

Published in final edited form as:

Nat Rev Cancer. 2019 April; 19(4): 197-214. doi:10.1038/s41568-019-0123-y.

Diverging inflammasome signals in tumorigenesis and potential targeting

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Abstract

Inflammasomes are molecular platforms that assemble upon sensing various intracellular stimuli. Inflammasome assembly leads to activation of caspase-1, thereby promoting the secretion of bioactive interleukin-1 β and interleukin-18 and inducing an inflammatory cell death called pyroptosis. Effectors of the inflammasome efficiently drive an immune response, primarily providing protection against microbial infections and mediating control over sterile insults. However, aberrant inflammasome signaling is associated with pathogenesis of inflammatory and metabolic diseases, neurodegeneration, and malignancies. Chronic inflammation perpetuated by inflammasome activation plays a central role in all stages of tumorigenesis, including immunosuppression, proliferation, angiogenesis, and metastasis. Conversely, inflammasome signaling also contributes to tumor suppression by maintaining intestinal barrier integrity, which portrays the diverse roles of inflammasomes in tumorigenesis. Studies have underscored the significance of environmental factors, such as diet and gut microbiota [G] in inflammasome signaling, which in turn influences tumorigenesis. In this review, we deliver an overview of the interplay between inflammasomes and tumorigenesis and discuss their potential as a therapeutic target.

ToC blurb

Inflammasome signaling in myeloid cells largely protects against microbial infections. Aberrant inflammasome signaling promotes chronic inflammation, which contributes to tumorigenesis. This Review presents an overview of the diverging roles of inflammasomes in cancer and discuss its targeting potential in anti-cancer therapy.

Introduction

Inflammasomes are macromolecular complexes that trigger central and rapid inflammatory responses to cytosolic insults. Inflammasome sensors are grouped based on their structural features into nucleotide-binding oligomerization domain and leucine-rich repeat receptors

Both authors contributed equally to researching data for the article, and writing and editing the article.

Conflicts of Interest

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The authors have no conflicts of interest to disclose.

(NLRs), absent in melanoma 2 (AIM2)—like receptors (ALRs), and the recently identified Pyrin. The NLR family is subdivided into NLRP or NLRC based on whether the N-terminus contains a pyrin domain (PYD) or caspase activation and recruitment domain (CARD), respectively¹. NLRP1 (mouse NLRP1b), NLRP3, and NLR family apoptosis inhibitory protein (NAIP)-NLRC4 are well-established NLRs for their ability to assemble inflammasome^{2,3}. Several other NLR sensors, including NLRP6, NLRP7, NLRP9, NLRP12, NLRC3, NLRC5, and non-NLR sensors, such as interferon gamma-inducible protein 16, and retinoic acid-inducible gene I may form inflammasome complexes in context-dependent manners^{4–6}. Inflammasomes are largely described in immune cells, such as macrophages and dendritic cells, but are also expressed and assembled in non-hematopoietic cells⁴.

Previous studies have indicated that the inflammasome-dependent biological responses—both inflammation and cell death—regulate the pathogenesis of a broad range of diseases including obesity, diabetes, atherosclerosis, gout, and ulcerative colitis⁷. Additionally, the complex roles of inflammasomes in tumorigenesis and antitumor immunity have been revealed over the past decade. The hallmarks of tumor are determined by the central biological characteristics that tumors acquire during the multistep process of tumorigenesis⁸. Remarkably, inflammasome signaling is implicated in virtually every aspect of tumor development, performing either tumor-suppressive or pro-tumorigenic functions⁹(TABLE 1). In this review, we describe the dynamic and divergent roles of inflammasome signaling in multiple tissues and organs, highlighting its major functions in shaping inflammatory responses, cellular proliferation and survival, immunosuppression, angiogenesis, and metastasis and gut microbiota, all of which are critical for modulating tumorigenesis. We also discuss recent advances made in translational research that motivate potential pharmacological approaches aiming the inflammasome crossroads in tumorigenesis.

