

1 *Review*

2 **Regulation and sensing of inflammasomes and their** 3 **impact on intestinal health**

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12 **Abstract**

13 Pattern recognition receptors such as nucleotide-binding oligomerization domain (NOD)-containing
14 protein receptors (NLRs) and the pyrin and HIN domain (PYHIN) receptors initiate the inflammatory
15 response following cell stress or pathogenic challenge. When activated some of these receptors
16 oligomerize to form the structural backbone of a signalling platform known as the inflammasome.
17 The inflammasome promotes the activation of caspase-1 and the maturation of the proinflammatory
18 cytokines, interleukin (IL)-1 β and IL-18. In the gut dysregulation of the inflammasome complex is
19 thought to be a contributing factor in the development of inflammatory bowel diseases (IBD), such
20 as ulcerative colitis (UC) and Crohn's disease (CD). The importance of inflammasomes to intestinal
21 health has been emphasized by various inflammasome deficient mice in dextran sulphate sodium
22 (DSS) models of intestinal inflammation and by the identification of novel potential candidate genes
23 in population based human studies. In this review we summarise the most recent finding with
24 regard to formation, sensing and regulation of the inflammasome complex and highlight their
25 importance in maintaining intestinal health.

26 **Keywords:** inflammasomes; ulcerative colitis; Crohn's disease; interleukin (IL)-1 β ; IL-18

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28 **1. Introduction**

29 The gastrointestinal environment is a continuous system with dual function. Firstly, it provides the
30 human body with the energy it needs to grow and develop and aids in the elimination of waste
31 material. Secondly, it plays an important role in preventing infection by providing a vast array of
32 immune cells close to the mucosal surface to target environment toxins and potential pathogens.
33 Several disease are known to occur in the gastrointestinal tract, notably are ulcerative colitis (UC) and
34 Crohn's disease (CD). Both are characterised by chronic and relapsing inflammation of unknown
35 aetiology. In CD the inflammation is discontinuous, transmural and often associated with intestinal
36 wall thickening, ulcerations, bowel strictures, luminal narrowing and abscesses. While in UC the
37 inflammation is continuous usually spreading proximally from the anal verge and affecting only the
38 mucosa and submucosa layers [1]. For both diseases mechanisms that regulate the gastrointestinal
39 innate immune system have been highlighted as contributing to disease pathology.

40 At the mucosal/gut lumen interface surveillance for pathogen-associated molecular pattern
41 molecules (PAMPs) and damage-associated molecular pattern molecules (DAMPs) is carried out by

42 membrane bound pattern recognition receptors and intracellular pattern recognition receptors. Upon
43 activation many of these receptors promote the secretion of proinflammatory cytokines, transcription
44 mediators, and initiate pathways responsible for pathogen neutralisation and elimination. In
45 addition, some receptors are known to form the structural backbone of the multimolecular complex
46 known as the inflammasome. The inflammasome complex is a core component of the inflammatory
47 response and its activation enhances the maturation of pro-interleukin (IL)-1 β and proIL-18 to their
48 biologically active IL-1 β and IL-18 forms [2]. Transcription of proIL-1 β is induced by Toll-like
49 receptor (TLR) and C-type lectins receptor (CLR) stimulation via the nuclear factor kappa-light-chain-
50 enhancer of activated B cells (NF- κ B) transcription pathway, whereas proIL-18 is constitutively
51 expressed and its expression is increased after receptor activation [3, 4]. For activated macrophages
52 and monocytes of the lamina propria inflammasome maturation of IL-1 β and IL-18 is crucial for
53 cytokine secretion [5].

54 In the intestine, the inflammasome can also promote an inflammatory form of cell death, known as
55 pyroptosis. Pyroptosis halts the replication of intracellular pathogens by destroying the infected
56 immune cell and exposing the surviving bacteria to circulating phagocytes and neutrophils [6]. Both
57 canonical (caspase-1) and non-canonical (caspase-11) inflammasome pathways are able to induce
58 pyroptosis, however caspase-11 does not produce mature IL-1 β or IL-18. Caspase-11 induced
59 pyroptosis is thought to occur upstream of canonical inflammasomes in response to
60 lipopolysaccharides (LPS) sensed in Gram-negative bacteria. Both mechanisms are considered
61 important for microbial defences in the gut [6, 7].

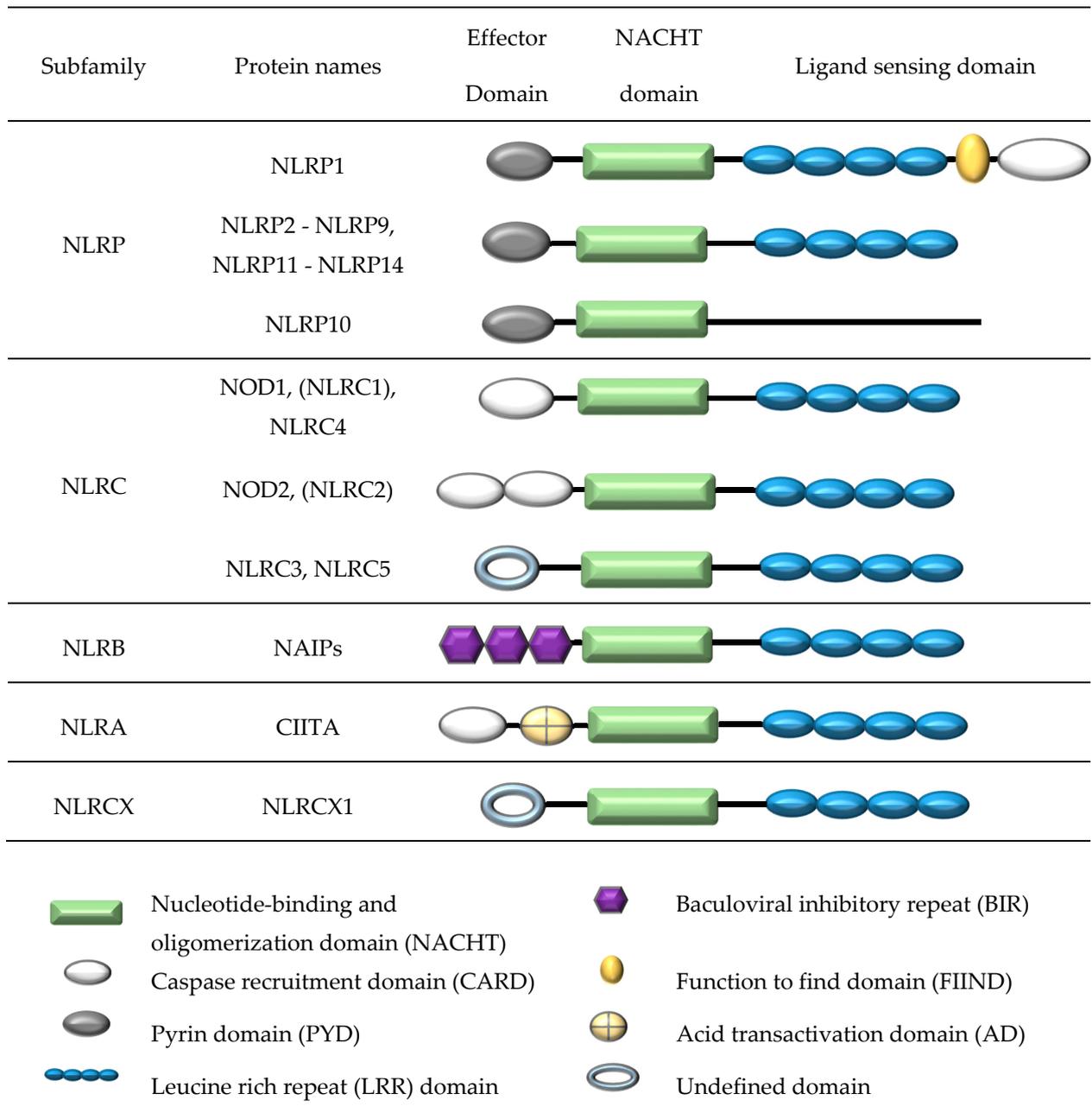
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63 **2. Formation of a NOD-like receptor protein (NLRP) inflammasome complex**

