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BRIEF REVIEWS

The P2X₇ Receptor: A Key Player in IL-1 Processing and Release¹

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Human IL-1 family proteins are key mediators of the host response to infections, injury, and immunologic challenges. The mechanism by which IL-1 activates proinflammatory responses in target cells, and the plasma membrane receptors involved, is fairly well known. This has led to the development of innovative drugs that block IL-1 downstream to its synthesis and secretion. On the contrary, the mechanism of IL-1 and other IL-1 family members (e.g., IL-18) maturation and release is incompletely understood. Accumulating evidence points to a plasma membrane receptor for extracellular ATP, the P2X₇ receptor, as a key player in both processes. A deeper understanding of the mechanism by which the P2X₇ receptor triggers IL-1 maturation and exteriorization may suggest novel avenues for the treatment of inflammatory diseases and provide a deeper insight in the fundamental mechanism of protease activation and cellular export of proteins lacking a leader sequence. The Journal of Immunology, 2006, 176: 3877–3883.

Interleukin-1 β is a key mediator of host response to infections and a primary cause of inflammation (1, 2). Bacterial products (e.g., LPS) and host-derived inflammatory factors cause the synthesis of IL-1 β in the form of a biologically inactive procytokine (molecular mass, 31 kDa) that remains dispersed in the cytosol until a second stimulus drives processing and release of the 17-kDa active form. IL-1 α and IL-18, two additional members of the IL-1 superfamily with proinflammatory activity, are also synthesized as leaderless procytokines and accumulate in the cell cytoplasm in the absence of a maturation-promoting second stimulus (1, 3). Another member of the IL-1 superfamily, IL-1 receptor antagonist (IL-1Ra),^{3,3} is also synthesized and released in parallel to IL-1 β , IL-1 α , and IL-18 (4). IL-1Ra binds to type I IL-1 receptor (IL-1RI) and blocks IL-1-

dependent signal transduction, thus functioning as an endogenous, IL-1-selective inhibitor of inflammation (5).

In vivo, IL-1 β is elevated during infections and in several chronic inflammatory diseases such as arthritis, scleroderma, systemic lupus erythematosus, vasculitis, sepsis, septic shock, and in the presence of atherosclerotic lesions leading to myocardial infarction (2). However, the in vitro process of IL-1 β release is very inefficient, as activated monocytes release into the extracellular space < 10% of the IL-1 β accumulated intracellularly (6). This finding has led to postulate that IL-1 β release requires two stimuli (two hits), the first one driving gene transcription and pro-IL-1 β accumulation and the second one processing and release.

In recent years, increasing attention has been paid to extracellular ATP as a candidate danger signal locally released at the inception of inflammation (7, 8). One of the most striking features of this nucleotide is its unmatched ability to promote massive release of mature IL- β from LPS-primed mononuclear phagocytes and other cell types (9). ATP-driven maturation and release of IL-1 β are specifically mediated by the P2X₇ receptor (P2X₇R) for extracellular ATP (10–12). The molecular dissection of this novel pathway for cytokine release may disclose new targets for anti-inflammatory therapy.

IL-1

IL-1, the product of a member of a superfamily of related genes, some of which encode proteins not involved in inflammation (2), causes the accumulation of arachidonic acid metabolites, up-regulates inducible NO synthase, and sustains NO production. Furthermore, it enhances expression of adhesion molecules on endothelial cells, promotes extravasation of leukocytes, modulates muscle metabolism, and induces fever (2, 13). IL-1 is also a key activator of osteoclasts, thus causing bone resorption (14).

IL-1 α and IL-1 β share low sequence homology (20–30%) but high three-dimensional similarity. Upon cell activation,

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³ Abbreviations used in this paper: IL-1Ra, IL-1 receptor antagonist; IL-1RI, type I IL-1 receptor; casp, caspase; procasp, procaspase; ASC, apoptosis-associated speck-like protein containing a CARD; IL-1R-AcP, IL-1R accessory protein; DC, dendritic cell; SNP, single nucleotide polymorphism; P2X₇R, P2X₇ receptor.

