

Sterile inflammation and pregnancy complications: a review

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Abstract

Inflammation is essential for successful embryo implantation, pregnancy maintenance and delivery. In the last decade, important advances have been made in regard to endogenous, and therefore non-infectious, initiators of inflammation, which can act through the same receptors as pathogens. These molecules are referred to as damage-associated molecular patterns (DAMPs), and their involvement in reproduction has only recently been unraveled. Even though inflammation is necessary for successful reproduction, untimely activation of inflammatory processes can have devastating effect on pregnancy outcomes. Many DAMPs, such as uric acid, high-mobility group box 1 (HMGB1), interleukin (IL)-1 and cell-free fetal DNA, have been associated with pregnancy complications, such as miscarriages, preeclampsia and preterm birth in preclinical models and in humans. However, the specific contribution of alarmins to these conditions is still under debate, as currently there is lack of information on their mechanism of action. In this review, we discuss the role of sterile inflammation in reproduction, including early implantation and pregnancy complications. Particularly, we focus on major alarmins vastly implicated in numerous sterile inflammatory processes, such as uric acid, HMGB1, IL-1 α and cell-free DNA (especially that of fetal origin) while giving an overview of the potential role of other candidate alarmins.

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Introduction

Inflammation is essential for successful female reproduction. Inflammatory processes are implicated in every step of fertility from menstrual cycle (ovulation and menses) to early pregnancy (implantation and decidualization) and later during labor (myometrial activation, cervical ripening and weakening of fetal membrane), whereas quiescence of these mechanisms is maintained by local immune cells during gestation to allow maternal tolerance of fetal antigen allograph. However, untimely inflammatory triggers shifting the immunological balance toward activation can lead to adverse pregnancy outcomes including preterm birth. Inversely, failure to mount a local inflammatory response in early or late gestation can also lead to adverse conditions, including miscarriages. Evidence shows that impaired inflammatory response is implicated in numerous female reproductive tract pathologies including menstrual disorders (Sales & Jabbour 2003), endometriosis-associated infertility (Gupta *et al.* 2008), recurrent miscarriage (von Wolff *et al.* 2000, Laird *et al.* 2003), intrauterine growth restriction (Heyborne *et al.* 1994), preeclampsia (Redman *et al.* 1999,

Rinehart *et al.* 1999) and preterm labor (Romero *et al.* 2006, Christiaens *et al.* 2008). Infertility has an estimated global prevalence of 9% with >72 million infertile women worldwide (Boivin *et al.* 2007), whereas preterm birth and preeclampsia, the two leading causes of perinatal mortality and morbidity, have an estimated prevalence of >11% (Blencowe *et al.* 2013) and 3–5% (Ananth *et al.* 2013, Chaiworapongsa *et al.* 2014) respectively. Therefore, understanding the mechanisms by which inflammation is untimely triggered in the uterus is fundamental to developing effective therapeutics to improve fertility and decrease poor obstetrical outcomes.

Infection is not an essential component in reproductive disorders linked to inflammation. In animals, sterile inflammation is sufficient to recreate major features of common reproductive diseases (Romero *et al.* 1991, Scharfe-Nugent *et al.* 2012, Gomez-Lopez *et al.* 2016), whereas in humans, a significant part of patients suffering from preeclampsia, preterm labor or other inflammatory diseases during pregnancy display no clinical signs of infection. This has been extensively studied in the context of preterm birth; although observational, correlational and causal

data accumulated for >30 years have linked infection to preterm labor, preterm birth without infection is more prevalent (Romero *et al.* 2001). Furthermore, antibiotics are inefficient to prevent preterm labor in women with infection (Olson *et al.* 2008), suggesting that infection-induced pro-labor effects arise from inflammation (self) rather than infection (non-self).

Pro-inflammatory stimuli can be classified as 'danger' (or damage) and 'stranger' signals; both types of signals are pharmacologically active via pattern recognition receptors (PRRs), a class of phylogenetically conserved receptors ubiquitously expressed by mammalian cells. These receptors act as sensors of damage-associated molecular patterns (DAMPs) or pathogen-associated molecular patterns by operating a transduction cascade of intracellular and intranuclear signals leading to the mounting of cytokine-based inflammatory responses. PRRs include Toll-like receptors (TLRs) 1–11, scavenger receptors, C-type lectins, and NOD-like receptors and are expressed abundantly in decidua, placenta, membranes and myometrium throughout pregnancy, in immune and non-immune cells (Koga & Mor 2010, Lappas 2013, Zhang *et al.* 2014). Therefore, the uteroplacental compartment is a sensor of 'danger' and 'stranger' inflammatory stressors. We suggest that inflammatory processes implicated in physiological human reproduction are triggered mainly through sterile pathways (e.g. via tissue injury or cell death) compared to exogenous signals such as pathogens (bacteria or viruses, namely stranger signals), whereas pathological inflammatory events implicated in pregnancy complications can be triggered by both sterile and infectious pathways. This review focuses on the role of sterile inflammation in common pathologies of pregnancy.

Major players in sterile inflammation and their mechanism of action

Sterile inflammation is triggered when DAMPs activate PRRs (or other receptors including RAGE and IL-1R) to mount an acute immune response in order to solve the adverse condition that initially led to DAMP release. As DAMPs are endogenous intracellular molecules primarily released as a result of non-programmed cell death to convey danger cues in the first few hours of an injury, they are also referred to as alarmins (Matzinger 1994). Candidate alarmins include, but are not limited to, high-mobility group box 1 (HMGB1), uric acid, interleukin-1 α (IL-1 α) and cell-free DNA. A detailed description of these alarmins and their mechanism of action can be found below and in Fig. 1, whereas their roles in pathological conditions of pregnancy are presented in the next section.