64 In general, the NLRP inflammasome complex consists of a nucleotide-binding oligomerization
65 domain (NOD)-like receptor (NLR) protein, a caspase and often an adaptor protein known as
66 apoptosis-associated speck-like protein containing a CARD (ASC) [2, 8]. Several receptors from the
67 NLR family, NLRP1, NLRP2, NLRP3, NLRC4, NLRP6, NLRP7 and NLRP12 (Figure 1) have all shown
68 the ability to form the structural backbone of an inflammasome complex. The ASC adaptor protein is
69 identical for all inflammasomes and contains two transduction domains, a pyrin domain (PYD)
70 domain and a caspase recruitment domain (CARD) domain [9].

71 Formation of a NLRP inflammasome is initiated by ligand activation of the receptor protein and this
72 causes the NLR proteins to oligomerize through their nucleotide-binding and oligomerization
73 (NACHT) domains (Figure 2). This oligomerization creates a platform of NLR^{PYD} molecules at the N-
74 terminal and through NLR^{PYD}/ASC^{PYD} interactions nucleates helical ASC clusters to form an ASC
75 filament structure. The aggregation of multiple ASC^{CARD} molecules promotes ASC^{CARD}/caspase-1^{CARD}
76 interactions which in turn brings caspase domains into close proximity for dimerization, *trans*-
77 autocleavage and activation [9]. The binding of ASC to both the NLR protein and caspase-1 is
78 facilitated by a 23-residual linker which orientates ASC^{PYD} and ASC^{CARD} back to back hence
79 preventing steric interference of binding sites, while enhancing binding partner prospects [10]. ASC
80 is sequestered in the nucleus but rapidly translocates to the cytoplasm upon stimulation where it
81 participates in inflammasome formation [11]. Interestingly, inflammasome formation can be
82 abolished by preventing the cellular redistribution of ASC [11].

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Figure 1: Structure of the human NOD-like receptor subgroups

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The NOD-like receptor (NLR) family comprises 23 human members [12, 13]. All NLR proteins contain a central nucleotide-binding and oligomerization (NACHT) domain flanked by a C-terminal LRR domain and N-terminal effector domain. The NACHT domain facilitates self-oligomerization and has ATPase activity. The N-terminal domain participates in protein-protein interactions while the LRR domain is involved in ligand recognition. Subgroup classification is based on the structure of the N-terminal effector region which generally comprises a CARD, PYD or BIR domain. The NLRP1, NLRP2, NLRP3, NLRC4, NLRP6, NLRP7 and NLRP12 receptors have all shown the ability to form inflammasome complexes.

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95 Caspase-1 is synthesized as an inactive, monomeric zymogen (procaspase-1) and initially is cleaved
96 into a p35 fragment containing a CARD and p10 fragment. Autoproteolysis results in the generation
97 of a large p20 subunit and a small p10 subunit and the removal of the N-terminal CARD domain.
98 Dimerization of caspase molecules (p20 and p10) results in the catalytically active caspase-1 enzyme
99 (Figure 3) [14, 15]. Inflammasome activated caspase-1 cleaves its substrates, proIL-1 β and proIL-18 at
100 recognition sites adjacent to aspartic acid residues, resulting in mature IL-1 β and IL-18 [8].

101 In contrast to other members of the NLRP subfamily, NLRP1 contains both a function to find (FIIND)
102 and CARD domain at the C-terminal, and a PYD domain at the N-terminal [16] (Figure 1). Given that
103 NLRP1 contains two signal transduction domains (PYD and CARD) it can activate caspase-1 through
104 its C-terminal CARD domain without the need for the ASC adaptor protein, however ASC has been
105 shown to greatly enhance inflammasome formation and IL-1 β processing [17]. The FIIND domain is
106 a highly conserved protein region and based on amino acid sequencing is only present in two human
107 proteins, NLRP1 and the caspase recruitment domain family, member 8 (CARD8) protein [18].
108 CARD8 is thought to function as an adaptor molecule that negatively regulates NF- κ B activation,
109 caspase-1 dependent IL-1 β secretion and apoptosis, and is often overexpressed in many types of
110 cancers [19-21].

111 NLRP1 inflammasome formation is strictly dependent on autolytic proteolysis within the FIIND
112 domain and after cleavage the two fragments remain associated to form a processed NLRP1. Dimers
113 of ASC joined by ASC^{PYD}/ASC^{PYD} are recruited to the C-terminal NLR^{CARD} domain and bind via
114 NLR^{CARD}/ASC^{CARD} interactions. This is in contrast to other NLRP proteins which recruit ASC to the
115 N-terminal PYD domain and bind via NLR^{PYD}/ASC^{PYD} interactions to form the inflammasome
116 complex. Subsequently, caspase-1 through its CARD domain interacts with ASC^{CARD} which leads to
117 dimerization, *trans*-autocleavage and activation of caspase-1 and IL-1 β , IL-18 processing [22]. The
118 formation of ASC filaments in the activation of the NLRP1 inflammasome remain to be defined.

