and disease tolerance. While this added level of complexity should not be ignored, here we focus instead on the mechanisms through which tissue damage control impacts on defense against disease.

STRESS-RESPONSES AND TISSUE DAMAGE CONTROL

Stress-responses emerged at an early stage of evolution as the means to provide ancestral forms of life with the possibility of adaptation to environmental changes²⁵⁻²⁷. In general, such environmental changes are related to essential components of homeostasis, such as i) oxygen tension ii) cellular redox iii) osmolarity and iv) glucose or ATP/ADP cellular concentrations, disturbance of which leads to, respectively, hyperoxia or hypoxia, oxidative stress, osmotic stress and metabolic stress (*Fig.2*).

The common outcome of stress-responses is metabolic adaptation, which enables the maintenance of cellular, tissue and organ function under different forms of stress²⁵. Metabolic adaptation aims at preserving core cellular functions at the expense of accessory ones, while minimizing macromolecular and organelle damage²⁵⁻²⁷. This is achieved via the expression of a number of immediate-early responsive genes coupled to broad inhibition of protein synthesis²⁸, repressing non-essential gene functions²⁹. An illustrative rather than comprehensive overview of different stress-responses potentially regulating tissue damage control is provided in [Fig.3](#).

Systemic spreading of pathogens from the initial site of infection is countered by an immediate host response characterized by the activation of the clotting cascade associated with platelet activation/aggregation and recruitment of activated PMN and monocyte/macrophages (M ϕ). One of the “trade offs” of this defense strategy is local deregulation of microvascular circulation, eventually leading to hypoxia, which depending on the tissue can have more or less severe pathologic consequences⁷. Hypoxia triggers an evolutionarily conserved stress-response regulated by the transcription factor hypoxia-inducible factor 1 alpha (HIF-1 α)([Fig.3](#))³⁰. When activated in immune cells, HIF-1 α can promote resistance to infection (reviewed in^{32,33}). In some instances, activation of HIF-1 α in immune cells can compromise disease tolerance, as suggested by the observation that HIF-1 α deletion in myeloid cells exacerbates lethality from endotoxic shock in mice³¹. Whether adaptive responses to hypoxia in parenchyma tissues, such as orchestrated by HIF-1 α , promote tissue damage control and disease tolerance remains to be tested.

Resistance mechanisms often rely on targeting pathogens for oxidative damage via PMN cell and M ϕ activation³⁴. The “trade-off” of this defense strategy includes oxidative stress imposed on host tissues, possibly leading to tissue damage, organ dysfunction and disease. This is likely counteracted by an adaptive cellular response regulated by the evolutionarily conserved transcription factor nuclear factor-erythroid 2-related factor 2 (NRF2)^{35,36}. Activation of NRF2 provides tissue damage control and disease tolerance to malaria caused by *Plasmodium* infection^{37,38} and presumably to sepsis caused by polymicrobial infections in mice³⁹. When activated in cellular components of host immunity, NRF2 modulates resistance to infection, as demonstrated for *Salmonella* infection in mice⁴⁰ ([Box.3](#)).

Some forms of stress associated with infection can decrease mitochondrial ATP output, reducing cellular ATP availability. This is sensed by the infected host via the

evolutionarily conserved AMP-activated protein kinase (AMPK), which adjusts cellular metabolism to available energy (*Fig.3*)⁴¹. While it is likely that when activated in the host parenchyma this adaptive response should confer some level of tissue damage control and disease tolerance, this remains to be established. Expression of AMPK in immune cells exerts immunoregulatory effects that modulate resistance mechanisms^{22,23}.

Infection is often associated with local or systemic “growth factor” deprivation, whether associated or not to oxidative and metabolic stress. This is sensed by the infected host via activation of the evolutionarily conserved Forkhead box O (FOXO) family of transcription factors⁴² (*Fig.3*). Activation of FOXO during *Mycobacterium* infection in flies is essential to provide metabolic adaptation, e.g. regulation of glycogen and triglyceride synthesis, and to limit host disease severity, irrespectively of pathogen load⁴³. Thus, FOXO regulates a stress-responsive program that confers disease tolerance to infection in flies⁸. Whether the same is true in mammals remains to be tested. Moreover, when activated in cellular components of the host immune system, FOXO family members also exert immunoregulatory effects that can impact on resistance mechanisms^{22,23}.

Maintenance of cellular osmolarity is a central component of homeostasis and perturbations of osmolarity associated with systemic infections are probably sensed and counteracted by osmoregulatory stress-responses, which provide systemic as well cellular adaptation to higher or lower than physiologic osmolarity^{44,45} (*Fig.3*). These stress-responses can act both systemically and in a cell autonomous manner^{44,45}, presumably contributing to tissue damage control and disease tolerance, although this remains to be established.