HMGB1

HMGB1 is a highly conserved non-histone protein (25 kDa) with cytokine-like activity in the extracellular space. HMGB1 is abundantly and ubiquitously expressed in nucleus where it plays a role in DNA replication, transcription and repair, and nucleosome stabilization (Boonyaratanakornkit *et al.* 1998, Stros 2010, Celona *et al.* 2011). HMGB1 is structured into two DNA-binding domains, HMG box A and B and an aspartic and glutamic acid-rich C-terminal tail. Although originally discovered in the nucleus, HMGB1 is also found in cytosol, mitochondria, and on membrane surface and can be released to the extracellular milieu through active (secretion) and passive pathways (Erlandsson Harris & Andersson 2004). First, active pathways are triggered by

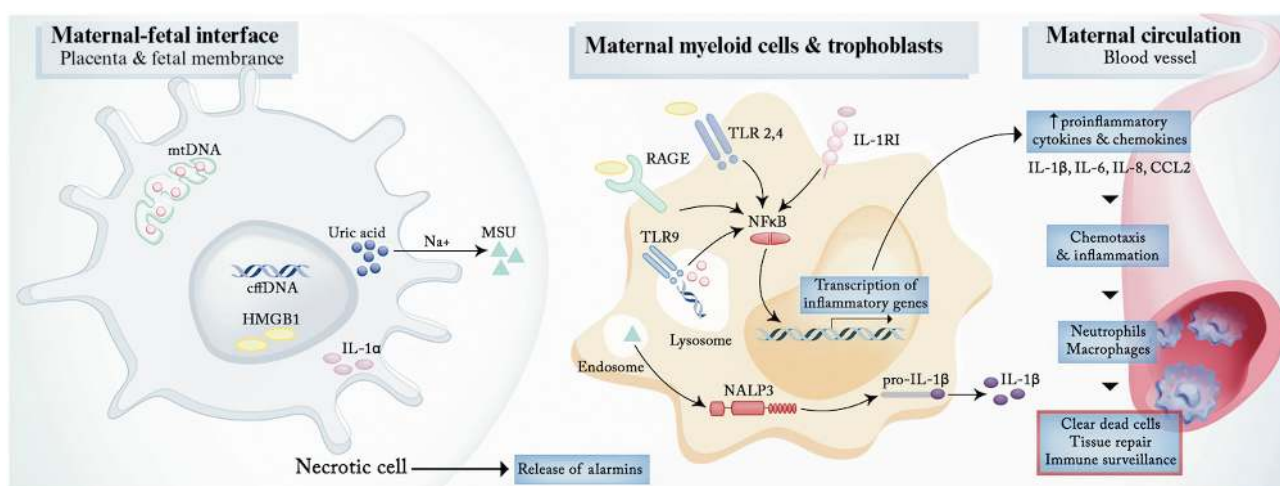


Figure 1 Inflammatory mechanism of action of HMGB1, uric acid, IL-1 α and cell-free DNA. The general mechanism of action of alarmins at the maternal–fetal interface is shown, with alarmins (uric acid/MSU, HMGB1, cffDNA and IL-1 α) being released from cells of the maternal–fetal interface (i.e., placenta and fetal membranes) following a stimulus or necrosis. They act on placental cells (primarily trophoblasts) and maternal myeloid cells to induce an inflammatory response. The inflammatory cascade leads to the secretion/release of cytokines/chemokines, which stimulate the recruitment of immune cells from the maternal circulation.

pathogenic products (e.g. bacteria and viruses) or other stressors (e.g. oxidative stress and cytokines), which have been shown in immune cells and non-immune cells (Tsung *et al.* 2007, Tang *et al.* 2011, Harris *et al.* 2012). Secondly, whereas (ii) passive release is observed following tissue injury and cell death, especially necrosis (Scaffidi *et al.* 2002) and in specific cases of apoptosis (Qin *et al.* 2006) – including when triggered by sterile injury events (e.g. hypoxia, senescence and autoimmune disease). The latter happens immediately (Scaffidi *et al.* 2002), whereas the former is a slower mechanism mediated by cellular signal transduction (Tsung *et al.* 2014). Once HMGB1 accumulates in the extracellular milieu, it conveys danger signals by triggering inflammatory pathways, including NF- κ B, ERK and p38, in neighboring cells via numerous cell surface receptors such as TLRs 2, 4 and 9; RAGE; CD24; and others (Venereau *et al.* 2013). This leads to the activation of innate and adaptive immunity, cytokine, chemokine, and metalloprotease release and ensued pro-migration and pro-inflammatory outcomes (Andersson *et al.* 2000, Scaffidi *et al.* 2002, Rouhiainen *et al.* 2004, Andersson & Tracey 2011). Of interest, HMGB1 has also been shown to form complexes with many pro-inflammatory mediators and enhance their respective actions in a synergistic manner (Hreggvidsdottir *et al.* 2009). Furthermore, HMGB1 levels are elevated in multiple animal models of sterile injurious events (Tsung *et al.* 2014) and in humans with acute organ injury, autoimmune diseases or cancer (Tong *et al.* 2011, Wang *et al.* 2014). *In vitro* and *in vivo*, HMGB1 administration induces inflammation (Yang *et al.* 2005), and more importantly, HMGB1 antagonism protects against sepsis (Yang *et al.* 2004). This evidence highlights a critical alarmin role of HMGB1 as an endogenous sterile driver of inflammation.

Uric acid

Uric acid (160 Da) is a product of metabolic breakdown of purine nucleotides by xanthine oxidase, with normal blood concentration ranging between 40 and 60 μ g/mL. Upon achieving concentrations of >70 μ g/mL, uric acid forms needle-like, immunostimulatory monosodium urate (MSU) crystals, which cause acute inflammation of gout. In the last few years, uric acid has been vastly regarded as an alarmin of sterile inflammation because of the high cytosolic concentration (\approx 4 mg/mL) released upon cell death, which reacts with extracellular sodium to form MSU in the immediate vicinity of cellular injury (Shi *et al.* 2003). Transport of MSU inside antigen-presenting cells through phagocytosis promotes its interaction with NALP3 inflammasome and induces IL-1 β maturation and release thereby triggering an inflammatory response (Martinon *et al.* 2006, Shi 2010). This is an important step in sterile inflammation that enables immune cells to sense injuries. Concordantly, administration of MSU

causes acute inflammation (Faires & McCarty 1962), and in mice, blocking uric acid is sufficient to inhibit the immunological and inflammatory responses associated with cellular death or injury in numerous cell types and tissues (Shi *et al.* 2003, Kono *et al.* 2010).