typically via plasma membrane TLRs, IL-1 α and IL-1 β are translated as 31-kDa leaderless secretory proteins (pro-IL-1 α and pro-IL-1 β). Although IL-1 α is already active in this form, IL-1 β needs a proteolytic step to generate the 17-kDa mature cytokine. Pro-IL-1 β can be processed in the extracellular milieu by several proteases activated during inflammation, whereas the IL-1 β -converting enzyme, later named caspase (casp)-1, is the key protease responsible for intracellular IL-1 β processing (15, 16). Recently, IL-33, an IL-1 β -like cytokine acting at the ST2 receptor, has also been shown to be processed by casp-1 (17). In resting cells, casp-1 is normally present as an inactive 45-kDa precursor, procaspase (pro-casp)-1. Proteolytic activation of procasp-1 occurs in a multimeric specialized structure named “IL-1 β inflammasome protein complex” (18) comprising at least four different proteins (casp-1, casp-5, apoptosis-associated speck-like protein containing a CARD (ASC), and NACHT-, LRR-, and PYD-containing protein) that transiently oligomerize upon cell activation (19). The mechanism of inflammasome assembly and activation is a focus of intense investigation.

IL-1 α and IL-1 β bind to the same receptor named IL-1RI. Upon IL-1 binding, IL-1RI recruits the accessory protein IL-1R-AcP, a member of the Ig superfamily, and initiates a stimulatory signal transduction cascade. A decoy receptor is also present, IL-1RII, that is unable to complex with IL-1R-AcP and to generate a biological signal (20). IL-1RII competes with IL-1RI to down-modulate IL-1 activity (21).

IL-1Ra

The IL-1Ra is secreted in response to the same stimuli that drive IL-1 release and binds to IL-1RI and IL-1RII (4). However, IL-1Ra lacks the IL-1R-AcP interacting domain, thus its binding results in inhibition of the IL-1 signaling cascade (22). IL-1Ra is generally secreted without requiring maturation, its function being to silence IL-1-dependent cell activation. Different IL-1Ra isoforms have been identified, of which three are intracellular (23).

The IL-1Ra knockout mouse spontaneously develops diseases similar to human rheumatoid arthritis and arteritis (24,

25). Administration of anakinra, a recombinant form of IL-1Ra, reduces local inflammation of joints and bone erosions in patients with rheumatoid arthritis (26, 27).

IL-18

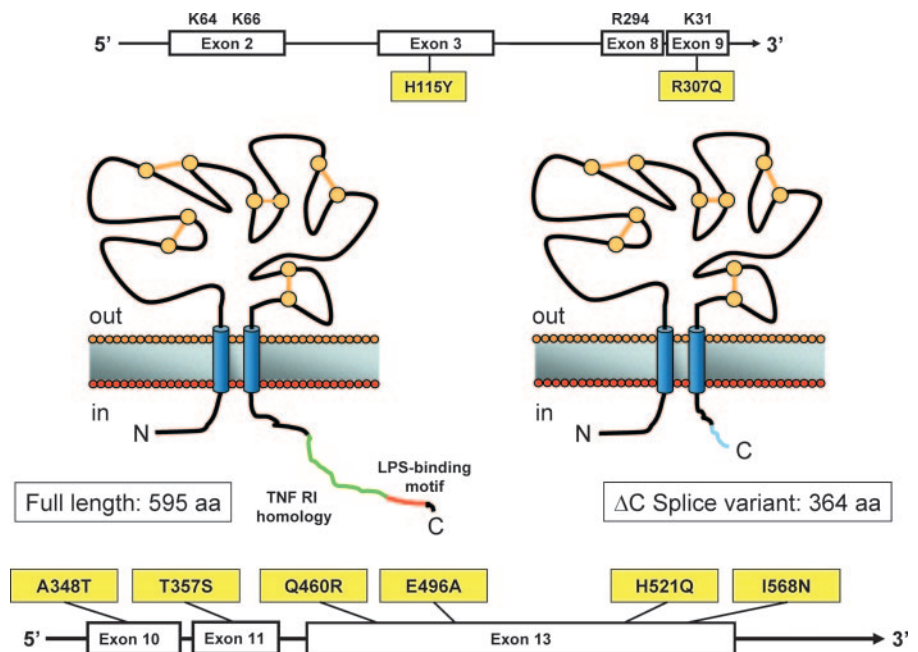
IL-18 shares structural features with IL-1 (3). Like IL-1, IL-18 also lacks a signal peptide, and it is synthesized as a biologically 24-kDa inactive precursor (pro-IL-18), which is converted by casp-1 to its mature 18-kDa form (28, 29). In contrast to IL-1 β , IL-18 is not an endogenous pyrogen (2). IL-18 binds to an $\alpha\beta$ heterodimeric receptor inducing the synthesis of other proinflammatory cytokines (IL-6, IL-8, TNF- α , IL-1 β , and IFN- γ), CD95 ligand, and several chemokines. It also increases the expression of ICAM-1 and VCAM-1 on endothelial cells (2). IL-18 is secreted by a variety of cells, including epithelial cells, keratinocytes, synovial fibroblasts, monocytes, macrophages, and dendritic cells (DCs) (30). Like IL-1, IL-18 behaves as an angiogenic factor through increased expression of vascular endothelial growth factor.