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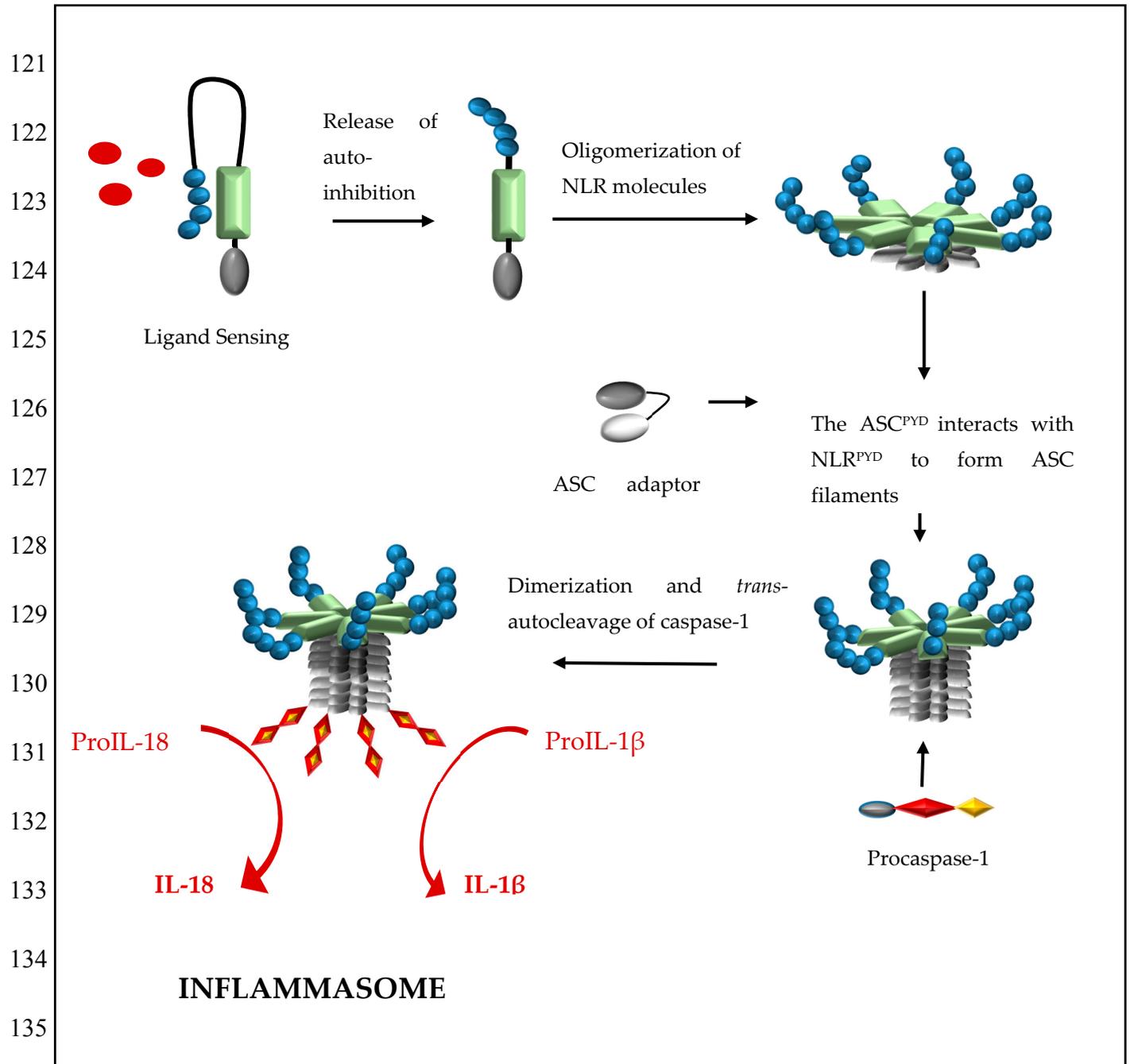


Figure 2: Formation of a NOD-like receptor protein inflammasome containing an N-terminal Pyrin domain

Formation of a nucleotide-binding oligomerization domain (NOD)-like receptor protein (NLR) inflammasome is initiated by ligand activation of the NLR protein. This causes the NLR proteins to oligomerize through their NACHT domains to create a platform of NLR^{PYD} molecules at the N-terminal and through NLR^{PYD}/ASC^{PYD} interactions, nucleates helical ASC clusters to form a filament ASC structure. The aggregation of multiple ASC^{CARD} molecules promotes ASC^{CARD}/caspase-1^{CARD} interactions which in turn brings caspase domains into close proximity for dimerization, *trans*-autocleavage, activation and the processing of pro-interleukin (IL)-1 β and proIL-18 to their biologically active form, IL-1 β and IL-18 respectively.

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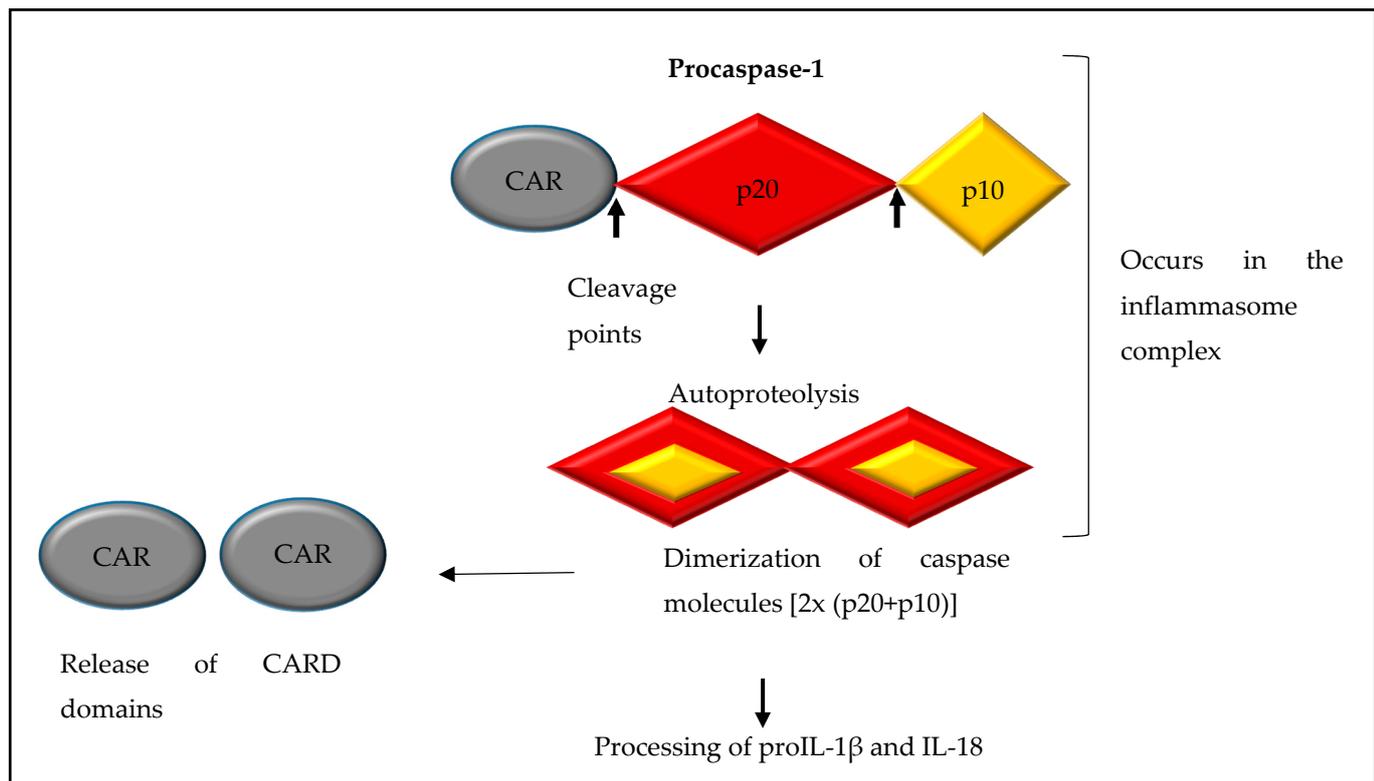