Interleukin-1

The interleukin-1 family comprises 11 cytokines that regulate inflammatory response to injuries and stressors. Two major members of the family are IL-1 α and IL-1 β , which bind to ubiquitous IL-1R1 to activate the translocation of transcription factors NF- κ B and AP-1, thereby triggering the expression of numerous cytokines including itself and initiating or sustaining an inflammatory response (Di Paolo *et al.* 2009, Dinarello 2009). Although IL-1 α and IL-1 β bind to the same receptor and convey similar biological effect, the two cytokines are encoded by different genes and have distinct mode of action. Unlike IL-1 β , IL-1 α is not actively secreted but instead translocates to the nucleus to participate in the regulation of gene transcription (Werman *et al.* 2004). Furthermore, while IL-1 β precursor requires exogenous (or endogenous in rare cases) signals to trigger its transcription and to initiate its inflammasome-dependent cleavage into a functional cytokine, IL-1 α precursor is, on the other hand, ubiquitously expressed in the cytoplasm of healthy cells, in the form of a biologically active precursor. Consequently, only IL-1 α is released in a functional form upon necrosis; therefore, IL-1 α is regarded as an alarmin, whereas IL-1 β is not (Eigenbrod *et al.* 2008, Lukens *et al.* 2012). Accordingly, sterile cell death-induced neutrophil inflammatory response in mice requires both IL-1 α and IL-1R, but not IL-1 β (Chen *et al.* 2007), suggesting that IL-1 β is not essential for the mounting of a functional sterile inflammatory response to cell death. However, evidence shows that both IL-1 α and IL-1 β are implicated in sterile inflammation but have distinct timing of effect and roles (Rider *et al.* 2011), suggesting that IL-1 β contributes to sterile inflammation, not as an initiator but as a redundant mechanism to amplify the initial trigger. Accordingly, it is documented that IL-1 β can be produced to contribute to sterile inflammation in response to non-cytotoxic sterile stressors as those released upon necrosis (Lukens *et al.* 2012). This was also recently reported for IL-1 α (Idan *et al.* 2015). Interestingly, the release of IL-1 α is tightly regulated during programmed cell death via chromatin sequestration, which significantly reduces its pro-inflammatory effect during apoptosis; this is not observed during necrosis (Cohen *et al.* 2010). These data suggest a critical role of IL-1 α in sterile inflammation, and a contributive, albeit non-essential, role of IL-1 β . The major role of IL-1 α in sterile inflammation has been reviewed elsewhere (Lukens *et al.* 2012).

Cell-free DNA

Circulating cell-free DNA refers to double-stranded, cell-unbound DNA fragments in the blood of humans. Cell-free DNA originates from genomic or mitochondrial DNA released subsequently to cell death. Cell-free DNA is present in small amounts in the blood of healthy individuals, but its concentration is increased in patients suffering from chronic diseases. In this context, studies suggest that it acts as a contributor to chronic diseases by inducing inflammation via TLR9, a PRR classically activated by unmethylated CpG motif-containing bacterial and viral DNA fragments (Chan & Lo 2002, Breitbach *et al.* 2012, Nishimoto *et al.* 2016). Mitochondrial DNA also triggers TLR9 to induce inflammation (Zhang *et al.* 2010).

Circulating blood of pregnant women contains an additional type of cell-free DNA, referred to as cell-free fetal DNA (cffDNA) that originates from the placenta. Evidence for the placental origin of cffDNA includes the following: (1) it is detected in anembryonic gestation (Alberly *et al.* 2007); (2) it is still detected after therapeutic abortion in which placenta is incompletely removed, albeit undetectable after normal delivery (Lo *et al.* 1999, Wataganara *et al.* 2005); (3) it is detected in cases of invasive placenta, a postpartum pregnancy complication in which trophoblasts invade myometrium (Sekizawa *et al.* 2002); and (4) it carries the placental genotype in patients with confined placental mosaicism (Masuzaki *et al.* 2004). In contrast to maternal cell-free DNA, of which 32% of the fragments are >356bp, cffDNA are short hypomethylated fragments (<313bp) and potent inducer of sterile inflammation (Chan *et al.* 2004, Scharfe-Nugent *et al.* 2012, Schroeder *et al.* 2013). The release of cffDNA is a physiological process present in all mammals, but its possible roles and implications in normal pregnancy (and more importantly parturition) remain poorly understood. Placental growth involves proliferation, differentiation and syncytial fusion of cytotrophoblasts, which is associated with significant release (grams per day) of microvesicles-encapsulated, cffDNA-containing apoptotic trophoblasts content into maternal circulation (Nelson 1996, Huppertz *et al.* 1998, Huppertz & Kingdom 2004, Bischoff *et al.* 2005, Taglauer *et al.* 2014). These microparticles, also referred to as syncytiotrophoblast microvesicles (SCTMs), were first described more than 100 years ago in lung capillaries of women who died from preeclampsia (Schmorl 1893) and were later described as a feature of normal pregnancy, although increased in preeclampsia (Johansen *et al.* 1999). SCTMs as well as cffDNA alone are pro-inflammatory (Redman *et al.* 1999, Redman & Sargent 2000, Phillippe 2015). Interestingly, once pregnancy is past 20 weeks, the levels of cffDNA in maternal circulation consistently increase 1% per additional week of gestation to abruptly rise (up to 13-folds) when gestation nears the end (Ariga *et al.* 2001,

Majer *et al.* 2007, Wang *et al.* 2013). This evidence, along with the established pro-inflammatory effects of cffDNA, underpins the theory that cffDNA may represent a common trigger to parturition in mammals (Phillippe 2014). Furthermore, elevated cffDNA in the maternal circulation has been observed in pathological pregnancies (Levine *et al.* 2004, Alberly *et al.* 2009, Girard *et al.* 2014) in association with placental dysfunction and inflammation. For these reasons and others, cffDNA is increasingly used for diagnostic purposes to decrease the use of invasive amniocentesis.

Mechanistically, cffDNA can bind to TLR9 to induce a conformational change in the homodimers of the receptor resulting in the close apposition of the TIR signaling domains and downstream activation of NF- κ B and transcription of inflammatory cytokine genes (Latz *et al.* 2007). Importantly, this TLR9, NF- κ B-dependent pro-inflammatory effect of cffDNA was shown in pregnant mice and is characterized by IL-6 production in human peripheral blood mononuclear cells (Scharfe-Nugent *et al.* 2012). Classically, TLR9 is localized intracellularly in endoplasmic reticulum (ER), endosomes and lysosomes (Latz *et al.* 2004). Therefore, cffDNA must be transported by endocytosis inside immune cells in order to convey inflammatory effects via TLR9; this is likely occurring through phagocytosis of cffDNA-containing SCTMs by placental or circulating granulocytes. Given the half-life of cffDNA (16.3 min in humans) (Lo *et al.* 1999), this inflammatory stimulation is short-lived, but is likely sustained by unabated trophoblast turnover.