Another stress-response possibly regulating disease tolerance relies on the recognition of exogenous and/or endogenous ligands by the evolutionary conserved ligand-activated transcription factor aryl hydrocarbon receptor (AhR), best known for its involvement in orchestrating a stress-response to xenobiotics⁴⁶. Several studies have shown that activation of this stress-response acts in an immunoregulatory manner that maintains barrier tissue function and limits the pathogenesis of immune mediated inflammatory conditions (*reviewed in*⁴⁷). A recent study, published while this review was in preparation, proposes that activation of AhR by L-kynurenine, an endogenous intermediate product of the host tryptophan catabolism, confers disease tolerance to bacterial infections⁴⁸.

Microbial toxins, such as bacterial pore forming toxins¹⁹, are another form of stress,

sensed via several host stress sensors including those belonging to the Nod like receptor protein (NLRP) family^{19,49}. Activation of NLRP3 by pore forming toxins triggers interleukin (IL)-1 β secretion, a pro-inflammatory cytokine that activates the stress-responsive p38 MAPK and the c-Jun N-terminal kinase (JNK) signal transduction pathways, which are protective against pore forming toxins⁵⁰. Presumably, osmoregulatory stress-responses are also involved in adaptive responses to pore forming toxins, given that these can disrupt cellular osmolarity⁵⁰.

In some cases stress-responses are maladaptive, that is, they fail *per se* to provide sufficient level of metabolic adaptation to different forms of stress, allowing therefore the accumulation of macromolecular and organelle damage in cells. This is sensed and countered by damage-responses (*Fig.2*).

DAMAGE-RESPONSES AND TISSUE DAMAGE CONTROL

Cells have distinct sensors that trigger specific damage-responses associated with different types of cellular damage. These share as a common biologic output repair of macromolecular and/or organelle damage, aiming at maintenance of cellular function within the boundaries of essential outputs and at the expense of accessory ones. An illustrative rather than comprehensive overview of damage-responses possibly involved in tissue damage control is provided (*Fig.4*).

Accumulation of misfolded proteins is a form of macromolecular damage associated with different forms of stress⁵¹. When misfolded proteins accumulate in the cytosol or in the ER these trigger two distinct damage-responses, namely the heat shock response^{52,53} and the unfolded protein response (UPR)^{51,54,55}, respectively (*Fig.4*). The hallmarks of these proteotoxic responses are: i) broad suppression of protein synthesis and ii) transcriptional up-regulation of a subset of immediate early-responsive genes that escape translational repression, and repair protein damage and/or destroy unfolded proteins^{29,51}. To what extent the heat shock and the UPR impact the severity of infectious diseases is not clear. While the expression of heat shock factor 1 (HSF-1) has been associated with some level of host protection against *Listeria monocytogenes* infection⁵⁶ as well as against endotoxic shock⁵⁷ in mice, whether this occurs via a mechanism involving tissue damage control and disease tolerance remains to be established. The UPR on the other hand confers tissue damage control in mice; the expression of X-box binding protein 1 (XBP1) by gut epithelial cells is required to sustain epithelial barrier integrity and anti-microbial activity, preventing gut epithelial damage

and colitis⁵⁸. Expression of XBP1 also protects *Caenorhabditis elegans* against *Pseudomonas aeruginosa* infection without interfering with pathogen load⁵⁹, arguing for an evolutionarily conserved role for the UPR in the regulation of tissue damage control in barrier epithelia and presumably elsewhere. It is likely that the salutary effects exerted by the UPR in gut epithelial cells relate both to protection from damage imposed by host resistance mechanisms⁵⁹ and also by pathogens⁵⁸, such as triggered by bacterial pore forming toxins that can disrupt the gut epithelium^{10,19}.

DNA damage arising from infections⁶⁰ must be promptly repaired to avoid accumulation of mutations and genomic instability, i.e. the hallmarks of tumorigenesis and cancer. This notion is in keeping with the growing recognition that a number of cancers are directly or indirectly associated with history of infection⁶⁰. Pharmacologic targeting of DNA-damage-responses regulated by the Ser/Thr protein kinase ataxia telangiectasia-mutated (ATM)⁶¹ provides a robust protective response against severe sepsis elicited by polymicrobial infection in mice⁶² (*Fig. 4*). This protective effect acts via a mechanism that does not interfere with host pathogen load, conferring tissue damage control and disease tolerance to sepsis⁶². More specifically, DNA-damage-responses appear to act predominately at the level of the lung epithelium to confer tissue damage control, arguing for a central pathologic role exerted by damage to the lung epithelium in the pathogenesis of severe sepsis⁶². Whether ATM and/or other regulators of DNA damage-responses act under pathophysiologic conditions to confer tissue damage control during different types of infection is likely, but this remains to be established (*Fig. 4*).