The P2X₇R for extracellular ATP

Basically all cell types express plasma membrane receptors for extracellular nucleotides named P2 receptors. As of now, 15 members have been cloned and classified into two subfamilies: P2Y and P2X. P2YRs are G protein coupled, whereas P2XRs are cation-selective channels (31, 32). The P2X₇R (Fig. 1) is a most peculiar receptor/channel in that sustained activation by extracellular ATP causes the formation of a reversible plasma membrane pore permeable to hydrophilic solutes of molecular mass up to 900 Da (33, 34). Pore formation is essential for P2X₇R-stimulated IL-1 release (35).

The P2X₇R gene is located at position 12q24 and encodes a 595-aa long polypeptide with two transmembrane stretches, a bulky extracellular domain and N- and C-terminal residues both on the cytoplasmic side of the plasma membrane (34, 36). The extracellular loop contains 10 cysteine residues that may form disulfide bonds and a sequence stretch (aa 170–330) likely containing six-stranded β -pleated sheets (37). This region has been proposed to host the ATP binding site (38). The

FIGURE 1. The P2X₇R: membrane topology and aa substitutions caused by the main SNPs so far described. The full-length and truncated (Δ C) splice variant of the P2X₇R are shown. The truncated form lacks almost the entire COOH tail (249 aa, green, red, and short black traits) but bears an extra 18 aa (light blue trait) due to inclusion of the intron between exons 10 and 11 (94). TNFRI homology domain (green) and putative LPS-binding region (red) are shown. Cysteine residues forming putative disulfide bridges are also shown. Amino acid changes are highlighted in yellow boxes, whereas residues involved in ATP binding in exons 2, 3, 8, and 9 are indicated in black.



main structural distinctive feature of the P2X₇R is a long C-terminal tail (244 aa) harboring multiple potential protein and lipid interaction motifs (see Fig. 1) (39). Although other receptors of the P2X subfamily have been shown to form functional hetero-oligomers, the P2X₇ subunits seem to associate only with each other to form homomeric P2X₇R (40).

Unique in the P2XR subfamily, P2X₇R is highly polymorphic. More than 260 single nucleotide polymorphisms (SNPs) have been described in the human *P2X₇R* gene, but only a few have been functionally characterized. Wiley and coworkers (41–43) have identified four loss-of-function single amino acid substitutions, three located in the cytoplasmic tail of the receptor (T357S, E496A, and I568N), and one in the putative ATP binding site (R307Q) (38). Our group has characterized the first gain-of-function polymorphism so far identified (H155Y) (44). Wiley and coworkers (45) have also described a splice site mutation in the first intron of the *P2X₇R* gene that produces a null allele. Polymorphisms in the promoter region of the gene have also been identified (46). No convincing disease association has been so far demonstrated for these SNPs.