Others

Different levels of evidence have been accumulated, suggesting that many other intracellular factors can induce acute inflammation once released in their environment and therefore may represent potential alarmins. These include S100 proteins (Hofmann *et al.* 1999, Ryckman *et al.* 2003), nucleosomes (Decker *et al.* 2005), purines (Cronstein *et al.* 1990), heat-shock proteins (Basu *et al.* 2000), saturated fatty acids (Lee *et al.* 2001) and antimicrobial peptides (Yang *et al.* 1999, De *et al.* 2000, Zanetti 2004). Interestingly, possible alarmin activity has been reported for molecules of mitochondrial provenance such as mitochondrial DNA (Zhang *et al.* 2010), N-formylated mitochondrial peptides (Carp 1982) and others (Raouf *et al.* 2010), which could arise from their probable prokaryote origin. Noteworthy, the role and mode of action of the aforementioned candidates *in vivo* are mostly unknown. Along these lines, the possible alarmin activity of heat-shock proteins is still under debate. Early studies have shown that purified HSPs activate DCs *ex vivo* (Basu *et al.* 2000) and *in vivo* (Binder *et al.* 2000) to trigger an inflammatory response. This pro-inflammatory effect has latter been attributed to bacterial contaminant (Bausinger *et al.* 2002, Gao & Tsan 2003), and the

enthusiasm of a possible alarmin role of HSPs was consequently severely dampened.

By definition, any endogenous molecule physiologically expressed in low concentrations in the extracellular milieu, which is upregulated and released during pathological events, could be considered as an alarmin candidate. Therefore many other mediators could potentially be included in this category, such as glucose that has recently been shown to have pro-inflammatory actions in human trophoblast (Han *et al.* 2015).

A role for sterile inflammation in pathological conditions of pregnancy

Alarmin release, caused by tissue injury, hypoxia/ischemia, cellular senescence or other stressors, is implicated in pathologies of pregnancy independently of infection. In the next section, we will focus on the role of alarmins in miscarriages, recurrent pregnancy loss (RPL), intrauterine growth restriction (IUGR), preeclampsia and preterm labor. The proposed sites of release of alarmins in diseases of pregnancy are shown in Fig. 2.

Early pregnancy

Many inflammatory mediators (and immune cells) are implicated in the early events of pregnancy, primarily

embryo implantation. A tight regulation of the immune system is required for proper invasion and remodeling of the spiral arteries by fetal trophoblasts, which has been recently reviewed (Erlebacher 2013). The involvement of DAMPs in RPL or miscarriages has only recently been addressed. Elevated HMGB1 levels in uterine fluids have been associated with pregnancy failure in rats and lower abundance of HMGB1 observed in the receptive phase of implantation in humans (Bhutada *et al.* 2014). Additionally, a genetic polymorphism of HMGB1 characterized by higher expression of HMGB1 in placenta has been associated with RPL (Jin *et al.* 2015). Furthermore, HMGB1 was shown to induce inflammation, characterized by an NF- κ B- and reactive oxygen species-dependent increased secretion of IL-6, IL-8 and CCL2 in first-trimester trophoblast (Shirasuna *et al.* 2016). Other alarmins, including S100A8 (Nair *et al.* 2015) and cell-derived microparticles (Martinez-Zamora *et al.* 2016), were also found to be elevated in early pregnancy loss. Likewise, increased inflammatory cytokine levels (namely IL-18, LIF, MIF, IL-12, IFN- γ and ICAM-1) in the blood and endometrium were also associated with RPL (Comba *et al.* 2015). Correspondingly, increased expression of the NALP3 inflammasome and its products IL-1 β and IL-18 was observed in the endometrium of patient with RPL (D'Ippolito *et al.* 2016). This evidence points toward a potential role of DAMPs in early pregnancy failure, although there are still many unresolved issues.

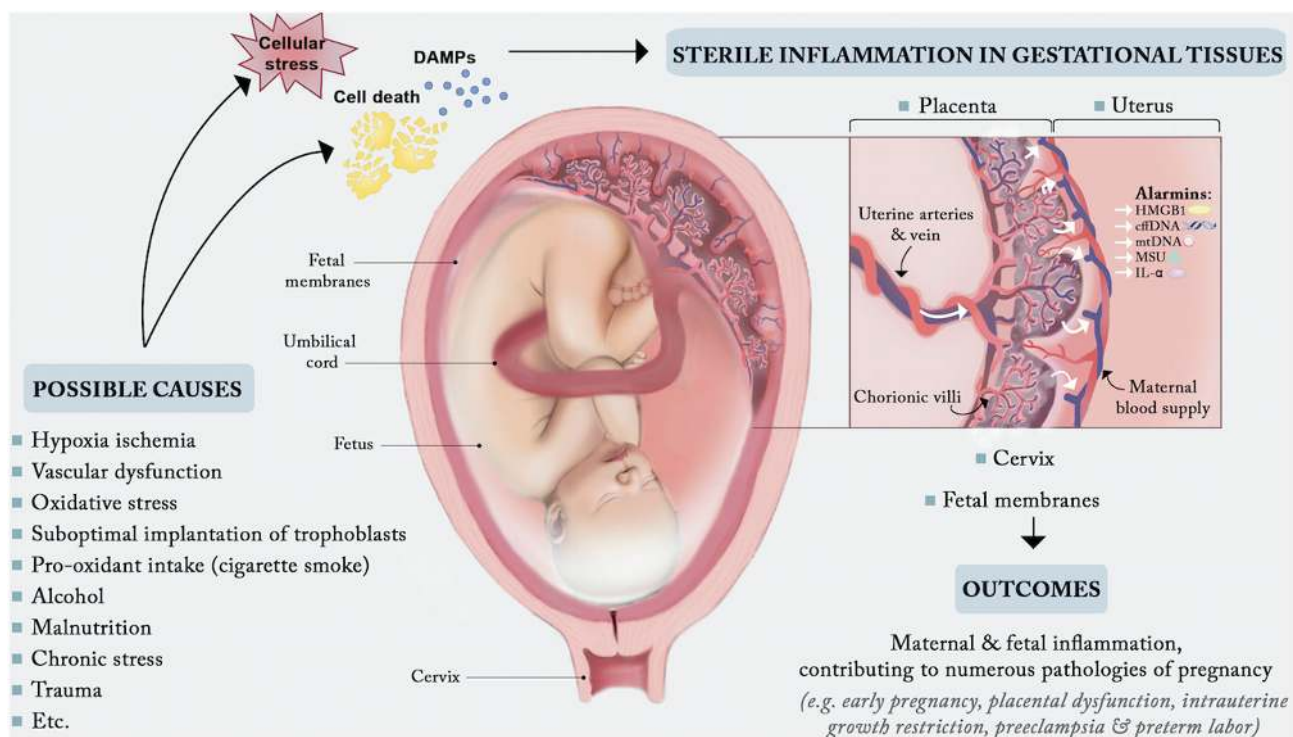


Figure 2 Principal sites of release and actions of alarmins in pathological pregnancy. Multiple causes of cellular stress will affect cell viability and lead to the release of DAMPs (alarmins) by the fetal membranes and the placenta. These DAMPs will then act not only on the placenta itself but also on the uterus, cervix and fetal membranes inducing inflammation and contributing to many complications of pregnancy.