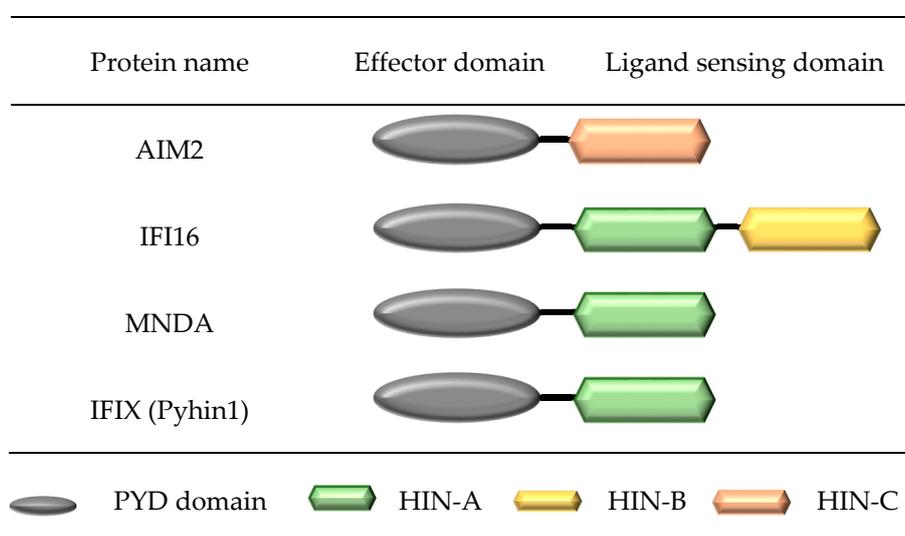
Figure 3: The mechanism for the inflammasome mediated catalytic conversion of procaspase-1 to caspase-1

Caspase-1 is initially synthesized as the inactive monomeric zymogen, procaspase-1. Binding of the procaspase-1^{CARD} to ASC^{CARD} filaments on the inflammasome complex results in the cleavage of procaspase-1 into a p35 fragment containing a CARD and a p10 fragment. Dimerization of the p10 and p20 and the removal of the procaspase-1^{CARD} domain produces catalytically active caspase-1.

174 3. Structure and formation of a pyrin and HIN domain (PYHIN) inflammasome complex

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176 Two receptor in the pyrin and HIN domain (PYHIN) receptor family, absent in melanoma 2 (AIM2)
 177 and interferon inducible protein 16 (IFI16) have shown the ability to form inflammasome complexes
 178 (Figure 4). Similar to NLRP inflammasomes, PYHIN inflammasomes, such as AIM2, upon ligand
 179 activation oligomerize through their PYD domains to form a platform of AIM2^{PYD} molecules which
 180 preferentially associates with ASC^{PYD} to form ASC filaments. The flexibly linked ASC^{CARD} clusters
 181 along the ASC^{PYD} to form a platform for the binding of caspase-1^{CARD}. Similar to other NLRP
 182 inflammasomes, the ASC filament structure forms the main body of the inflammasome. The
 183 interaction of ASC^{CARD}/caspase-1^{CARD} brings caspase domains into close proximity for dimerization,
 184 *trans*-autocleavage and activation, and the subsequent maturation of IL-1 β and IL-18 [9].
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188 **Figure 4: Structure of the human pyrin and HIN domain (PYHIN) family**

189 The human pyrin and HIN (PYHIN) family of receptors comprises 4 members including, the
 190 interferon inducible protein 16 (IFI16), absent in melanoma 2 (AIM2), myeloid nuclear differentiation
 191 antigen (MNDA) and interferon inducible protein X [IFIX (Pyhin1)], while mouse contains 11
 192 confirmed members [23]. All members consist of an N-terminal pyrin domain (PYD) domain attached
 193 to one or more hemopoietic expression, interferon-inducibility, nuclear localisation (HIN-200)
 194 domains at the C-terminal. Three distinct forms of HIN-200 have been characterised (HIN-A, -B and
 195 -C) and are classified according to specific consensus motifs [24].

196 4. Ligand sensing of inflammasome complexes

197 Depending on the type of receptor protein in the complex, inflammasomes have the ability to respond
198 to a wide array of pathogens and cellular danger signals. The LRR domains of the NLRP receptors
199 and the HIN200 domains of the PYHIN receptors are thought to be involved in ligand interactions,
200 however direct binding of an activating ligand to a receptor has only been demonstrated for the AIM2
201 and IFI16 inflammasomes.

202 203 5. The NLRP1 inflammasome

204 The NLRP1 inflammasome was one of the first inflammasomes to be described however efforts to
205 unravel the processes that lead to activation have been hampered by species variations in the *NLRP1*
206 gene. In humans the *NLRP1* gene is singular, while in mouse the gene encoding *Nlrp1* is polymorphic
207 with three homologs, *Nlrp1a*, *Nlpr1b* and *Nlrp1c* [14]. Furthermore, the structure of mouse *Nlrp1* lacks
208 the N-terminal PYD domain found in human NLRP1 and five different strain specific *Nlrp1b* alleles
209 exist in inbred mice [25].