The mechanism of pore formation by the P2X₇R is a matter of debate: while some investigators hold the conservative opinion that pore formation is due to an ATP-dependent increase in size of the P2X₇R channel itself (47), others believe that the pore is a separate molecular structure activated by the P2X₇R (48, 49). Early studies by Dubyak and coworkers (48, 49) suggested that it might coincide with the plasma membrane pore activated by the sea toxin maitotoxin. More recently, Elliott et al. (50) have hypothesized that P2X₇R-dependent transitions in plasma membrane permeability might involve the modulation of the multidrug transporter P-glycoprotein. Whichever the molecular basis of pore formation, there is no doubt that P2X₇R activation causes a massive upset of cytoplasmic ion homeostasis (51). Because the P2X₇R is nondesensitizing, the pore stays open as long it is bound by ATP. Removal of the nucleotide, by rinsing or apyrase-catalyzed hydrolysis, causes pore closure, thus allowing a reversible plasma membrane permeabilization. Should ATP stimulation be prolonged (over 15–30 min in most cell types), the cells become irreversibly injured and committed to death (52).

The P2X₇R and IL-1 release

LPS, the best known inducer of IL-1 secretion, is an incomplete stimulus because it causes massive accumulation of pro-IL-1 β in the cytosol while acting as only a very weak stimulator of IL-1 β maturation and externalization (6). This has led investigators to postulate a second stimulus to trigger efficient IL-1 β conversion and release. Early observations showed that extracellular ATP was a strong IL-1 β -releasing agent (53–55). Although at that time the identity of the plasma membrane receptor(s) involved and the signal transduction cascade activated was unknown, the massive efflux of intracellular K⁺ triggered by extracellular ATP suggested a mechanism based on cytoplasmic K⁺ depletion (51, 54, 56). Experiments performed *in vitro* and *in vivo* in *P2X₇R*^{-/-} mice conclusively identified the receptor responsible for ATP-dependent IL-1 β release as the P2X₇R (10–12, 57, 58).

The ATP effect is very fast, as externalization of mature IL-1 β is near maximal within 10–20 min. The main IL-1 β released form is the 17 kDa, but sustained ATP stimulation can also cause release of the 31-kDa form and of cytoplasmic markers

suggestive of a late nonspecific damage of the plasma membrane (11, 54). However, if care is taken to use ATP concentrations in the 0.5–1 mM range and short incubation times (15 min), a selective release of mature IL-1 β occurs and cells fully recover from the ATP challenge (11). Furthermore, it has been shown that cell lysis *per se* is unable to support pro-IL-1 β conversion (59).

It is currently debated whether extracellular ATP needs LPS priming to activate casp-1. Although until recently it was thought that priming was unnecessary (60, 61), two novel studies suggest that LPS pretreatment might indeed be needed to achieve substantial generation of casp-1 activation fragments in mouse macrophages (62, 63). Furthermore, blockade by YVAD-CHO shows that casp-1 activity is necessary for P2X₇R-dependent release of mature IL-1 β (Refs. 60 and 61 but see Ref. 64). The role of K⁺ efflux in supporting P2X₇R-dependent IL-1 β processing and release seems to be crucial as both processes are suppressed by inhibition of intracellular K⁺ efflux (11, 54, 61, 65, 66). Conversely, release of IL-1 β is enhanced in sucrose-containing medium, a condition in which K⁺ efflux is strongly potentiated (11, 61). Incidentally and in further support of the view that P2X₇R-dependent IL-1 β secretion does not require cell lysis, in sucrose medium, ATP-stimulated release of cytoplasmic markers is negligible (11, 67). Mutations in the human P2X₇R that prevent pore formation and reduce ATP-stimulated K⁺ efflux (e.g., the E496A substitution) inhibit IL-1 β release (35). Interestingly, this inhibitory effect is more marked in isolated macrophages than in whole blood (68), suggesting that in the presence of blood cells additional stimulatory factors are released. Altogether, there is consensus that the drastic upset of K⁺ homeostasis caused by P2X₇R opening has a key role in triggering IL-1 β maturation, whereas other intracellular ions (e.g., Ca²⁺) seem to be more involved in IL-1 β release (66, 69). This view is also supported by the casp-1 activating effect of nigericin-induced K⁺ depletion (70). A recent article (62) by Dixit's laboratory shows that mice deficient in the adaptor protein ASC fail to process pro-IL-1 β in response to ATP, thus suggesting that P2X₇R-dependent casp-1 cleavage may require assembly of a fully functional inflammasome. How the change in intracellular K⁺ concentration drives this process is an open question. On the other hand, a direct physical interaction of the P2X₇R with the inflammasome is as yet undocumented.