Inflammasome activation

Upon sensing stimuli, inflammasome sensors generally recruit the common adaptor molecule apoptosis-associated speck-like protein containing a CARD (ASC), which forms a platform for the activation of caspase-1. Recruitment and oligomerization of these components by homotypic CARD-CARD or PYD-PYD interactions are the basis of inflammasome assembly, which is followed by proximity-induced autoprocessing of caspase-1. ASC is a bipartite protein containing both PYD and CARD. PYD-containing AIM2, NLRP3, and Pyrin interact with CARD of caspase-1 via ASC, whereas, CARDcontaining NLRP1b and NLRC4 do not necessarily require ASC for their interaction with caspase-1⁴. Active caspase-1 proteolytically cleaves the pro-inflammatory cytokines pro-IL-1β and pro-IL-18 into bioactive IL-1β and IL-18². Similarly, active caspase-1 cleaves gasdermin D (GSDMD), which subsequently forms pores in the cell membrane, thereby allowing the secretion of mature IL-1β and IL-18 as well as certain damage-associated molecular patterns (DAMPs). IL-1β can pass through the GSDMD [G] pore in the absence of membrane rupture suggesting that pyroptosis is not prerequisite for the release of this cytokine¹⁰. Moreover, vesicular release has been described as an alternative mechanism for slow release of mature IL-1\beta, however, effective and robust release of IL-1\beta depends on GSDMD^{11,12}. Unlike in myeloid cells where caspase-1 is required for processing of IL-18 and IL-1β, it appears that caspase-1-independent IL-18 processing by caspase-4 occurs in

human intestinal epithelial cells 13 . These distinctive features suggest mechanistic differences in the processing and release of cytokines between cell types.

There are two distinct molecular mechanisms governing the ability of different inflammasome sensors to initiate inflammasome assembly. NLRP1, NLRP3, and Pyrin assemble inflammasomes without directly binding ligands, but caspase-11 (caspase-4 and caspase-5 in humans; sensor for non-canonical NLRP3), AIM2, and NAIPs directly bind with their ligands for inflammasome activation⁷.

Non-ligand binding sensors

NLRP1—Human NLRP1 has 3 paralogs NLRPI(a–c) in mouse. Unlike human NLRP1, mouse NLRP1 lacks PYD. NLRP1 b responds to lethal toxin of *Bacillus anthracis*. Lethal factor component of the anthrax lethal toxin or any protease that induces N-terminal proteolytic cleavage at the amino terminus or function to find domain of NLRP1 can activate this inflammasome ^{14,15} (FIG. 1 a). It has been proposed that lethal factor-mediated cleavage relieves an intramolecular autoinhibition or induces conformational changes that subsequently leads to oligomerization of the receptor.

Canonical NLRP3—Although no direct ligands of NLRP3 have been identified yet, it is known to respond to cellular aberrations characterized by lysosomal rupture, potassium efflux, mitochondrial DNA or disruption, calcium influx or decrease in cellular cAMP levels, all caused by various PAMPs and DAMPs, including toxins, pathogens, crystalline substances, and metabolites⁷. The serine/threonine-protein kinase NEK7 and MAP kinase TGF-β activated kinase-1 (TAK1) are shown to regulate NLRP3 activation^{16–18}(FIG. 1b). In addition, Z-DNA-binding protein regulates NLRP3 inflammasome activation during influenza A virus infection¹⁹. Due to the broad nature of NLRP3 activation, it is unlikely that direct structural recognition or ligand binding is involved for its activation. NLRP3 may act as a sensor for homeostasis-altering molecular processes (HAMPs)²⁰.

Pyrin—Activation of the most recently identified inflammasome, Pyrin, depends on the inactivation of host small GTPases of the Rho family via Rho-modifying toxins, which inhibits the action of serine-threonine kinases PKN1 and PKN2 to relieve the phosphorylation of Pyrin and promote its activation^{21,22} (FIG. 1e). RhoA inactivation occurs in different residues which can be sensed by Pyrin, indicating that Pyrin responds to perturbation of cytoplasmic homeostasis rather than directly recognizing a conserved PAMP/DAMP²⁰.