210 *Nlrp1* is activated mainly by lethal toxin (LeTx) produced by *Bacillus anthracis* with variations in
211 *Nlrp1b* providing sensitivity or resistance to the toxin [26]. LeTx is a bipartite toxin consisting of a
212 protective antigen binding subunit and a catalytic lethal factor moiety. Binding of the protective
213 antigen to anthrax binding sites translocates lethal factor into the host cytosol where it cleaves the N-
214 termini of mitogen-activated protein kinase (MAPK) thereby disrupting cell signalling pathways.
215 Initially lethal factor blocks cytokine production from numerous cell types, inhibits chemotaxis of
216 neutrophils, induces apoptosis in activated macrophages and later induces cytokine-independent
217 shock and death [27]. Caspase-1 and IL-1 β deficient mice are more susceptible to *B.anthraxis* infection
218 indicating IL-1 β production via the NLRP1b inflammasome is more important than ASC
219 independent pyroptosis in the host protective response to *B.anthraxis* [15, 27].

220 More recently NOD2 has been linked to NLRP1 dependent sensing of MDP and *B.anthraxis* in
221 activated cells where it produces a NOD2-NLRP1 inflammasome complex [28]. NOD2 is a known
222 intracellular sensor of MDP and has the ability to contribute to the induction of NF- κ B and MAPK
223 transcription factors, however TLRs are much more effective in triggering these responses [29]. The
224 absence of NOD2 prevents *B. anthracis* induced IL-1 β secretion but has little effect on the transcription
225 of proIL-1 β indicating the importance of the NOD2-NLRP1 association in host defences against *B.*
226 *anthracis* [28].

227 228 6. The NLRP3 inflammasome

229 The NLRP3 inflammasome has the ability to activate upon exposure to a wide range of whole
230 pathogens, environmental irritants and structurally diverse DAMPs and PAMPs [2, 30, 31].

231 While the mechanisms are not yet fully understood it is thought that activation of NLRP3 occurs in
232 response to host derived factors that are altered by these agents. While several models have been
233 proposed for the activation of NLRP3 none have been found to be unified for all activating agents.
234 The proposed mechanisms include;

- 235 1. K⁺ efflux [32]
- 236 2. The generation of mitochondrial derived reactive oxygen species (mROS) [33]
- 237 3. Phagolysosomal destabilisation and the release of cathepsins [34]
- 238 4. The release of mitochondrial DNA or the mitochondrial phospholipid cardiolipin [35-37]

239 5. Translocation to the mitochondria [33, 38, 39]

240 To add to the controversy, membrane permeation, phagolysosomal destabilisation, mitochondrial
241 damage and ROS production are all interrelated cellular events making the distinction between
242 bystander and causative activation events complicated.

243 In resting cells the basal expression of *NLRP3* is insufficient for inflammasome activation and
244 consequently two signals are required for the activation of the NLRP3 inflammasome [40, 41]. The
245 first signal is the NF- κ B mediated transcription of *NLRP3* and *proIL-1 β* from stimulation of TLR
246 antagonists or cytokines such as TNF- α and IL-1 β . The second signal is the ligand activation step
247 which culminates in the activation of caspase-1 and the maturation of IL-1 β and IL-18 [30, 42]. The
248 enhanced effect of guanylate binding protein (GBP5) on Nlrp3 inflammasome assembly in response
249 to bacteria and soluble but not crystalline inflammasome priming agents raises the possibility of
250 agent specific cofactors being required for inflammasome activation [43].

251 Particulate matter such as aluminium, silica, monosodium urate (MSU), calcium pyrophosphate
252 dehydrate crystals, cholesterol and amyloid β enters the cell by means of phagocytosis [34, 44-46].
253 The destabilisation of the phagolysosomal membrane and the release of the cysteine protease
254 cathepsins B into the cytosol is thought to also trigger NLRP3. Inhibitors of cathepsins B have been
255 shown to prevent caspase-1 activation induced by *N. gonorrhoeae* [47]. Interestingly, cathepsins
256 deficient mice show minimal defects in the activation of NLRP3 in response to particulate matter,
257 suggesting other off target effects may exist [48].

258 More recently, mitochondrial dysfunction and activation of the NLRP3 inflammasome has been an
259 area of intense research and much speculation. Mitochondrial reactive oxygen species (mROS) are
260 produced in response to cell stresses such as, hypoxia, starvation, pathogen infection, and growth
261 factor stimulation or membrane damage [49]. The release of mROS and oxidised mitochondrial DNA
262 have both been shown to activate the NLRP3 inflammasome [35, 50]. Interruption of ROS production
263 using inhibitors blocks NLRP3 activation suggesting ROS production upstream is necessary for
264 NLRP3 activation [50-52].

265 It has been proposed that NLRP3 associates with the mitochondria upon activation [38, 50] and when
266 exposed to non-crystalline activators, recruitment from the cytosol to the mitochondria is mediated
267 by the mitochondrial anti-viral signalling protein (MAVS) [39]. MAVS is also known as a
268 mitochondrial adaptor protein and plays a crucial role in RLR receptor signalling pathways leading
269 to type 1 IFN induction and NF- κ B activation [53]. MAVS is thought to directly associate with the N-
270 terminus of NLRP3 to promote optimal inflammasome formation [39]. Consistent with a role for
271 MAVS in NLRP3 activation, MAVS deficient mice exposed to dextran sodium sulphate (DSS)
272 induced colitis fail to upregulate IL-1 β [54].

273 Other work on mitochondrial dysfunction has demonstrated a ROS independent activation of *Nlrp3*
274 induced by the antibiotic linezolid whereby the mitochondrial specific lipid cardiolipin binds to *Nlrp3*
275 leading to the maturation of IL-1 β [37]. Cardiolipin is a phospholipid exclusively found in the inner
276 mitochondrial membrane of eukaryotic cells. Cardiolipin plays a critical role in the activation of
277 caspase-8 and caspase-3 in the apoptotic cell death pathway which raises the possibility that the
278 inflammasome pathways are linked to the apoptosis pathways by processes that control
279 mitochondrial homeostasis.