Placental dysfunction

Placental dysfunction is an early event in both IUGR and preeclampsia (and represents a defined etiology of preterm labor) but will be addressed mainly in this subsection. Causes of placental dysfunction include (but are not limited to) hemodynamic conditions (hypertension and reduced blood viscosity (e.g., in anemia or as a result of using blood thinner drugs)), diabetes, placental abruption and improper implantation. These conditions induce hypoxia/ischemia, oxidative stress and/or inflammation in placenta, which subsequently induces increased trophoblast cell death (Maxwell *et al.* 2015), hence favoring the release of alarmins, and can be a cause or a consequence of abnormal placental function, which likely differs from one patient to another. Nonetheless, elevated alarmin levels have been associated with placental dysfunction, which leads to the amplification of the effects of placental inflammation and dysfunction. Accordingly, levels of HMGB1, uric acid and cffDNA are all elevated in pregnancies at high risk of developing complications associated with placental dysfunction such as growth restriction or preterm labor (Girard *et al.* 2014). Given that these alarmins have been reported to induce placental inflammation (Mulla *et al.* 2011, 2013, Phillippe 2015, Shirasuna *et al.* 2016), their upregulation in high-risk pregnancies may plausibly contribute to placental dysfunction. Additionally, elevated placental mitochondrial DNA concentrations were associated with placental abruption (Qiu *et al.* 2015).

Intrauterine growth restriction

IUGR is characterized by a suboptimal fetal growth and is associated with perinatal morbidity and mortality. Numerous causes have been suggested for IUGR, among which placental dysfunction is predominant. Hence, a role for sterile inflammation in its onset has already been established in the previous section. Furthermore, studies assessing the levels of alarmins in maternal plasma have found elevation of multiple candidates in IUGR. An increase of S100B proteins in maternal plasma was reported in women with IUGR, which correlated with brain morbidity outcomes in neonates (intraventricular hemorrhage) (Gazzolo *et al.* 2006). Interestingly, amniotic fluid concentration of S100B was found to sensitively and specifically predict spontaneous intrauterine fetal death (Florio *et al.* 2004). Although an early study conducted by Sekisawa *et al.* found no significant difference in maternal plasma levels of cffDNA in nine women with IUGR compared with 20 gestation age-matched controls (Sekisawa *et al.* 2003), more recent studies using larger cohorts found significant increases in women with IUGR (Smid *et al.* 2006, Al Nakib *et al.* 2009, Alberly *et al.* 2009). Similarly, circulating mitochondrial DNA was also found to be increased in patients with IUGR (Colleoni *et al.* 2010). Furthermore, a study by Mert *et al.* found

a marginal increase in maternal plasma uric acid levels in pregnancies complicated with IUGR; this elevation was more pronounced in women with preeclampsia (PE) (Mert *et al.* 2012).

Preeclampsia

PE represents a leading cause of maternal and fetal mortality and morbidity and is characterized by maternal hypertension and proteinuria; additionally, it is often associated with fetal growth restriction (Srinivas *et al.* 2009). PE is mainly a consequence of deficient uteroplacental blood flow, and removal of placenta is the only known curative treatment. Along these lines, a major feature of the pathophysiology of PE is the failure of fetal trophoblasts to invade uterine arteries, resulting in reduced placental perfusion and ensued hypoxia/ischemia. This localized oxygen and nutrient deprivation is associated with exaggerated trophoblast cell death (Jones & Fox 1980, Chua *et al.* 1991, Knight *et al.* 1998, Johansen *et al.* 1999, Leung *et al.* 2001, Wu *et al.* 2012), which has been suggested to directly contribute to the disease by releasing mediators of inflammation that promote endothelial activation and systemic maternal inflammation (Smarason *et al.* 1993, Knight *et al.* 1998, Redman & Sargent 2003). Although the etiology of PE is mostly unknown, a major hallmark is a generalized inflammatory response characterized by high cytokine levels, such as IL-1 β , IL-6, IL-8 and tumor necrosis factor- α (Vince *et al.* 1995, Mellembakken *et al.* 2001, Laresgoiti-Servitje 2013, Harmon *et al.* 2016). Because this inflammatory response usually occurs in the absence of microbial infection, PE primarily represents a sterile inflammation.

Trophoblasts contain numerous alarmins, including uric acid, cffDNA, HMGB1 and IL-1 α , which can mount a sterile inflammatory response and whose contributions to PE are increasingly reported. These alarmins are released in maternal circulation as free mediators upon trophoblast necrosis, or as part of SCTMs consequently to trophoblast apoptosis; the latter form is subsequently prone to engulfment and clearance by phagocytes, wherein it can interact with intracellular targets including TLRs. Studies by Huppertz *et al.* and Chen *et al.* respectively reported that placental hypoxia, as observed in PE, favors trophoblast necrosis vs apoptosis (Huppertz *et al.* 2003), and that once cleared by phagocytes, necrotic (but not apoptotic) trophoblasts can induce an inflammatory response characterized by increased adhesion of monocytes to endothelial cells (Chen *et al.* 2006). This suggests that pathological trophoblast necrosis, as observed in PE, induces distinct inflammatory mechanisms than those observed with normal pregnancy, which may contribute to the pathophysiology. Complementary evidence by Aly *et al.* suggests that SCTMs from pregnancy complicated with preeclampsia exhibit different contents and induce

the generation of significantly increased amount of superoxide radicals from neutrophils, implying increased toxicity (Aly *et al.* 2004).