Ligand-binding sensors

Caspase-11—Mouse caspase-11 or the human analogues, caspase-4 and caspase-5 directly bind to cytoplasmic lipopolysaccharide that subsequently leads to non-canonical NLRP3 inflammasome activation²³ (FIG. 1b). The molecular events by which caspase-11 acquires protease function have been obscure. A recent report has shown that caspase-11 dimerization is sufficient for autoprocessing that generates the fully active caspase-11 responsible for cleaving GSDMD²⁴. Although it has been demonstrated that GSDMD is

required for non-canonical NLRP3 inflammasome activation, the proximal events leading to inflammasome activation are not fully understood.

AIM2—The HIN domain of AIM2 binds to cytoplasmic double-stranded DNA (dsDNA), irrespective of the sequence of the dsDNA^{25,26} (FIG. 1d). Binding of the sugar-phosphate backbone of dsDNA with the positively charged HIN-200 domain relieves PYD for self-oligomerization and its interaction with ASC for inflammasome activation.

NAIP-NLRC4—Recognition of bacterial ligands by NAIPs is an initial event in NLRC4 inflammasome activation. Human NAIP recognizes flagellin and components of the type 3 secretion system; mouse NAIP5 and NAIP6 bind directly to flagellin, and mouse NAIP1 and NAIP2 bind the needle and inner rod of the type 3 secretion system, respectively^{27,28}. This ligand-binding event is followed by NLRC4 recruitment and subsequent oligomerization for the assembly of a functional NAIP–NLRC4 inflammasome complex²⁹ (FIG. 1c). The production of NAIPs is under the control of IRF8, which therefore is required for optimal NLRC4 inflammasome activation³⁰.

Promoting tumorigenesis

Although the primary role of inflammasome activation is to restrict pathogenic insults, persistent activation of inflammasomes propagates undesirable inflammatory responses⁷. It is well established that chronic inflammation contributes to most stages of tumorigenesis³¹. The pro-tumorigenic roles of inflammasome components have been mostly studied in tumor cell transplantation models, and are centered on proliferation and survival, immunosuppression, angiogenesis, and metastasis (FIG. 2).

Proliferation and Survival.

A common feature of all cancers is that they possess the ability to undergo increased proliferation and reduced cell death, both of which are stimulated by inflammation-driven mechanisms 31 . The inflammasome effector cytokines IL-1 β and IL-1 β released during acute and chronic inflammation may function in both a paracrine and an autocrine manner to induce cellular proliferation (FIG. 2a)

Notably, IL-18 but not IL-1β, produced from gastric epithelium promotes the development of gastric tumor in *gp130*^{F/F} mice [G] as a downstream effect of inflammasome activation. IL-18 inhibits caspase 8–mediated apoptosis in gastric cancer cells thereby promoting cell survival in a cell-autonomous manner³². Furthermore, IL-18 production from immune cells in the particular study is not sufficient to drive gastric tumorigenesis, suggesting that IL-18 production from epithelial tumor cells rather than immune cells is detrimental. Perhaps IL-18 is produced in higher amounts from gastric epithelium, as the study has showed higher gene expression of IL-18 in these cells compared to immune cells. Although IL-1β does not have such a role in survival, it also accelerates gastric tumorigenesis by a different mechanism, discussed in detail in the immunosuppressive section³³. Therefore, the functional dichotomy between IL-18 and IL-1β in gastric cancer could be explained, at least in part, by IL-18 acting on epithelial (tumor) cells expressing higher levels of IL-18R to promote cell survival³², whereas IL-1β-responsive immune cells provide a tumor-supporting