280 In addition, agents that induce NLRP3 activation, such as nigericin have demonstrated an ability to
281 disrupt mitochondrial homeostasis by reducing the intracellular concentration of the coenzyme

282 NAD⁺. Low NAD⁺ inactivates the α -tubulin deacetylase sirtuin 2 (SIRT2) and causes the accumulation
283 of acetylated α -tubulin. Excess acetylated α -tubulin mediates the microtubule transport of
284 mitochondria which drives the apposition of ASC on the mitochondria to NLRP3 on the endoplasmic
285 reticulum. Microtubule transport of organelles creates optimal sites for signal transduction between
286 ASC and NLRP3 and directs activation of NLRP3. Work using inhibitors of tubulin polymerisation
287 have demonstrated suppression of IL-1 β [38].

288 Early work investigating caspase-1 activation by the NLRP3 inflammasome showed that K⁺ efflux
289 accompanies NLRP3 activation [51, 55] and a high extracellular concentration of K⁺ blocks the
290 activation of not only the NLRP3 inflammasome but also the NLRP1, NLRC4 and AIM2
291 inflammasomes [56, 57]. ATP levels have been linked to K⁺ efflux, such that high extracellular ATP
292 levels engage the ATP-gated purinergic P2X₇ receptor promoting the formation of the pannexin-1
293 pore, which induces K⁺ efflux [42, 58]. Previous work by Muñoz-Planillo [32] has shown that ROS
294 generation, opening of the pannexin-1 pore and K⁺ efflux all occur upon stimulation with a variety of
295 bacterial pore-forming toxins, nigericin, ATP and particulate matter. However in contrast to other
296 work the permeation of the cell membrane to K⁺ and Na⁺ was found to be the only common step
297 induced by all NLRP3 antagonists and the primary activity that was necessary and sufficient for
298 caspase-1 activation. In addition, cytosolic K⁺ efflux was found to be specific to NLRP3 activation and
299 was shown not to play a role in the activation of AIM2. These results await further clarification by
300 other independent researchers.

301

302 7. The NLRC4 inflammasome

303 The NLRC4 inflammasome has been well characterised in the mouse system and plays an important
304 role in the detection of pathogenic bacteria [14]. The pathogenicity of a bacteria is reliant on functional
305 secretion systems including the type III and IV which act as needle-like structures delivering virulent
306 factors into the host's cytosol. NLRC4 is activated by two critical components of pathogenic bacteria,
307 a sequence motif found in the basal rod components of the type III (T3SS) and IV (T4SS) bacterial
308 secretion systems, and a similar sequence motif found in flagellin which is a component of their
309 flagellum apparatus [59, 60]. NLRC4 has been shown to detect basal rod components in *Salmonella*
310 *typhimurium*, *Legionella pneumophila*, *Burkholderia pseudomallei*, *Escherichia coli*, *Shingella flexneri*,
311 *Pseudomonas aeruginosa* [61, 62] and leaked cytosolic flagellin from *Listeria monocytogenes*, *Salmonella*
312 *typhimurium*, *Pseudomonas aeruginosa* and *Legionella pneumophila* [60, 63, 64].

313 Activation of the NLRC4 inflammasome involves the initial binding of a receptor protein from the
314 neuronal apoptosis inhibitory protein (NAIP) subfamily of NLRs to the activating ligand. NAIP
315 receptor proteins differ from other NLRs in that they contain multiple BIR domains at the N-terminus
316 instead of a CARD or PYD domain (Figure 1). In humans only one NAIP homolog is expressed,
317 whereas in mice the NAIP locus is polymorphic and seven paralogs of Naip (*Naip1-Naip7*) exist [62].
318 Human NAIP and its mouse ortholog, Naip1 recognise cytosolic T3SS needle proteins, Naip2 binds
319 T3SS rod components while Naip5 and Naip6 bind directly to bacterial flagellin [62, 64]. Binding of
320 a NAIP protein to a bacterial motif leads to the formation of the NAIP-NLRC4 inflammasome
321 complex and activation of caspase-1. Interestingly, in human U937 monocyte derived macrophages
322 NLRC4 activation does not occur in response to flagellin or T3SS rod protein but occurs in response
323 to the T3SS subunit Cpr1 from *Chromobacterium violaceum* which raises the possibility that other
324 accessory proteins may be involved in activation of the human NLRC4 inflammasome [64].

325

326 8. The AIM2 and IFI16 inflammasome

327 Both the cytosolic AIM2 receptor and the nuclear IFI16 receptor directly bind their activating ligand
328 double stranded DNA (dsDNA) via the C terminal HIN200 domain [65-67]. Non-sequence specific
329 binding occurs at multiple sites along the dsDNA and is through electrostatic attractions between the
330 positively charged HIN domain residues and the dsDNA sugar phosphate backbone [68].

331 The mechanisms that enable AIM2 and IFI16 to respond to viral, bacterial, mammalian and synthetic
332 dsDNA while remaining unresponsive to self DNA are still unclear [14, 69].

333 Work using *Aim2* deficient mice have demonstrated an essential role for AIM2 in the recognition of
334 viruses and bacteria by the detection of cytosolic dsDNA. When compared to WT mice, *Aim2*^{-/-} mice
335 experience higher mortality rates, higher bacterial loads and decrease production of caspase-1
336 generated cytokines after infection with *Fransicella tularensis*, suggesting AIM2 is necessary for
337 detection of *Fransicella tularensis* [70, 71]. Similarly, mouse macrophages deficient for *Aim2* show an
338 impaired ability to recognise not only *Fransicella tularensis*, but also vaccinia virus, murine
339 cytomegalovirus (mCMV) with only partial recognition of *Listeria monocytogenes* being demonstrated
340 [65, 72].

341

342 9. The NLRP6, NLRP7 and NLRP12 inflammasomes

343 In addition to the well-known NLRP1, NLRP3, NLRC4, AIM2 and IFI16 inflammasomes NLRP6,
344 NLRP7 and NLRP12 have shown an ASC dependent activation of caspase-1. However, the signals
345 that activate the NLRP6 and NLRP12 inflammasomes are yet to be determined [73].

346 Indeed, two independent studies have reported a lack of caspase-1 activation and IL-1 β release in
347 *Nlpr6* deficient mouse macrophages in response to ATP and LPS which suggest the triggers that
348 activate the NLRP6 inflammasome are different to those that activate the NLRP3 inflammasome [74,
349 75]. Recently NLRP7, which is not expressed in mice, was shown to form an ASC dependent
350 inflammasome in human macrophages in response to microbial acylated lipopeptides [76].

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353 10. Regulation of the inflammasome complex

354 The potent inflammatory cytokines, IL-1 β and IL-18 and the pyroptosis pathway all have the
355 potential to cause tissue damage and disrupt an effective adaptive immune response. The
356 mechanisms that lead to maturation of IL-1 β and IL-18 are tightly controlled at several levels and
357 multiple checkpoints along this process ensuring response appropriate levels.