cffDNA

The most studied alarmin in PE is cffDNA. cffDNA is elevated in pregnancies complicated by preeclampsia (Levine *et al.* 2004, Lazar *et al.* 2009, Vlkova *et al.* 2015) and its levels correlate with the degree of impairment in placental perfusion (Sifakis *et al.* 2009). For these reasons, it is broadly investigated as a biomarker of PE (Martin *et al.* 2014). As mentioned above, cffDNA can trigger inflammation and adverse pregnancy outcomes in mice via TLR9 (Scharfe-Nugent *et al.* 2012). Similarly, mitochondrial DNA (mtDNA) is released by trophoblasts upon death and its levels in maternal circulation are increased in PE (and IUGR) (Lattuada *et al.* 2008, Goulopoulou *et al.* 2012, Qiu *et al.* 2012); the immunostimulatory and pro-inflammatory role of mitochondrial DNA in PE has been reviewed elsewhere (McCarthy & Kenny 2016). Activation of TLR9 by fetal or mitochondrial cell-free DNA, or other mediators (including HMGB1), has been suggested to lead to vascular dysfunction and hypertension (Goulopoulou *et al.* 2012). Interestingly, women with preeclampsia express higher levels of placental TLR9 (Pineda *et al.* 2011). Self DNA is becoming increasingly considered as a major immunostimulatory molecule responsible for adverse pregnancy outcomes (Hartley *et al.* 2015, Sifakis *et al.* 2015).

Uric acid

Hyperuricemia is commonly observed in pregnancies complicated by PE (Laughon *et al.* 2011). More importantly, plasmatic levels of uric acid positively correlate with PE severity (Voto *et al.* 1988), and hyperuricemia (serum uric acid >4–5.8 mg/dL) generally heralds poor maternal and fetal outcomes (Hawkins *et al.* 2012). This hyperuricemia may represent a consequence of the symptoms associated with PE, such as loss in renal function, tissue injury, acidosis and increased activity of xanthine oxidase (Johnson *et al.* 2003). However, whether uric acid is an inactive, dead-end consequence of PE or a contributor to the disease is controversial (Kang *et al.* 2004, Martin & Brown 2010). Evidence for a causal role of uric acid includes the following: (1) uric acid exerts pro-inflammatory and vasoconstrictive effects in rats (Kang *et al.* 2004); furthermore, rats rendered hyperuricemic with uric acid, and uricase inhibitor administration develop hypertension and many other major features of preeclampsia, which is reversed by the xanthine oxidase inhibitor allopurinol (Mazzali *et al.* 2001, Kang *et al.* 2004); (2) elevation of uric acid levels in maternal plasma often precedes hypertension and proteinuria in humans (Powers *et al.* 2006,

Laughon *et al.* 2011); (3) mechanistically, uric acid induces a pro-inflammatory, pro-contractile phenotype in vascular smooth muscle cells by activating NF- κ B, AP-1 and MAPK (p38, ERK p42/p44) pathways and downstream expression of Cox-2, MCP-1, CRP and thromboxane A₂, which plausibly contributes to many features of PE including inflammation (Kang *et al.* 2002, 2005, Kanellis *et al.* 2003); (4) hyperuricemic rats have decreased placental activity of eNOS (Kang *et al.* 2005), an enzyme catalyzing nitric oxide generation, which is a critical vasodilator for efficient placental perfusion given the absence of autonomic innervation in placenta; and (5) uric acid promotes the release of pro-inflammatory cytokines in rats challenged with LPS, and oppositely treatment of hyperuricemic rats with allopurinol or sodium bicarbonate, which decreases uric acid concentrations, decreases this inflammation (Netea *et al.* 1997). This suggests that uric acid, once released by trophoblasts upon necrosis, may play a role in the pathogenesis of PE. Interestingly, as PE is associated with decreased levels of ascorbate (Mikhail *et al.* 1994), an antioxidant enzyme responsible for reducing urate anions back into uric acid, it is possible that uric acid, via its oxidized form, induces oxidative stress specifically during PE. Accordingly, it was demonstrated that the pro-inflammatory effects of uric acid are attenuated in the presence of antioxidants, which suggests that urate anions are an important part of uric acid action (Kanellis *et al.* 2003).

HMGB1

Similar to cffDNA and uric acid, maternal plasma levels of HMGB1 have been found to increase during pregnancy, and more importantly to reach exaggerated levels in women with PE (Pradervand *et al.* 2014). This finding was corroborated in a study by Zhu *et al.*, with further evidence revealing increased levels of HMGB1 and RAGE in the placenta of women with severe PE, especially in the cytoplasmic compartment of trophoblasts (Zhu *et al.* 2015). Additionally, RAGE and TLR4, two receptors with affinity for HMGB1, were found to have higher expression in placentas from pregnancies complicated with PE (Kim *et al.* 2005, Chekir *et al.* 2006). Pro-inflammatory effects of HMGB1 via TLR9 have been suggested to contribute to the pathophysiology of PE (Scharfe-Nugent *et al.* 2012).

IL-1 α

An important role of IL-1 as a contributor to hypertension has been proposed (Voelkel *et al.* 1994, Zou *et al.* 2001, Krishnan *et al.* 2014). Additionally, IL-1 is known to exacerbate inflammation in placenta (Baergen *et al.* 1994, Nadeau-Vallee *et al.* 2015b), the key organ in PE. Accordingly, variation in the IL-1 α and IL-1Ra genes has been associated with increased risk of PE

(Hefler *et al.* 2001, Li *et al.* 2014, Ghasemi *et al.* 2015). Interestingly, antagonism of IL-1 dose dependently restores adequate placental perfusion following endotoxin exposure (Girard *et al.* 2010).

Overall, there is accumulating evidence that alarmins (1) are released in maternal circulation in numerous conditions, but mainly as a result of trophoblast death; (2) are elevated in pregnancies complicated with PE, systemically and locally in the placenta; (3) can initiate an inflammatory response via PRRs abundantly expressed in the uteroplacental compartment especially in women with PE; and (4) can directly contribute to the pathogenesis of the disease by mounting a sterile inflammatory response to placental hypoxia/ischemia. The establishment of animal models of preeclampsia is needed to test novel therapeutics to block alarmin activity and therefore achieve a greater knowledge of the importance of alarmins in PE.