microenvironment³³. However, IL-1R signaling is important for proliferation of tumor cells in a spontaneous model of breast cancer³⁴. IL-1 β acts on breast cancer cells to enhance nuclear translocation of β -catenin that results in induction of multiple oncogenes responsible for cell proliferation³⁵. IL-18 production from gastric epithelial cancer cells is dependent on ASC, and ablation of ASC correlates with reduced NF-kB activation³² (FIG. 2a). NF-kB being a mediator of ASC in the gastric epithelium is consistent with NF-kB promoting cecal carcinogenesis in which ASC has been assigned a pro-tumorigenic role³⁶. ASC suppresses IL-1R-mediated NF-kB signaling in primary melanoma cells to inhibit proliferation, whereas such a suppressive function is inert in metastatic melanoma cells and instead ASC contributes to an inflammasome-mediated positive feedback loop of IL-1R signaling in metastatic melanoma to promote proliferation³⁷.

Furthermore, studies have highlighted the role of individual inflammasome sensors in tumor proliferation and survival. NLRP3 activation in lymphoma cells produce IL-18 which attenuates dexamethasone-induced apoptosis³⁸ thereby promoting their survival (FIG. 2a). The decreased tumor growth of cutaneous squamous cell carcinoma (SCC) in the absence of AIM2 is associated with its ability to suppress cell death and promote cellular proliferation by inducing the expression of several genes involved in cell cycle regulation³⁹. Although the precise regulatory mechanisms by which AIM2 induces these genes has not been reported, this might be due to the indirect effect of cytokines released by SCC cells in response to AIM2 inflammasome activation.

Another consequence of inflammasome activation, besides cytokine maturation, is GSDMD cleavage, which generates cytokine-releasing pores and culminates in pyroptosis³. The precise relevance and function of the pyroptosis executioner GSDMD in tumorigenesis is largely unknown. *Gsdmd*-silenced non-small cell lung cancer cells exhibit reduced EGFR– AKT signaling and enhanced caspase-3 cleavage and apoptosis, leading to suppression of tumor growth in transplanted mice⁴⁰. Together, these studies show how inflammasome signaling provides proliferative and survival cues by activating NF-KB or β -catenin and inhibiting apoptosis during tumorigenesis. But how these diverse signals are distributed among, and finally integrated in different cell types in distinct tumor settings requires further investigation.

Immunosuppression.

In response to invading tumor cells, our immune system launches a potent anti-tumor response with an influx of inflammatory cells into the tumor microenvironment [G] (TME) 41 . However, cancer cells can employ multiple mechanisms to evade immune surveillance. The release of inflammasome-dependent cytokines IL-18 and IL-1 β , and other costimulatory molecules (either directly from cancer cells or from neighboring cells) is a well-known process for shaping an immunosuppressive TME during the progression of various cancers 33,42,43 .

Myeloid-derived suppressor cells (MDSCs) are one of the key components of the TME and are characterized by their ability to produce inhibitory cytokines and inducible nitric oxide synthase, express arginase and induce regulatory T-cells, all of which collectively exert potent immunosuppressive activity 44 . IL-1 β is instrumental in suppressing the tumour

immune response by recruiting MDSCs. Xenograft tumors that overexpress IL-1β show a greater accumulation of immunosuppressive MDSCs and more rapid tumor progression⁴⁵, and *IIIr*^{-/-} mice implanted with mammary carcinomas exhibit delayed accumulation of MDSCs and tumor growth⁴⁶. The key role of IL-1β in MDSCs recruitment and activation is also shown in gastric cancer. Here, overexpression of IL-1β leads to early recruitment of MDSCs during the spontaneous development of gastric adenocarcinoma, and IL-1β directly activates these MDSCs³³. IL-18 suppresses the immune response through a distinct mechanism, which involves activation of T-cell immune checkpoints. In particular, IL-18 promotes melanoma or colon carcinoma metastasis likely by inhibiting natural killer (NK)-cell tumoricidal function through surface induction of the immunosuppressive costimulatory molecule PD-1⁴² (FIG. 2b). IL-18 also facilitates the immune escape of gastric cancer cells by downregulating CD70, a costimulatory molecule that increases the cytotoxicity of NK-cells and induces tumor-specific T-cell memory⁴³. Although these studies illustrate the direct immunosuppressive functions of IL-1β and IL-18, the specific inflammasome complexes to regulate these effectors are still being explored.