358 In most cells the basal levels of many of the inflammasome constituents is insufficient for
359 inflammasome formation. Consequently, the expression of the inflammasome components is
360 regulated by NF- κ B induced transcription and requires sensitization by a TLR or CLR ligand or
361 stimulus from cytokine signalling pathways [30, 77]. In contrast to most cytokines IL-1 β and IL-18
362 are produced as inactive zymogens requiring caspase-1 cleavage between Asp and Ala for
363 maturation [3, 78]. The synthesis of precursor cytokines requiring activation prevents aberrant
364 secretion of the leaderless IL-1 β and IL-18 cytokines. Serine proteinases such as cathepsins G, elastase
365 and in particular proteinase 3 found in neutrophils have also been shown to cleave proIL-1 β to active
366 IL-1 β . While in monocytes autocrine production of ATP can activate caspase-1 and cleave proIL-1 β ,
367 thereby releasing IL-1 β by transcription only [79]. Worth noting is that during acute inflammatory
368 conditions non-canonical maturation of IL-1 β can also occur via caspase-11 and the NLRP3
369 inflammasome [6].

370

371 11. Regulation by autoinhibition of the ligand sensing domain

372 For most of the receptor proteins autoinhibition of the ligand sensing domain prevents unproductive
373 intramolecular interactions by providing a tight on-site repression of the protein in the absence of a
374 suitable activating ligand. For NLRP1, NLRP3, NLRP12 and NLRC4 receptors autoinhibition is
375 achieved by the association of two chaperone proteins, ubiquitin ligase-associated protein (SGT1)
376 and heat-shock protein 90 (HSP90) to the LRR domain. Upon ligand sensing SGT1 and HSP90
377 dissociate resulting in a conformation change within the protein which favours the recruitment of the
378 ASC adaptor protein [80]. Whether autoinhibition of the sensing region occurs for the NLRP6 protein
379 remains to be determined. For the PHYIN subfamily autoinhibition is provided by the molecular
380 interactions between the PYD and HIN-200 domain and binding of DNA releases this autoinhibition
381 [68].

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383 12. Priming events that regulate activation

384 Specific priming events are known to regulate the activation of inflammasomes. The K-63 specific
385 deubiquitinating enzyme BRCC3 mediates the deubiquitylation of NLRP3 which has recently been
386 shown to occur in response to pattern recognition receptor stimulation [81]. Similarly, and as
387 mentioned above, GBP5 enhances NLRP3 assembly in response to bacterial but not crystalline agents
388 [43]. A priming event involving the phosphorylation of Ser533 by kinases like PKC δ is necessary
389 before *Salmonella typhimurium* can activate the NLRC4 inflammasome. The phosphorylation of Ser533
390 is thought to result in a conformation change within the NLRC4 protein [82].

391 The anti-apoptotic proteins B-cell lymphoma 2 (Bcl-2) and B-cell lymphoma extra-large (Bcl-X_L) have
392 been shown to regulate the NLRP1 inflammasome. By associating with NLRP1 via their loop domains
393 Bcl-2 and Bcl-X_L are able to suppress caspase-1 activation and IL-1 β processing [83, 84]. Similar
394 experiments for NLRP3 in Bcl-2 deficient macrophages have shown more caspase-1 processing while

395 Bcl-2 overexpressing macrophages demonstrated less caspase-1 processing suggesting NLRP3 may
396 also be regulated by Bcl-2 protein [35].

397 Activation of the NLRP3 inflammasomes is thought to be influenced by K⁺ levels, indeed low
398 intracellular K⁺ level enhance caspase-1 activation [51, 55]. Similarly, high extracellular K⁺ levels block
399 IL-1 β release from the NLRC4 and AIM2 inflammasome suggesting the regulatory effect of K⁺ may
400 be extended to other inflammasome complexes [70, 85]. Interestingly, the levels of extracellular K⁺
401 need to block IL-1 β release for the NLRP3 inflammasome is less than that needed for the NLRC4 or
402 AIM2 complex, while for the NLRP7 inflammasome high K⁺ levels only slightly reduced IL-1 β release
403 [76]. More work is needed to exclude off target effects and to determine the reasons for inflammasome
404 specific thresholds to K⁺ levels.

405 13. Regulation by POPs and COPs

406 In humans, pyrin only proteins (POPs) and CARD-only proteins (COPs) regulate the inflammasome
407 at the level of death fold interactions. With the exception of caspase-12, POPs and COPs are lacking
408 from the mouse genome which suggests humans have evolved more complex inflammasome
409 regulatory systems [86]. The POPs include, POP1 (also known as PYDC1) and POP2 (also known as
410 PYDC2) and both inhibit PYD interactions between the receptor protein and the ASC adaptor
411 molecule. POP1 shows a higher homology to ASC^{PYD} than POP2 and therefore inhibits inflammasome
412 formation by sequestering ASC from other inflammasome forming NLRs [87]. POP2 is surprisingly
413 similar to the PYD domain of NLRP2 and NLRP7 and is thought to interact with other NLR^{PYD}
414 proteins thereby preventing inflammasome formation [88]. Both POP1 and POP2 can prevent NF- κ B
415 activation [87, 88].

416 The COPS proteins consists of several members including, CARD16 (also known as pseudo-ICE or
417 COP1), CARD17 (also known as INCA), CARD18 (also known as ICEBERG), caspase-12s and Nod2-
418 S.[89] COP proteins act as decoy inhibitors and sequester procaspase-1 via CARD-CARD interactions
419 thereby preventing its activation in the inflammasome. For example, CARD 17 is upregulated by IFN-
420 γ in the monocytic cell lines THP-1 and U937 and interacts with procaspase-1 to suppress IL-1 β
421 processing and release in LPS stimulated macrophages [90].

422

423 14. Regulation by Type I interferons

424 Type I interferons restrict IL-1 β production by two distinct mechanisms. Depending on the cell type,
425 type I interferons through the STAT3 signalling pathway can induce autocrine and paracrine
426 production of the anti-inflammatory cytokine IL-10 which inhibits the synthesis of proIL-1 β and
427 proIL-18. Additionally, type I interferons signalling through the STAT1 transcription factor can
428 repress the activity of the NLRP1 and NLRP3 inflammasome thereby subduing IL-1 β production [91].
429 For the AIM2 inflammasome, *Irf3* deficient mouse macrophages, which are unable to secrete type I
430 interferons, have impaired AIM2 activation in response to *Francisella tularensis* infection indicating
431 that an intact type I interferon response is required for AIM2 activation [70]. Interestingly, activation
432 of the AIM2 inflammasome in response to mouse cytomegalovirus does not require an intact type I
433 interferon response [72]. The mechanisms pertaining to the selective requirement of type I interferons
434 for the clearance of certain infections remain unclear.