Lipid damage is another form of macromolecular damage associated with different types of stress, including lipid peroxidation driven by a self-propagating oxidative chain-reaction catalyzed by divalent metals such as iron contained inside the lipophilic ring of heme⁶³. Lipid peroxidation can impair membrane functions and promote tissue damage, compromising disease tolerance, as illustrated for *influenza* virus infection in mice⁶⁴. Presumably effector mechanisms that restrain lipid peroxidation, such as for example mediated by glutathione peroxidase 4 (GPX4)⁶⁵ or by the lipophilic antioxidant bilirubin⁶⁶ (*reviewed in*⁶⁷), should promote tissue damage control and in turn disease tolerance, but this remains to be established.

Autophagy is an evolutionarily conserved damage-response triggered by organelle damage driven by different forms of stress including redox and metabolic stress, hypoxia or protein unfolding as well as driven by PRR signaling (*Fig. 4*) (*reviewed in*⁶⁸). Damaged

organelles are captured by the vesicular system and fused to lysosomes, initiating their degradation while promoting recycling of their components. Autophagy and its manipulation by pathogens modulates host resistance mechanisms⁶⁸. More recently autophagy has also been shown to modulate tissue damage control and disease tolerance, as illustrated in the context of polymicrobial infection in mice⁶². Briefly, pharmacologic induction of DNA-damage response by anthracyclines, a group of chemotherapeutic agents that activate DNA damage-responses involving ATM, provides robust protection against severe sepsis in mice⁶². This salutary effect acts via a mechanism involving two components of the autophagy damage response, namely the autophagy protein microtubule-associated protein 1 light chain-3B (LC3B) and the autophagy-related protein 7 (Atg7)⁶². Specific inhibition of Atg7 in the lung is sufficient to impair the protective effect of anthracyclines while Atg7 overexpression in the lung is protective against severe sepsis⁶². This argues strongly for the notion of autophagy providing tissue damage control in parenchyma tissues, i.e. the lung epithelium, and conferring disease tolerance to sepsis.

When damage-responses are maladaptive, that is, fail to provide a sufficient level of damage repair to enforce tissue damage control, the default outcome is programmed cell death leading eventually to irreversible tissue damage, organ dysfunction and severe disease (*Fig.2* and *Box 3*). We propose that the pathogenesis of infectious diseases is regulated to a large extent by the relative capacity of different stress- and/or damage-responses to provide metabolic adaptation and damage repair, at sufficient levels as to avoid cytotoxicity, tissue damage and disease (*Fig.2*). While we have argued that tissue damage control mechanisms are a central component of disease tolerance, this does not exclude other mechanisms from contributing to disease tolerance. One of such mechanisms is likely to involve tissue repair via compensatory proliferation of stem cells⁶⁹.

Stress- and damage responses must be tightly regulated during infection, so that cellular function can be restored to full capacity as soon as the cause of stress and damage, i.e. the pathogen, is eliminated by host resistance mechanisms. Moreover, it has been argued that in a similar manner to host resistance mechanisms, tissue damage control and disease tolerance operate in a pathogen-class specific manner, a notion proposed originally by Ruslan Medzhitov in scientific conferences, and demonstrated experimentally in the context of protozoan/bacterial⁷⁰ as well as viral/bacterial co-infection⁷¹ in mice. This imposes again the existence of a stringent regulatory

mechanism controlling stress- and damage-responses that allows for host protection against non-overlapping classes of pathogens.

TISSUE DAMAGE CONTROL IN NON-COMMUNICABLE DISEASES

Stress- and damage-responses also exert protective effects against non-communicable diseases in which inflammation or misdirected immunity act as the underlying cause of pathology. In keeping with this notion the stress-responsive program regulated by NRF2 is protective against organ ischemia and reperfusion injury (IRI), via a mechanism involving the expression of several effector genes, including the stress-responsive enzyme heme oxygenase-1 (HO-1, encoded by the *HMOX1* gene)⁷² and the iron sequestering protein ferritin heart/heavy chain (encoded by the *FTH* gene)⁷³ (*Box 3*). This salutary effect is also observed in the context of heart and brain IRI⁷², presumably limiting the pathogenesis of myocardial infarction and stroke, the two major non-communicable diseases in terms of global impact on human morbidity and mortality. Other adaptive responses conferring protection against IRI include the metabolic stress-response regulated by AMPK⁷⁴ and the UPR⁷⁵. Moreover ischemic pre-conditioning, a hormesis-like protective response against IRI (*Box 4*)⁷⁶, acts via a mechanism involving HIF-1 α ³⁰. Stress-responses regulated by NRF2⁷⁷ and HIF-1 α ³² also prevent the rejection of transplanted organs via a mechanism involving tissue damage control, and driven most probably by HO-1 expression⁷². Transplanted organs can also undergo a hormesis-like response⁷⁶ (*Box 4*) termed accommodation⁷⁸, which prevents graft rejection via a mechanism involving again the expression of HO-1⁷⁹.