Preterm labor

Labor is the culmination of an inflammatory cascade wherein leukocytes invade the uterus to produce a broad range of uterotrophins (cytokines, chemokines and others) leading to uterine activation (cervical ripening, weakening of fetal membranes and myometrial contractility intensification). Once prematurely triggered by pathological inflammation, this pathway can lead to preterm labor, independent of infection (Romero *et al.* 2006, Christiaens *et al.* 2008). Efforts are underway to identify the most early or upstream event in this cascade to develop effective preventive treatments. Alarmins are interesting candidate as their release represents an initiating step in sterile inflammation following an injury, and because most preterm births happen without any evidence of infection, which raises interrogations about what factor (or group of factors) initiates pro-labor pathways in women with preterm labor and no infection. Accordingly, it is reported that sterile intra-amniotic inflammation is observed significantly more often than microbial-associated intra-amniotic inflammation in patients with preterm labor and intact membranes (Romero *et al.* 2014), and recent advances have found increased expressions of alarmins, namely cffDNA (Leung *et al.* 1998, Farina *et al.* 2005, Jakobsen *et al.* 2012), HMGB1 (Bredeson *et al.* 2014), interleukin-1 (Romero *et al.* 1989, Puchner *et al.* 2011), uric acid (Roberts *et al.* 2005, Homer *et al.* 2008) and S100B (Friel *et al.* 2007), in maternal serum or gestational tissue of women at risk of preterm labor or having delivered preterm. This increase in alarmins could be a link between numerous causes of preterm labor wherein tissue injury and cell death are implicated, and the initiation of a pro-inflammatory, pro-labor response. These causes include placental and uterine senescence, breakdown of maternal/fetal tolerance, uterine and cervical structural insufficiency, hemorrhage, multiple pregnancy, vascular disorders

and hypoxia/ischemia. Establishment of such a link could convey major implications for the development of effective therapeutics and diagnosis. Along these lines, cell-free DNA fraction ≥ 95 th percentile as screened between 14 and 20 weeks' gestation has been suggested as an effective biomarker to assess the risk of preterm birth (Dugoff *et al.* 2016).

Although most of the data linking a rise in alarmin levels and the onset of preterm labor are correlational, causal and mechanistic data have also been documented, especially for cffDNA and HMGB1. First, administration of cffDNA was found to induce placental inflammation and fetal resorption via TLR9 when injected i.p. to pregnant mice, contrastingly with the lack of effects of adult DNA (Scharfe-Nugent *et al.* 2012). This suggests that high levels of circulating cffDNA, as achieved in women with preterm or term labor (referenced above), can trigger pathological inflammation in gestational tissue via TLR9. Accordingly, hypomethylated CpG fragments, the TLR9-responsive element in cffDNA, have been found to induce prompt (24–48 h) leukocyte migration to uterus, TNF α production and preterm labor/birth in IL-10-deficient mice (Thaxton *et al.* 2009). Secondly, recent evidence shows that stimulation with HMGB1 induces the expression of uterine activation genes including *Tnfa*, *Il6* and *Pgbs2* in human myocytes (Menon *et al.* 2016), and labor in mice when administered intra-amnion (Gomez-Lopez *et al.* 2016); and correspondingly, an association between high HMGB1 amniotic levels and earlier deliveries in patients with intra-amniotic sterile inflammation has been reported (Romero *et al.* 2014, Baumbusch *et al.* 2016). Furthermore, HMGB1 administration *ex vivo* in human fetal membranes induces p38-mediated IL-6 and IL-8 production (Bredeson *et al.* 2014). In this setting, a potential role in labor for the HMGB1 pathway was reported using transcriptomics and bioinformatics analysis (Stephen *et al.* 2015, Menon *et al.* 2016). Additionally, HMGB1 and its receptors RAGE, TLR2 and TLR4 are found in cervix and extranuclear fraction of HMGB1 increases with labor onset at term and preterm (Dubicke *et al.* 2010), suggesting that HMGB1 may play a role in cervical ripening. Interestingly, stimulation with endotoxins triggers HMGB1 expression and release *in vitro* in human fetal membranes (Bredeson *et al.* 2014) and *in vivo* in murine fetuses when endotoxins are administered in dams (i.p.) (Buhimschi *et al.* 2009); concordantly, women with intra-amniotic infection/inflammation and women with chorioamnionitis have higher amniotic fluid levels of HMGB1 (Romero *et al.* 2011, Romero *et al.* 2012). The latter suggests that HMGB1 may also have an implication in the infectious etiology of preterm birth.

IL-1 α was the first alarmin to be associated with preterm labor and labor at term (Romero *et al.* 1989). However, as IL-1 β is released in response to infection by immune and non-immune cells in the uteroplacental

Table 1 Therapeutic molecules targeting the alarmin activity of HMGB1, uric acid, IL-1 α and cell-free DNA.