IL-1 β is a leaderless protein that does not appear to be contained within classical exocytotic vesicles. Thus, how it is externalized has long been a mystery. In the last few years experiments by Rubartelli and coworkers (66) and Surprenant and colleagues (71) have shed light on this issue suggesting a vesicular mechanism (Fig. 2). However, there are two crucial differences in the pathways proposed by the two groups: Rubartelli suggests that IL-1 β is accumulated into endocytic vesicles (secretory lysosomes) together with casp-1, then a P2X₇R-induced loss of intracellular K⁺ activates phosphatidylcholine-specific phospholipase C, which in turn causes an increase in cytosolic Ca²⁺, Ca²⁺-dependent phospholipase A₂ activation, and exocytosis of the IL-1 β -containing lysosomes. According to this model, casp-1 activation and IL-1 β processing are triggered by the K⁺ loss-stimulated activation of a Ca²⁺-independent phospholipase A₂ within the lysosomes.

In the model proposed by Surprenant, upon P2X₇R-mediated macrophage activation, IL-1 β is packaged into small

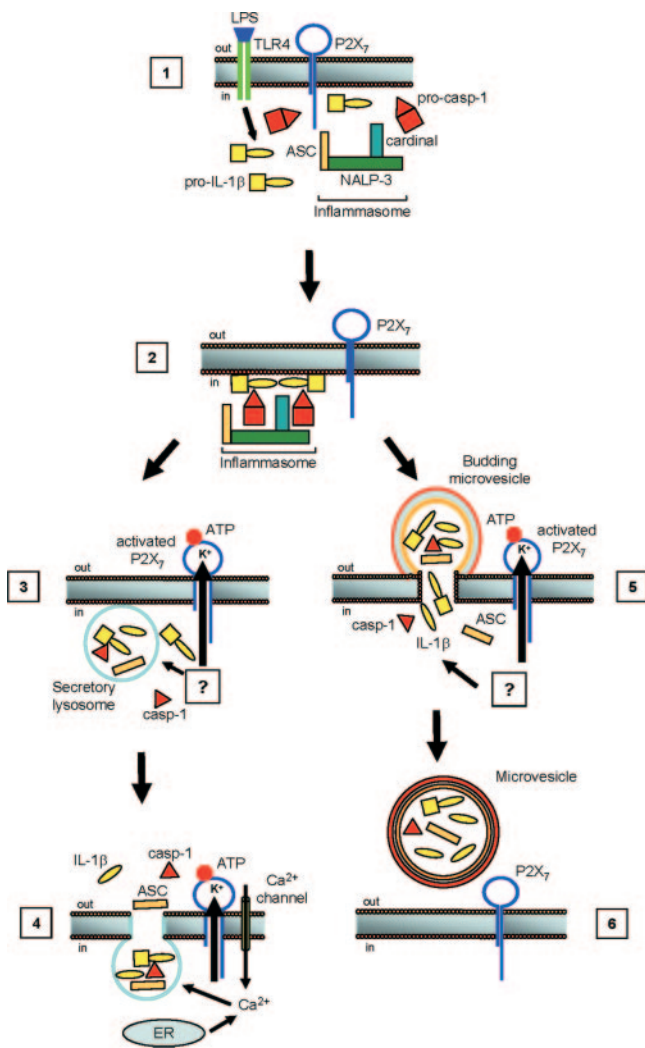


FIGURE 2. Pathways for P2X₇-stimulated IL-1 β cleavage and release. Activation of TLRs by LPS causes cytoplasmic accumulation of pro-IL-1 β and aggregation of the inflammasome components (step 1). Pro-IL-1 β and the inflammasome localize below the inner leaflet of the plasma membrane (step 2). Activation of the P2X₇R triggers K⁺ efflux, which in turn drives loading of some components of the inflammasome (e.g., pro-IL-1 β , casp-1, and ASC) into secretory lysosomes (66). During this process, procasp-1 is cleaved, and pro-IL-1 β is converted into mature IL-1 β (step 3). The secretory lysosome content is then secreted via a process requiring P2X₇R-dependent K⁺ efflux, Ca²⁺ increase, activation of phosphatidylcholine-specific phospholipase C, and both Ca²⁺-independent phospholipase A₂ and Ca²⁺-dependent phospholipase A₂ (step 4). An alternative model hypothesizes that after the inflammasome has aggregated below the inner leaflet of the plasma membrane (step 2), activation of the P2X₇R triggers budding of small membrane blebs (microvesicles, notice phosphatidylserine flip in the outer leaflet, red) that trap some of the inflammasome components (e.g., pro-IL-1 β , casp-1, and ASC). During this process, which is driven by the K⁺ loss, procasp-1 is cleaved, and pro-IL-1 β is converted into mature IL-1 β (step 5). Eventually, plasma membrane blebs pinch off and diffuse into the pericellular space (step 6).