Autoimmune diseases are another group of non-communicable diseases in which stress- and damage-responses can act in a salutary manner. This is illustrated by the oxidative stress-response regulated by NRF2, which prevents the onset of diabetes⁸⁰, systemic lupus erythematosus⁸¹, rheumatoid arthritis⁸² and multiple sclerosis⁸³ in murine models for these diseases. Damage responses also exert protective effects against autoimmune diseases, as illustrated for the UPR in the context of type 1 diabetes, where impaired expression of the the UPR components activating transcription factor 6 (ATF6) and XBP1 in β -cells of the pancreas are associated with disease progression in both mice and humans⁸⁴. Importantly, targeting the UPR pharmacologically in β -cells inhibits the pathogenesis of experimental type 1 diabetes in mice, a salutary effect associated with β -cell cytoprotection and reduced inflammatory infiltrates⁸⁴. The UPR also exerts protective effects against autoimmune neuroinflammation, as illustrated in mice for the

expression of the UPR component protein kinase RNA-like ER kinase (PERK) in oligodendrocytes⁸⁵. As referred above, expression of the UPR component XBP1 in intestinal epithelial cells inhibits colitis in mice while hypomorphic variants of the human XBP1 allele are associated with susceptibility to inflammatory bowel disease⁵⁸. It is worth noticing that the salutary effects exerted by the UPR against the pathogenesis of these immune-mediated inflammatory diseases appear to act essentially in parenchyma cells in which protein synthesis is overabundant, as illustrated for β -cells, oligodendrocyte and intestinal epithelial cells, which produce high levels of insulin, myelin and mucins, respectively. Whether hormesis-like responses (*Box 4*)⁷⁶ involving stress- or damage-responses confer protection against autoimmunity remains to be established.

THERAPEUTIC TARGETING OF TISSUE DAMAGE CONTROL

The widespread and often uncontrolled usage of anti-microbial drugs and in particular antibiotics, in the treatment of infectious diseases led to the selection of multidrug-resistant pathogens¹. Targeting tissue damage control and disease tolerance might be a major therapeutic option when treating infectious diseases caused by multidrug resistant pathogens. This therapeutic approach, referred as supportive therapy, is already widely used in severe sepsis, severe forms of malaria, severe diarrheal diseases, severe febrile illness as well as fatal hemorrhagic fevers. Presumably a more rational development of pharmacologic agents targeting specifically central regulators of different stress- or damage-responses, e.g. NRF2³⁵, HIF1- α ³², AMPK or ATM⁶², conferring tissue damage control should be of therapeutic value in the treatment of these pathologic conditions. The same rationale can be applied to the treatment of non-communicable diseases in which inflammation and/or immunity act as the underlying cause of disease. In support of this notion, pharmacologic use of antioxidants confers disease tolerance to *Plasmodium* infection in mice^{86,87}. Also, activation of DNA damage responses and autophagy by anthracyclines - involving ATM, LC3B, ATG7 - confers disease tolerance to polymicrobial infections, acting therapeutically against severe sepsis in mice⁶². Pharmacologic administration of amphiregulin, an epithelial growth factor family member, confers disease tolerance to bacterial pneumonia after *influenza* virus infection in mice⁷¹ and as mentioned above pharmacologic induction of the UPR in β -cells also provides tissue damage control and mitigates the pathogenesis of type-1 diabetes in mice⁸⁴. These findings argue strongly for the potential therapeutic targeting of these stress- and damage-responses outside the specific

context of infectious diseases.

CONCLUDING REMARKS

Vaccination and anti-microbial drugs resulted in global protection of mankind against a variety of pathogens. These approaches however, failed to confer robust protection against insidious infectious diseases that remain a major cause of morbidity and mortality worldwide. Moreover the emergence of a growing number of highly virulent multidrug-resistance pathogens compromises the current therapeutic handling of infectious diseases. In these cases, disease tolerance may play a major role that is often not considered in terms of our understanding of the pathogenesis of infectious diseases or their treatment. Therefore, a fuller understanding of disease tolerance and underlying mechanisms, including tissue damage control, is of clear basic and clinical relevance.

A major challenge is to identify and characterize the molecular mechanisms regulating disease tolerance to specific classes of pathogens. Assuming that disease severity reflects more or less pronounced disruption of homeostasis one should monitor in a quantitative manner “homeostatic parameters” as read-outs of disease driven by infection. Such “homeostatic parameters” include those related to the functional outputs of vital organs essential for maintenance of homeostasis, including the heart/vascular, lung, kidney, liver and brain. This approach used in a daily basis clinically should be adapted to experimental systems addressing at molecular level the mechanism underlying disease tolerance. The expectation is that disease severity will be reflected by quantitative variations of those parameters and that mechanisms controlling disease tolerance should modulate those parameters within the boundaries of homeostasis, without interfering with pathogen load. Another major challenge is the identification and characterization of the functional points of integration between immune-driven resistance and tissue damage control mechanisms regulating disease tolerance. The prediction is that immunoregulatory mechanisms will modulate stress- and damage-responses and hence tissue damage control and disease tolerance. It is expected that these endeavors will enable further understanding of host-pathogen interactions and the rational targeting of disease tolerance mechanisms in the treatment of infectious diseases.