NLRP3 is crucial for accumulating MDSCs in tumors and inhibiting antitumor T-cell immunity after dendritic cell vaccination⁴⁷. NLRP3 signaling in tumor-associated macrophages (TAMs) [G] drives immunosuppressive CD4⁺ T-cell polarization in the TME of pancreatic ductal adenocarcinoma (PDA) via IL-1β ⁴⁸. Also, NLRP3-dependent release of IL-1β affects immune cells, primarily CD4⁺ T-cells, to express and release IL-22, which has been associated with aggressive growth of multiple cancers including lung, breast, gastric and skin cancer⁴⁹. In contrast to NLRP3 which mediates its effects by secreting inflammasome effector cytokines, studies point to AIM2 having a role in inflammasomedependent release of alarmins [G] that promotes tumorigenesis. Immunosuppressive tumorassociated plasmacytoid dendritic cells [G] in lung cancer are associated with a heightened ability to secrete IL-1a that depends on AIM2 and subsequent calpain activation⁵⁰. Mitophagy proteins PINK1 and PARK2 suppress oncogenic Kras-driven pancreatic tumorigenesis by keeping mitochondrial iron levels in check. Mechanistically, disrupted mitochondrial iron metabolism in the absence of these proteins induces AIM2-dependent HMGB1 release in PDA cells, which promotes upregulation of the immune checkpoint protein PD-L1. Blocking of HMGB1, but not IL-1β or IL-18, reduces neoplastic lesions and prolongs survival of the mice⁵¹. These two studies highlight the significance of understudied inflammasome-mediated alarmins in tumorigenesis.

Lastly, NLRP1 inflammasome-mediated IL-18 production in multiple myeloma augments the generation of MDSCs in the immune niche, leading to accelerated disease progression⁵² (FIG. 2b). While the NLRP1 inflammasome is known to be activated by anthrax lethal toxin, *Toxoplasma* infection, and hematopoietic stress¹⁵, the mechanism of its activation in the TME is largely unknown. NLRP1 may sense hematopoietic stress or the disturbance of intracellular homeostasis in the TME of multiple myeloma. Overall, inflammasomes and their effector cytokines lead to the accumulation of MDSCs and expression of immune checkpoint molecules, thereby inhibiting tumoricidal function of T-cells and NK-cells.

Angiogenesis.

Angiogenesis, the process by which new capillaries and vessels emerge from pre-existing vasculature, is vital for the progression from a small localized tumor to an enlarging tumor with the ability to metastasize. It is tightly regulated by numerous proangiogenic and antiangiogenic factors 53 . Inflammasome effector cytokines have been shown to regulate angiogenesis in several settings. Rapid tumor growth in mice implanted with IL-1 β –expressing lung cancer cells is associated with hyperneovascularization induced by proangiogenic factors secreted into the TME 54 . IL-1 β produced from tumor cells induces the production of proangiogenic factors, such as vascular endothelial growth factor (VEGF) and hepatocyte growth factor 54 , and chemokines such as CXCL2. Moreover, IL-1 β –mediated hypoxia-inducible factor-1 α upregulation stimulates VEGF production in lung cancer cells 55 (FIG. 2c). Although these studies exemplify the angiogenic functions of IL-1 β , how distinct inflammasome complexes regulate this cytokine to modulate angiogenesis need further investigations.

Metastasis.