plasma membrane blebs that are released into the extracellular space as microvesicles of size ranging from 200 nm to 1 μ m. These microvesicles are akin to the tissue factor-containing microparticles released from various cell types (72) and different from the large plasma membrane blebs that are also produced in cells stimulated via the P2X₇R (71, 73). Microvesicle budding and release are preceded by phosphatidylserine flip and loss of membrane asymmetry (71), a change in the membrane phospho-

lipid structure that might have a relevant signaling function (50). Recent experiments have shown that a vesicle-mediated mechanism for IL-1 β release is also present in mouse microglia and human DCs (Ref. 74; C. Pizzirani and F. Di Virgilio, submitted for publication). In DCs, casp-1 and -3 are also loaded into the vesicles, thus providing a mechanism for intravesicular pro-IL-1 β processing.

The microvesicle model proposed by Surprenant raises an obvious criticism: how does mature IL-1 β get through the microvesicle membrane and reaches the extracellular space to activate IL-1Rs? Recent observations from Verderio's laboratory and from our own group provide a possible answer: microvesicles shed from microglia and DCs, express the P2X₇R (together with several other markers), and lyse when exposed to extracellular ATP (Ref. 74; C. Pizzirani and F. Di Virgilio, submitted for publication). Thus, it can be hypothesized that once the microvesicles approach the plasma membrane of the target cells, where the ATP concentration is higher than in the bulk solution due to active cellular release (75), the P2X₇R is activated, the microvesicles lyse, and IL-1 β is released. In both the Rubartelli and Surprenant models, P2X₇R activation is crucial, but how and if this receptor is activated under physiological conditions is as yet an open question.

P2X₇R activation by extracellular ligands

The only known physiological activator of the P2X₇R is ATP. Scattered evidence suggests that ADP, but not other nucleotides, may also cause IL-1 β release via P2X₇R, but it is likely that this needs priming with ATP (76, 77). Since the cytoplasmic ATP concentration is in the millimolar range, acute cell injury or death will cause massive ATP release into the extracellular milieu. However, there is compelling evidence for nonlytic ATP secretion via as yet unidentified pathways activated by host- or pathogen-derived factors (76, 78–81). Measurements performed with membrane-bound probes in platelets, human neuroblastoma cells, and P2X₇R-transfected HEK293 cells show that the ATP concentration at the plasma membrane surface is much higher than in the bulk solution and may range from 20 to 200 μ M (75, 82). This suggests that ATP levels sufficient to activate the P2X₇R may be reached in the pericellular space. In addition, proinflammatory cytokines or bacterial products up-regulate P2X₇R expression and increase its sensitivity to extracellular ATP (83–85). In principle, pericellular ATP levels can also be increased by ecto-ATPase inhibition. It has been recently shown that Abs raised against a surface expressed ATPase known as regeneration and tolerance factor potentiate ATP-stimulated IL-1 β release from macrophages (86). In mouse, but not in human, thymocytes ADP-ribosylation due to extracellular NAD can also activate the P2X₇R, although it is not clear whether this mechanism is operative in macrophages (87). More recently, an antimicrobial peptide derived from human cathelicidin (LL37) was reported to directly activate the P2X₇R and trigger IL-1 β secretion (80). Thus, it is likely that as our knowledge of the P2X₇R expands, we will find additional physiologically relevant ligands for this receptor.

P2X₇R-dependent secretion of other IL-1 family members

IL-1 α , as with IL-1 β , is retained mostly within the cytoplasm unless extracellular ATP is added (88). Stimulation of IL-1 α release occurs via the P2X₇R and follows a time course similar to that of IL-1 β . Both pro-IL-1 α and mature IL-1 α are released.