BOX 1:

An historical perspective of disease tolerance: Disease tolerance was first recognized as a plant defense strategy against infection^{88,89}, with its original description dating back to as early as the end of the XIX century⁹⁰. The concept was refined by mid XX century, as the ability to sustain infection without a concomitant reduction in host fitness⁸⁹. These studies posit that disease tolerance does not rely on reducing host pathogen load for preservation of health⁸⁸ but instead acts via mechanisms that limit parenchyma damage⁸⁹. While the concept of disease tolerance was rapidly expanded to different types of infection in plants⁸⁹, it took over a century to extrapolate this notion beyond the plant literature. This was achieved by a series of studies on the immune response of *Drosophila melanogaster* to infection, which revealed that loss of function mutations in genes encoding inflammatory cytokines, e.g. the tumor necrosis factor (*TNF*) homolog *eiger* or in genes controlling metabolic stress-responses, i.e. forkhead box transcription factor (*FOXO*) and *AKT* ([Fig.3](#)) modulate host survival without interfering with pathogen load^{8,9,43}. These and other studies revealed the involvement of specific genes in the regulation of “endurance” to infection, now referred as disease tolerance by analogy to the plant literature^{8,9}, while the same phenomenon is often referred to as “resilience” as well⁹¹. Contemporary with these studies is the finding that a symbiont of flies, i.e. the intracellular bacteria *Wolbachia*, regulates not only host resistance but also disease tolerance to viral infections⁹². In addition to demonstrating that disease tolerance is operational in flies, these studies revealed that host interaction with a given microbe can regulate disease tolerance and as such the pathologic impact of infection by other pathogens⁹². Again contemporary to these studies, is the finding that disease tolerance also occurs in animals, including worms⁵⁹ as well as mice^{86,93}. Overall, these studies “opened the way” to the cellular and molecular characterization of the mechanisms involved in disease tolerance, which have now started to become elucidated, and shown to rely on evolutionarily conserved stress- and damage-responsive programs that adapt and maintain host parenchyma function during infection ([Fig.3&4](#)).

BOX 2:

Disease tolerance in mammals: Disease tolerance was first demonstrated formally in mammals, and interpreted as such, in the context of *Plasmodium* infection⁹³, the causative agent of malaria. Namely, mice from different genetic backgrounds were found to develop varying levels of disease severity, irrespectively of their corresponding pathogen loads⁹³. This observation and the conceptual framework under which it was interpreted were instrumental in extrapolating the notion that genetically encoded mechanisms confer disease tolerance mammals⁹³. Contemporary to this study, is the finding that the *Kcnj8* gene, encoding the ATP-sensitive potassium (K_{ATP}) channel Kir6.1, is essential for protection against viral infections in mice, without interfering with pathogen load⁹⁴.

The cellular and molecular mechanisms regulating tissue damage control and disease tolerance remain poorly understood. In the specific context of *Plasmodium* infection⁹³ these have been linked functionally to a evolutionary conserved stress-responsive and cytoprotective program that provides metabolic adaptation to cellular iron overload^{87,95}. Two effector genes have been functionally implicated, namely the heme catabolizing enzyme HO-1^{86,96,97} and the ferritin heart/heavy chain (FTH)^{87,95}. These provide a systemic adaptive response to tissue iron overload in the infected host, which prevents cytotoxicity and tissue damage caused by the accumulation of iron-heme during the blood stage of *Plasmodium* infection^{86,96,97}. The same stress-responsive program is involved in conferring tissue damage control and disease tolerance to severe sepsis driven by polymicrobial infection⁹⁸.

Assuming that unfettered cytotoxicity is a common underlying mechanism driving tissue damage during infection, stress- and damage-response that confer tissue damage control and disease tolerance to infection should protect host parenchyma cells from programmed cell death. In support of this notion is the finding that deletion of the RIP kinase 3 (RIPK3) gene, a master regulator of programmed cell death by necroptosis⁹⁹, is sufficient *per se* to confer tissue damage control and disease tolerance to systemic polymicrobial infection in mice¹⁰⁰. Moreover, deletion of the *Birc3* (cIAP2) gene, encoding a E3 ubiquitin ligase that suppresses necroptosis, impairs tissue damage control and disease tolerance to *influenza* virus infection in mice¹⁰¹. These findings suggest that stress- and damage-responses conferring tissue damage control may target directly or indirectly the RIPK1/3-driven necroptosis signal transduction pathway to confer disease tolerance or resistance to infection, a hypothesis that remains to be tested.