Tumor metastasis is a complex process that involves all sequential events from tumor cell dissemination from the primary foci to the formation of metastatic nodules in distant organs⁵⁶. The environment of the distant metastatic target organs undergoes reprogramming, mostly by recruiting immune cells, to favor the growth of the tumor ^{56,57}. Tumor cell invasion and migration are key events in the metastatic cascade⁵⁷. Several mechanisms are shown for IL-1β or IL-18–mediated invasion and migration of cancer cells (FIG. 2d). These cytokines facilitate the invasion of malignant cells into the circulatory system and enhance the expression of adhesion molecules on endothelial and malignant cells, allowing dissemination and implantation into remote tissues⁵⁸. II1b^{-/-} mice have reduced lung metastasis and increased survival following inoculation of B16 melanoma cells⁵⁹. Similarly, systemic administration of IL-1 receptor antagonist (IL-1RA) reduces the size and numbers of hepatic metastases of melanoma and improves survival of the mice⁶⁰. IIIb-/- mice are comparatively less resistant to hepatic metastasis than Casp1-/- Casp11-/mice, which fail to produce both mature IL-1β and IL-18, suggesting that both cytokines contribute to metastasis. In this particular model, IL-18 acts downstream of IL-1β to facilitate inflammation-augmented hepatic metastasis by increasing vascular cell adhesion molecule-1 (VCAM-1) expression in hepatic-sinusoidal endothelial cells (HSECs) [G], which allows cancer cell adhesion⁵⁸. IL-18 also induces very late antigen-4 in melanoma cells⁶¹, which facilitates VCAM-1-dependent melanoma cell adhesion to HSECs⁶². Depletion of IL-18 in transplanted melanoma cells or systemic neutralization of IL-18 in recipient mice reduces lung metastasis⁴² indicating that IL-18 from cancer cells also contributes to metastasis. The outcome of metastasis appears to be greatly affected by the cancer cell type and source of IL-18 production. For instance, IL-18 promotes melanoma⁵⁸, but suppresses colon cancer⁶³ metastasis to the liver. Colon carcinoma-induced IL-18 production from liver Kupfer cells promotes Fas-Fas ligand (FasL)-driven cell death⁶³ (FIG. 2d). It is interesting to note that despite using the same intrasplenic injection model, these two studies presented with contrasting outcomes of hepatic metastasis indicating that IL-18 production induced by different cancer cell types dictates metastasis.

Similarly, the effect of NLRP3 activation may differ according to the cancer type, route of inoculation, and metastatic site. Hepatic metastasis following splenic injection of colon cancer cells is enhanced in Casp1^{-/-}Casp11^{-/-} and Nlrp3^{-/-} mice, which is dependent on IL-18 but not IL-1β⁶³. In contrast, a similar study has suggested that NLRP3-dependent IL-1β secretion from macrophages may shift tumor cells to a more migratory phenotype to drive hepatic dissemination and metastasis of colon cancer ⁶⁴. However, a critical flaw in the latter study is that different strains of WT and KO mice have been used, which generates difficulty in assessing the contribution of the gene of interest. On the other hand, the reduced lung metastasis in Casp1^{-/-} and NIrp3^{-/-} mice after orthotopic implantation or intravenous injection of EO771 breast cancer cells supports the idea that inflammasome activation regulated by NLRP3 encourages metastasis in this setting⁶⁵. Furthermore, there is evidence that NLRP3 also promotes metastasis independently of its inflammasome activity. Nlrp3^{-/-} mice, but not Casp1^{-/-} mice, have lower numbers of lung metastases after intravenous inoculation of melanoma or prostate carcinoma cells. Resistance to metastasis is attributed to enhanced NK-cell activity in the Nlrp3^{-/-} mice⁶⁶. Although tumor growth and lung metastasis in Casp1^{-/-}Casp11^{-/-} mice are comparable to that in WT mice in a model of breast cancer with spontaneous metastasis (PyMT-MMTV transgenic mice)³⁴, lung metastasis is reduced in Nlrp3^{-/-} mice implanted with tumors derived from PyMT-MMTV transgenic mice⁶⁵. Further study is required to explain whether this discrepancy results from inflammasome-independent functions of NLRP3 or from the differential contribution of inflammasomes in tumor cells versus host cells.