The physiological meaning of P2X₇R-dependent pro-IL-1 α cleavage is not clear because this cytokine, in contrast to pro-IL-1 β , is a full agonist at IL-1Rs.

In response to ATP, macrophages and endothelial cells (HUVECs) also release IL-1Ra. In macrophages, but not in HUVECs, release occurs via P2X₇R-stimulated microvesicle release (89). In monocytes, P2X₇R-stimulated release of IL-18 occurs with a time course similar to that of IL-1 β , requires priming with LPS, and is prevented by the P2X₇R E496A loss-of-function polymorphism (64, 90).

IL-1 and ATP as danger signals

There is increasing awareness that stressed cells release soluble signals (danger signals) that activate the immune system (7). Such signals can be classified into constitutive and inducible. While IL-1 is an obvious inducible danger signal, intracellular nucleotides, and among them chiefly ATP, are good candidates to the role of ubiquitous constitutive danger signals (Fig. 3) (7, 8, 91). Several features make ATP well suited to the role of danger signal: high intracellular:extracellular concentration ratio, hydrophilicity, ubiquitous expression of very efficient degrading systems (ecto-ATPases), presence of specific receptors with widely different affinity, and strong DCs maturing activity (8, 92).

Inflammation is a complex response generated by an interacting network of stimulatory and inhibitory signals. Immune cells primed by soluble factors produced by infections or tissue damage may or may not progress to a full-activated phenotype depending on the additional signals that they receive by neighboring cells (93). We think that the P2X₇R may act as a "sensor of danger" that monitors the release of danger signals (ATP) at inflammation sites and drives mononuclear phagocytes primed by bacterial products into fully activated inflammatory effectors (IL-1-secreting cells). Thus, in the coordinate response to pathogens, P2X₇R might be a "checkpoint" where the choice is made to progress to a full-blown response or put inflammation on hold.

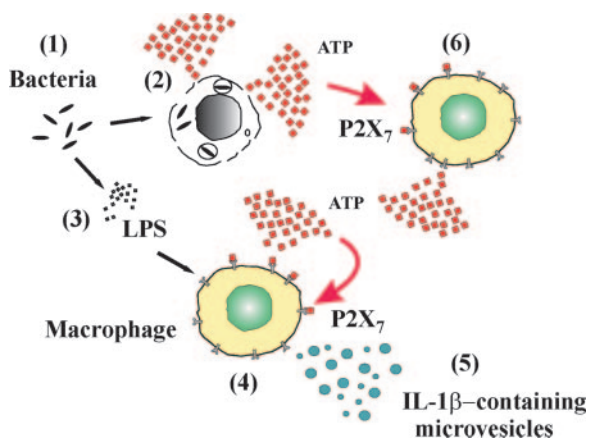


FIGURE 3. Extracellular ATP as a diffusible danger signal generated during bacterial infections. Bacteria enter tissues (step 1) and may directly injure cells and cause ATP release (step 2). Bacterial products (e.g., LPS, step 3) may also cause ATP release (step 4). Extracellular ATP diffuses to activate neighboring cells by paracrine or autocrine pathways (step 4). Macrophages stimulated by LPS and ATP release IL-1-containing microvesicles (step 5). The P2X₇R may function as an amplification device to spread the ATP wave as its activation triggers further ATP release (step 6) (75).

Perspectives

The more we learn about inflammation and its role in pathogen fighting, the more we appreciate that living organisms need to exert a tight control on this process to harvest its most beneficial effects. IL-1 family members have a central role in inflammatory diseases. Several novel molecular inhibitors targeting sites downhill to IL-1 synthesis have been introduced in the clinic or are in preclinical trials (e.g., anti-IL-1 β or IL-1RI Abs, rIL-1Ra or IL-1T trap). Now, the many points of control of IL-1 synthesis, processing, and release suggest alternative strategies. Cell permeant casp-1 inhibitors are a viable option, but in the light of the recent discoveries on the role of the P2X₇R, we anticipate that also blockers of P2X₇R may have a future as anti-inflammatory drugs.

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