BOX 3:

Metabolic adaptation to iron overload and disease tolerance. Based on its relative abundance and ability to exchange electrons with a number of donor/acceptor molecules iron is at the center stage of many vital biological functions. Pathogens rely strictly on iron acquisition for the progression of infection, evolving strategies that fuel host iron into their own metabolic pathways¹⁰². It follows that host strategies that deny pathogen access to iron are a central and evolutionarily conserved host resistance mechanism^{95,102,103}. This defense strategy relies to a large extent on the expression of: i) hepcidin antimicrobial peptide gene (*HAMP*), a master regulator of systemic iron metabolic adaptation during infection that reduces iron acquisition from diet and suppresses iron cellular export¹⁰³, ii) lipocalin-2, a soluble iron chelator encoded by the *LCN2* gene that prevents extracellular pathogens from accessing iron¹⁰⁴ and iii) natural resistance associated macrophage protein function (*NRAMP-1*), an intracellular iron transporter encoded by the *SLC11A1* gene, that removes iron from phagolysosomes and limits iron supply to intracellular pathogens¹⁰⁵.

Systemic regulation of pathogen access to host iron has a major “trade off”, namely, host tissue iron overload compromising host parenchyma function⁹⁵. Moreover, systemic disruption of cellular iron export can interrupt iron supply to hemoglobin synthesis and erythropoiesis, causing anemia of chronic disease¹⁰⁶. Therefore systemic modulation of host iron metabolism during infection provides a paradigm for the requirement of an integrated host defense strategy in which resistance mechanisms must be coupled to tissue damage control as to limit the severity of infectious diseases^{87,95}. This is accomplished via metabolic adaptation to tissue iron overload, via a mechanism involving the expression of ferritins^{87,95}.

Ferritins are multimeric nanocage-like structures made of FTH (heavy/heart) and FTL (light/liver) chains, that can incorporate up to 4,500 iron atoms in the form of inorganic ferrihydrite aggregates¹⁰⁷. FTH ferroxidase activity converts reactive iron (Fe^{2+}) into inert iron (Fe^{3+}) that does not partake in the production of free radicals via the Fenton chemistry⁹⁵. This anti-oxidant effect confers tissue damage control and disease tolerance to infection in mammals^{87,95} as well as in plants¹⁰⁸, arguing for the evolutionarily conserved nature of this host defense strategy.

BOX 4:

Overlapping protection, evolution and hormesis. There is an overlapping profile of gene expression associated different stress- and damage-responses in evolutionary disparate organisms^{25-27,53}. This argues for the involvement of a core number of evolutionarily conserved effector genes in the regulation of those stress- and damage-responses and as such on the regulation of tissue damage control and disease tolerance. Presumably, stress- and damage-responses evolved from ancestral forms of life where they provided adaptation to environmental changes²⁶ being co-opted through evolution to provide host protection against infection^{25,27}. These ancestral adaptive responses preceded most probably those underlying host resistance mechanisms, co-evolving thereafter to decouple potentially damaging resistance mechanisms from tissue damage and disease severity. This is in keeping with the notion that some host resistance mechanisms can *per se* elicit cellular stress and damage, which in the absence of a countervailing protective response would be pathogenic. We propose that stress- and damage-responses conferring tissue damage control and disease tolerance to infection are required to decouple potentially deleterious resistance mechanisms from disease severity. The overlap of signal transduction pathways and profiles of gene expression associated with different stress- and damage-responses (*Fig.2-4*) also argues for some level of cross-protection against seemingly unrelated forms of stress and damage⁶⁸. This phenomenon known as hormesis⁷⁶, is also referred as pre-conditioning in the context of organ IRI, or energy restriction in the context of ageing as well as accommodation in the context of organ transplantation⁷⁸. The shared principle being that sub-toxic forms of stress and/or damage can elicit adaptive responses in cells, tissues, organs or organisms that are protective against subsequent exposure to toxic levels of the same or unrelated forms of stress and/or damage⁷⁶. The impact of this phenomenon for infectious diseases is supported by the finding that the protective effect exerted by sickle hemoglobin against malaria, relies on a hormesis-like effect involving the activation of the stress-response regulated by NRF2 and providing tissue damage control and disease tolerance to *Plasmodium* infection⁹⁷. A similar effect has been assigned to the protective effect of nitric oxide against the development of severe malaria in mice³⁸. This suggests that targeting hormesis-like mechanisms may be used as a strategy induce tissue damage control and disease tolerance to other types of infection, a notion supported by the protective effect exerted by pharmacologic targeting of the DNA damage-responses against severe sepsis in mice⁶².

FIGURE LEGENDS:

Figure 1: Tissue damage control in host microbe interactions. Homeostasis is governed to a large extent by parenchyma tissues that do not exert a negative impact (-|) on pathogens. Toxins and other virulence factors expressed by pathogens can elicit cellular stress and damage to the host parenchyma (lightning bolt arrow), disrupting homeostasis. This is a major driver in the pathogenicity of infectious diseases. Recognition of pathogens (PRR/PAMP) activates (->) the host innate and adaptive immune response, reducing pathogen load and hence pathogenicity. This defense strategy, called host resistance to infection, can have a direct negative impact (-|) on host parenchyma (immunopathology) or an indirect negative impact (-|) in combination with toxins. This is another major driving force in the pathogenesis of infectious diseases. Tissue damage control refers to a protective mechanism that limits the extent of stress and damage imposed to host cells by toxins and other virulence factors as well as by host resistance mechanisms. When exerted in parenchyma, tissue damage control reduces disease severity without interfering with pathogen load, and is said to confer disease tolerance to infection. Toxins and virulence factors as well as host resistance mechanisms (not depicted in *figure*) can exert a negative impact (-|) on host epithelial cells, disrupting barrier functions. When exerted in host epithelial cells, tissue damage control enforces barrier function, contributing to host resistance mechanisms. Toxins and virulence factors can also exert a negative impact (-|) on components of the host immune system, impairing resistance to infection. Therefore, when exerted in the immune system, tissue damage control can act in an immunoregulatory manner and modulate resistance mechanisms.