435 Evidence suggests that cells of the adaptive immune response can also dampen inflammasome
436 activation. In mouse macrophages and dendritic cells, effector CD4⁺ T cells and memory T cells
437 suppress activation of the NLRP1 and NLRP3 inflammasomes. For the NLRP3 inflammasome the

438 inhibitory effect requires the cell-to cell contact and could be mimicked by macrophage stimulation
439 with members of the TNF family such as, CD40L, OX40L and RANKL. Interestingly, the negative
440 feedback loop exerted by T cells is only evident for the NLRP1 and NLRP3 inflammasome and was
441 absent for the NLRC4 inflammasome [92].

442 **15. Regulation from inflammasome components**

443 Inflammasomes components can themselves indirectly impact on inflammasome formation and IL-
444 1 β release. For example, NLRP12 acts as a negative regulator of the NF- κ B pathway through its
445 interaction and regulation of NIK and TRAF3, and dysregulation of NF- κ B is associated with colonic
446 inflammation and cancer [93]. NLRP10 interacts with ASC, even though it lacks a ligand sensing
447 LRR, and is thought to negatively regulate the inflammasome by sequestering ASC [94, 95]. The ASC
448 adaptor protein, in addition to the full length ASC also exists as three novel isoforms, ASC-b, ASC-c
449 and ASC-d. ASC-c exerted an inhibitory effect on NLRP3 inflammasome formation by only colocalise
450 with caspase-1 and not NLRP3. ASC-d failed to colocalise with either caspase-1 or NLRP3 suggesting
451 an undetermined function for this isoform [11].

452 Emerging evidence indicates NLRP7 is able to regulate inflammasomes, however conflict reports
453 argue the nature of the negative regulation. Reconstitution experiments in HEK293 cells have shown
454 that NLRP7 inhibits NLRP3 and caspase-1 mediated release of IL-1 β and co-immunoprecipitation
455 studies indicated NLRP7 directly interacts with procaspase-1 and proIL-1 β [96]. While other work
456 focusing on NLRP7 overexpression and gene specific mutations have indicated that NLRP7 inhibits
457 NF- κ B activation by an unknown mechanism or inhibits release of IL-1 β [97]. Positive regulation is
458 affirmed by the formation of the NLRP7 inflammasome in response to microbial acylated
459 lipopeptides [76].

460

461 **16. Inflammasome complexes and the intestinal environment**

462 Mouse models that stimulate colitis, such as DSS, have provide an accessible framework for
463 investigating the role of inflammasomes in diseases that affect the gastrointestinal tract. Differences
464 in the experimental conditions used for colitis induction and pathogen infection have resulted in
465 many discrepancies regarding the redundant or necessary role of individual inflammasome
466 complexes in protecting against colitis [16].

467 Mice deficient in *Nlrp3*, *Nlrc4*, *IL-1 β* , *Casp1/11* and *Asc*, when challenged by DSS, have all shown
468 increased susceptibility to colitis, disease exacerbation, frequent mortality and increased tumor
469 formation when compared to DSS challenged wild type mice, suggesting these components aid in
470 colitis protection [98-104]. Disease exacerbation has also been a feature of DSS challenged *Nlrp6*
471 deficient mice [105]. Not reported in *Nlrc4* and *Nlrp3* deficient mice but associated with *Nlrp6*
472 deficiency is a reduction in the thickness of the mucus layer and the development of a transferable
473 colitis forming microbiota dominated by TM7 and *Prevotellaceae* species (*Bacteroidetes* phyla). The
474 reduction in mucus has been attributed to defects in mucin granule exocytosis and reduce autophagy
475 mechanisms in goblet cells which suggests that, unlike NLRP3 and NLRC4, NLRP6 orchestrates
476 downstream mechanisms involved in bacterial defences [105, 106].

477 Alterations in the composition of the gut microbiota have been reported for IBD patients [107, 108].
478 In general, UC patients exhibit higher overall bacterial counts while in CD the bacterial counts are
479 lower but associated with a higher proportion of unclassified *Bacteroidetes* spp. and a higher diversity
480 of TM7 phylotypes. Increases in *Enterobacteriaceae*, adherent-invasive strains of *Escherichia coli* and

481 *Ruminococcus gnavus* populations and a decrease in *Faecalibacterium* and *Roseburia* have been reported
482 for ileal CD [109-111]. Interestingly, disease remission in UC induces microbial populations
483 comparable to healthy patients while in CD the microbial population is reportedly not altered by
484 disease remission, remaining constant in active and quiescent disease states [109].

485 Human work investigating the role of individual inflammasomes on gastrointestinal diseases are
486 currently lacking. It has however been demonstrated that the expression of inflammasome
487 components such as *CASP1*, *IL-1 β* , *IFI16* and *AIM2* increases in active disease [112-114].

488

489 **17. Future direction**

490 The dysregulation of inflammasomes and their importance in maintaining intestinal health has been
491 demonstrated by mice deficient in inflammasome components in DSS models of intestinal
492 inflammation. Population based studies have identified possible risk polymorphisms associated with
493 UC and CD. IL-1 neutralising agent have provided remarkable reduction in clinical symptoms for
494 CAPS patients. Taken altogether, it highlights the potential therapeutic benefits of targeting
495 individual inflammasome complexes to complement mainstream therapeutic options.

496 Currently, the focus of treatment for IBD patients is to induce and maintain clinical remission. This
497 is usually achieved by a combination of antibiotics, vitamin support, immunomodulators,
498 corticosteroids, 5-aminosalicylates, biologic therapies and surgery [1]. For many patients however
499 active disease persists despite treatment. Recently, the compound MCC950 was shown to inhibit
500 NLRP3 non-canonical and canonical IL-1 β production in both mouse bone-marrow derived
501 macrophages and human monocyte-derived macrophages [115]. The ability of this compound to
502 consistently inhibit inflammasome mediated IL-1 β production provides promise for clinical trials and
503 future therapeutic options.

504 While mice work has been pivotal to determining the regulatory role of inflammasomes in intestinal
505 health, questions still remain. Firstly, what is the exact role of inflammasomes, such as the NLRP3
506 complex, in intestinal immune responses? Secondly, how accurately do the finding in mice translate
507 to the mechanisms that induce colitis in humans? Future research now needs to focus on individual
508 inflammasomes complexes; how they present in active human disease, what mechanisms they
509 influence downstream and if blockading alleviates disease symptoms.

510

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513

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524

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