| Target | Therapeutic molecule | Description | Mode of action | References |
|--|--|---|---|---|
| HMGB1/RAGE | Recombinant box A | Truncated N-terminal domain of HMGB1 (~10 kDa) | Competitive antagonist of the receptor RAGE | Kokkola <i>et al.</i> (2003), Li <i>et al.</i> (2003) |
| | S100P-derived RAGE antagonistic peptides | Small peptide inhibitors derived from S100P, a RAGE ligand (~1 kDa) | Binds with RAGE and inhibits HMGB1-mediated NF- κ B activation | Arumugam <i>et al.</i> (2012) |
| | Ethyl pyruvate | Derivative of pyruvate (~116 Da) | Downregulates the HMGB1–RAGE axis <i>in vitro</i> and <i>in vivo</i> | Dave <i>et al.</i> (2009), Li <i>et al.</i> (2012) |
| | Methotrexate | Antimetabolite and anti-folate drug used in the treatment of cancer and autoimmune diseases (~454 Da) | Binds to HMGB1 and prevents its interaction with RAGE | Kuroiwa <i>et al.</i> (2013) |
| | Neutralizing HMGB1 antibody | Polyclonal antibody against the B box domain of HMGB1 | Binds to HMGB1 and prevents its interaction with RAGE | Kokkola <i>et al.</i> (2003) |
| | Anti-HMGB1 mAB | Monoclonal antibody against HMGB1 (IgG2b 2G7) | Binds to HMGB1 and prevents its interaction with RAGE | Schierbeck <i>et al.</i> (2011) |
| | Glycyrrhizin | Natural anti-inflammatory and antiviral triterpene in clinical use (~822 Da) | Binds to HMGB1 and reduces its activity | Mollica <i>et al.</i> (2007) |
| | Quercetin | Plant-derived flavonoid (302 Da) | Inhibits the cytokine activity of HMGB1 | Tang <i>et al.</i> (2009) |
| | Lycopene | Natural carotenoid (~536 Da) | Inhibits the cytokine activity of HMGB1 | Lee <i>et al.</i> (2012) |
| | Vasoactive intestinal peptide (VIP) and urocortin | Endogenous neuropeptides | Inhibits HMGB1 secretion | Chorny and Delgado (2008) |
| | Pituitary adenylate cyclase-activating polypeptide (PACAP) | Endogenous neuropeptide (~4.5 kDa) | Inhibits HMGB1-induced cytokine release <i>in vitro</i> and <i>in vivo</i> | Tang <i>et al.</i> (2008) |
| | <i>Chim 2A</i> | Kinked oligonucleotide duplexes (18bp) | Interacts with HMGB1; potentially blocks a number of HMGB1 extracellular effects | Musumeci <i>et al.</i> (2011) |
| Uric acid | Allopurinol | Uric acid analog (~136 Da) | Reduces uric acid production by xanthine oxidase | Shi <i>et al.</i> (2003), Kono <i>et al.</i> (2010) |
| | Uricase, also known as urate oxidase | Homotetrameric enzyme specific to uric acid (~33 kDa) | Breaks down uric acid to allantoin | Shi <i>et al.</i> (2003), Kono <i>et al.</i> (2010) |
| | Sodium bicarbonate | Salt composed of sodium ions and bicarbonate ions (~84 Da) | Increases urine pH, thus increasing the dissolution and excretion of uric acid and decreasing its plasma concentrations | Netea <i>et al.</i> (1997) |
| | Benzbromarone | Small organic molecule (~424 Da) | Uricosuric agent and non-competitive inhibitor of xanthine oxidase | Hanvivadhanakul <i>et al.</i> (2002) |
| IL-1 α /IL-1R | Anakinra | Recombinant version of the interleukin-1 receptor antagonist (IL1-Ra) (~17 kDa) | IL-1R competitive antagonist | Dinarello <i>et al.</i> (2012) |
| | Riloncept also known as IL-1 Trap | Dimeric fusion protein (~251 kDa) | Soluble decoy IL-1R; competitive antagonist | Dinarello <i>et al.</i> (2012) |
| | 101.10, also known as rytvela | Small peptide (all-d) (~850 Da) | Non-competitive IL-1R antagonist, negative allosteric modulator of IL-1R-associated JNK, p38, c-jun and Rho/ROCK activity | Quiniou <i>et al.</i> (2008), Nadeau-Vallee <i>et al.</i> (2015b) |
| Cell-free DNA including cfDNA and mtDNA/TLR9 | ODN TTAGGG (A151) | Synthetic oligonucleotide | Interacts with TLR9; neutralizes the stimulatory effect of CpG-containing oligonucleotides | Kaminski <i>et al.</i> (2013) |
| | Chloroquine | Small organic molecule (~320 Da), diprotic weak base | Reduces NF- κ B and AP-1 activation induced by CpG oligonucleotides; also exerts other anti-inflammatory effects | Hong <i>et al.</i> (2004) |
| | AT791 and E6446 | Small organic molecules | Inhibit DNA–TLR9 interaction and TLR9 signaling <i>in vitro</i> ; <i>in vivo</i> efficacy also reported | Lamphier <i>et al.</i> (2014) |

compartment, its role has been primarily investigated rather than IL-1 α . As mentioned previously, IL-1 β and IL-1 α bind to the same receptor and have similar effects. Evidence linking IL-1 α to preterm labor are as follows:

(1) stimulation of IL-1R induces the transcription of numerous pro-labor genes via MAPK p38, JNK, c-jun and small GTPase Rho in myometrial smooth muscle cells, which results in increased myometrial contractility

(Tribe *et al.* 2003, Chevillard *et al.* 2007, Nadeau-Vallee *et al.* 2015b); and preterm labor in mice and non-human primates (Romero *et al.* 1991, Sadowsky *et al.* 2006); (2) antagonism of IL-1R prevents all of these events (Romero & Tartakovsky 1992, Nadeau-Vallee *et al.* 2015b); (3) IL-1 α amniotic fluid levels are elevated in women that deliver preterm (Figuerola *et al.* 2005); (4) preterm labor is associated with increased IL-1 α activity in amniotic fluids (Romero *et al.* 1989); and (5) maternal polymorphisms and haplotypes in the IL-1 α gene (Sata *et al.* 2009), as well as fetal polymorphism in the endogenous IL-1R antagonist (Witkin *et al.* 2003), have been associated with increased risk of preterm birth. The critical role of IL-1 in preterm labor has been reviewed elsewhere (Nadeau-Vallee *et al.* 2015a).

Interestingly, sterile inflammation has been suggested to induce a common inflammatory pathway leading to labor at term in normal pregnancies (Kobayashi 2012, Phillippe 2014). Accordingly, transcriptomic analysis of chorionic decidua collected at term predicted HMGB1 as a potential upstream regulator of parturition (Stephen *et al.* 2015). As mentioned previously, cffDNA is another alarmin candidate initiator of labor at term (Phillippe 2014).

Perspectives

Inflammatory processes are key determinants of pregnancy outcomes, independent of infection. We hereby presented a body of evidence pointing to an important role of alarmins in numerous complications of pregnancy. Alarmins are released as a result of sterile tissue stress and trigger an inflammatory cascade via PRRs (and other receptors), which are abundantly expressed in gestational tissue in immune and non-immune cells. Of all candidate alarmins, HMGB1, uric acid, IL-1 α and cffDNA have been predominantly studied for their effect in pathological pregnancy events, particularly miscarriages, RPL, placental dysfunction, IUGR, preeclampsia and preterm labor. Data accumulated to date converge toward a deleterious contribution of alarmins to the pathophysiology of these diseases. Hence, effectively blocking alarmins could potentially result in favorable outcomes. This strategy has yielded positive outcomes in other inflammatory diseases, as it applies to HMGB1 (Gong *et al.* 2009), uric acid (Netea *et al.* 1997), IL-1 (Thaler *et al.* 2009) and cffDNA (Scharfe-Nugent *et al.* 2012). Therapies effective to block HMGB1, uric acid, IL-1 α and cffDNA are summarized in Table 1. Furthermore, the development of suitable animal models of IUGR and preeclampsia is an unavoidable step in assessing the efficacy and innocuousness of such therapy. Although many models have been described, none of them reproduce the complete spectrum of pathophysiological changes associated with IUGR or preeclampsia (McCarthy *et al.* 2011, Swanson & David 2015). Further efforts are also

needed to develop specific and potent antagonists of uric acid and cffDNA to gain better knowledge in their role during physiological and pathological pregnancy.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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