Figure 2: Stress- and damage-responses: Circles indicate signal transduction pathways regulating specific gene profiles, as triggered by different sensors represented by rectangles. Activation of stress- and damage-responses provides tissue damage control and disease tolerance to systemic infections. When stress-responses are maladaptive, that is, when these fail to provide sufficient levels of metabolic adaptation to different forms of stress, the result is macromolecular, i.e. protein, lipid, DNA, and/or organelle damage. This triggers a functionally different set of adaptive responses that are no longer aimed at providing metabolic adaptation but instead aim at repairing macromolecular and/or organelle damage, i.e. damage repair. Damage responses, act presumably as a second layer of tissue damage control to enforce disease tolerance.

When damage-responses are maladaptive, that is, fail to provide sufficient macromolecular and/or organelle damage repair, the default program is programmed cell death, leading to tissue damage, organ dysfunction and eventually to disease.

Figure 3: Stress-response pathways: Stress-responses are controlled by a number of master regulators (red rectangles) that provide cellular adaptation to specific forms of stress. **Hypoxia** is sensed by the prolyl hydroxylase (PHD)2, which uses O₂ to hydroxylate two proline residues in the transcription factor HIF-1α. This promotes the recruitment of the E3 ubiquitin ligase von Hippel-Lindau (VHL/Cul3), ubiquitinating (green circle; Ub) and targeting HIF-1α for proteolytic degradation by the 26s proteasome pathway³⁰. PHD2 activity is inhibited when O₂ pressure (pO₂) decreases below physiologic levels, i.e. hypoxia. This releases HIF-1α from VHL, allowing for HIF-1α nuclear translocation and binding to DNA hypoxia responsive elements (HRE) in the promoter of effector genes regulating metabolic adaptation to hypoxia³⁰. **Oxidative stress** is sensed by the Kelch-like ECH-associated protein 1 (Keap1) that controls the activation of the transcription factor NRF2, a member of the Cap'n'collar basic leucine zipper family of transcription factors that acts as a master regulator of cellular adaptive responses to oxidative stress³⁶. Under homeostasis, Keap1 acts as an ubiquitin E3 ligase, targeting NRF2 for ubiquitination (green circle; Ub) and proteolytic degradation by the 26s proteasome pathway³⁵. Oxidative stress causes several sulfhydryl groups in Keap1 to form disulfide bonds, inhibiting its ubiquitin E3 ligase activity and releasing NRF2, which associated with small Maf proteins¹⁰⁹ and undergoes nuclear translocation, binding to the DNA antioxidant responsive elements (ARE) in the promoter of genes regulating adaptation to oxidative stress³⁵. **Metabolic stress.** Cellular AMP, ADP and ATP concentrations are maintained at constant levels by different mechanisms regulating ATP production in the mitochondria and ATP consumption. Moreover, adenylate kinase (ADK) catalyzes the conversion of 2 ADP into ATP + AMP. When cellular ATP concentration decreases, ADP to ATP ratio increases displacing the reaction catalyzed by adenylate kinase towards ATP and AMP. This is sensed by AMPK, which orchestrates a cellular adaptive response promoting catabolic pathways generating ATP while switching-off ATP consumption⁴¹. **Multiple forms of stress** can be sensed by the evolutionarily conserved Forkhead box O (FOXO) family of transcription factors⁴². Under homeostasis, FOXO activity is suppressed via the

insulin-signaling transduction pathway involving PI3K and AKT and promoting sustained FOXO binding to 14.3.3⁴². Inhibition of PI3K and AKT is associated with activation of upstream stress-activated mitogen activated protein kinases (MAPK), including the Jun N-terminal kinase (JNK). These trigger FOXO post-translational modifications (PTM) promoting its nuclear translocation and binding to specific DNA motifs in the promoter of genes that confer adaptation to multiple forms of stress. **Osmotic stress** elicits an immediate adaptive response modulating cellular volume and intracellular concentrations of inorganic ions and macromolecules, via a mechanism involving the aquaporin “water channels” (AQP) and solute carrier channels (SLC). Prolonged osmotic stress is sensed by the protein kinase A-anchoring protein 13 or Brx⁴⁵, which activate MAPK. These include the p38 MAPK that targets the transcription factor nuclear factor of activated T-cells 5 (NFAT5), also known as the tonicity-responsive element binding protein (TonEBP). Phosphorylated NFAT5 dimerizes and undergoes nuclear translocation binding to DNA osmotic response elements (ORE), in the promoter of osmoregulatory genes⁴⁴. A recent study proposes that activation of the xenobiotic stress-response regulated by AhR confers disease tolerance to bacterial infections⁴⁸ (not illustrated).

Figure 4: Damage response pathways. Damage-responses are controlled by a number of macromolecular and organelle damage sensors. These activate specific genetic programs providing cellular adaptation to different forms of cellular damage. **Unfolded protein response (UPR).** Accumulation of misfolded proteins in the ER lumen is sensed by the binding immunoglobulin protein (BiP)/78 kDa glucose-regulated protein (GRP-78) chaperone and the inositol requiring protein-1 (IRE1), two master regulators of the UPR^{54,55}. Dimerization and release of GRP78, de-repress IRE1 activity⁵⁵, which splices X-box binding protein 1 (XBP1) mRNA, promoting XBP1 translation, nuclear translocation and binding to DNA X-box elements in the promoter of effector genes regulating the UPR. Binding of GRP-78 to unfolded proteins in the ER lumen also triggers the activation of the protein kinase RNA-like ER kinase (PERK) and the transcription factor-6 (ATF6). PERK represses mRNA translation⁵⁵ and activates different substrates, including NRF2, which regulates the expression of several effector genes that provide disease tolerance to infection. ATF6 also induces the transcription of different genes contributing to the UPR, including *XBP1*. **Heat shock response.** Accumulation of misfolded proteins in the cytoplasm, as a result of cellular exposure to

higher than physiologic temperatures, i.e. fever, or other forms of stress associated with infection is sensed by heat shock proteins (HSP), e.g. chaperones⁵². Under homeostasis, components of the Hsp90 chaperone family repress the transcription factor heat shock factor 1 (HSF1), the master regulator of the heat shock response. Misfolded proteins recruit Hsp90. This releases HSF1, which homotrimerizes and undergoes nuclear translocation, binding to DNA heat shock elements (HSE) in the promoter of different classes of HSP genes. **DNA damage.** DNA double strand breaks, one of the most deleterious forms of DNA damage, are sensed by the Mre11/Rad50/Nbs1 complex, which activates ATM, a master regulator of the double stranded DNA damage-response⁶¹. Under homeostasis ATM exists essentially as a homodimer, dissociating into active monomers in response to DNA double strand breaks⁶¹. ATM orchestrates an adaptive cellular response involving substrate proteins that regulate cell cycle progression, metabolic adaptation or programmed cell death⁶¹. **Autophagy** relies on the cellular vesicular system initiated by a process of nucleation of damaged organelles, elongation and maturation leading to lysosome (Lys) fusion, and allowing for degradation and recycling of their components⁶⁸.

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ABBREVIATION:

ADK: adenylate kinase; **AMPK:** AMP-activated protein kinase; **AQP:** aquaporin; **ARE:** antioxidant responsive elements; **ATF6:** activating transcription factor-6; **ATM:** ataxia-telangiectasia mutated; **CBP:** CREB binding protein; **CO:** Carbon Monoxide; **CREB:** cAMP response element-binding protein; **ER:** endoplasmic reticulum; **Fe:** iron; **FOXO:** Forkhead box O; **FTH:** ferritin heart/heavy chain; **FTL:** ferritin liver/light chain; **GRP-78:** glucose-regulated protein; **HAMP:** hepcidin antimicrobial peptide gene; **HIF-1 α :** hypoxia-inducible factor 1 alpha; **HO-1:** HMOX1/heme oxygenase-1; **HRE:** hypoxia responsive elements; **HSE:** heat shock elements; **HSF1:** heat shock factor 1; **HSP:** heat shock proteins; **IRE1:** inositol requiring protein-1 ; **IRI:** ischemia and reperfusion injury; **JNK:** Jun N-terminal kinase; **Keap1:** Kelch-like ECH-associated protein 1; **MAPK:** mitogen activated protein kinases; **NFAT5:** nuclear factor of activated T-cells 5; **NRAMP-1:** natural resistance associated macrophage protein function; **NRF2:** nuclear factor-erythroid 2-related factor 2; **ORE:** osmotic response elements; **PAMP:** pathogen associated molecular patterns; **PERK:** protein kinase RNA-like endoplasmic reticulum kinase; **PHD2:** prolyl hydroxylase 2; **PRR:** pattern recognition receptors; **PTM:** post-translational modifications; **HSP:** small heat shock proteins; **SLC:** solute carrier channels; **TNF:** tumor necrosis factor; **TonEBP:** tonicity-responsive element binding protein; **Ub:** ubiquitinating; **UPR:** unfolded protein response; **VHL/Cul3:** von Hippel-Lindau; **XBP1:** X-box binding protein 1.

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