Tumor cells lose epithelial markers and gain mesenchymal traits during primary tumor invasion and metastasis 67 . IL-1 β and IL-18 have been reported to induce epithelial—mesenchymal transition [G] (EMT) in multiple cell types 68 . IL-1 β downregulates E-cadherin expression and upregulates Snail expression in SCC 69,70 and gastric cancer cells 71 . Tumor invasion also involves degradation of the extracellular matrix by matrix metalloproteinases 72 [G]. IL-1 β synergistically acts with growth factors to upregulate MMP-9 by increasing transcriptional activity of AP-1, thereby enhancing the invasiveness of breast ductal cancer cells 73 . Furthermore, interruption of cell–cell adhesion is a crucial step in invasion and metastasis. IL-18 enhances breast cancer cell migration via downregulation of claudins, which are junctional adhesion molecules 74 . Of interest, NLRP3 can promote EMT by enhancing TGF- β 1 signaling and Smad activation independently of caspase-1 or inflammasome-regulated cytokines 75,76 and reduced invasion of cutaneous SCC in the absence of AIM2 is associated with decreased production of MMP-13 and MMP-1 39 .

Together, these studies show that the role of inflammasomes in metastasis is bidirectional and the outcomes vary depending on factors such as the type of cancer and route of inoculation. Extending our knowledge gained from transplantable tumors, it would be exciting to explore how inflammasomes are involved in metastasis from primary tumor settings.

Suppressing tumorigenesis

The tumor-suppressive function of the inflammasome has been mostly demonstrated in the colorectal cancer (CRC) model. Mice lacking the inflammasome-initiating sensors

NLRP1b⁷⁷, NLRP3^{78,79}, AIM2^{80,81}, NLRC4^{82,83}, and Pyrin⁸⁴ are hypersusceptible to colitis-associated cancer induced by the DNA-damaging agent azoxymethane [G] (AOM) and chemical colitogen dextran sulfate sodium (DSS). AOM is a precursor of methylazoxymethanol, which can damage DNA by methylation of guanine. Tumors induced by AOM frequently carry mutations in K-Ras and β -catenin mimicking human CRC. AOM combined with DSS accelerates tumor development and is commonly used to study inflammation-mediated CRC⁸⁵. Inflammasome sensors assemble a fully functional inflammasome complex by recruiting ASC and caspase-1, which are also important in mediating protection against CRC^{77–80,82,83} (TABLE 1).

Protection in colorectal cancer

The ability of NLRP1b, NLRP3, and Pyrin to protect against CRC is attributed to the effector function of caspase-1 to mediate secretion of IL-18, a key cytokine that promotes epithelial barrier regeneration during the early stages of colitis^{78,79,86–89} (FIG. 3b). In addition, the ability of IL-18 to mount NK- or T-cell–mediated anti-tumor immune responses may contribute to this protection⁹⁰. Injection of recombinant IL-18 into *Casp1*^{-/-} mice reduces the prevalence of tumors in response to AOM and DSS⁷⁹. In contrast, another study found that mice with a conditional deletion of IL-18 in either epithelial cells or hematopoietic cells are more resistant to DSS-induced colitis⁹¹. Furthermore, amelioration of intestinal inflammation by neutralization of IL-18 suggests a detrimental role of IL-18 in colitis^{92,93}. Notably, IL-18 can inhibit the expression of soluble IL-22 binding protein largely in hematopoietic cells, which modulates the bioavailability of IL-22, a cytokine that suppresses early intestinal damage but also promotes tumorigenesis over time⁹⁴ (FIG. 3b). Therefore, early local production of IL-18 by enterocytes or cells residing in the lamina propria may contribute to epithelial repair after injury, whereas its excessive production during chronic inflammation potentially promotes tumorigenesis.

Signaling through the NLRP3 inflammasome in the hematopoietic⁷⁸ and non-hematopoietic compartment⁸⁶ are essential for mediating protection against colonic tumorigenesis. One study has suggested that NIrp3^{-/-} mice are more resistant to DSS-induced colitis than are WT mice⁹⁵, whereas another study has found similar tumor prevalence between WT mice and Nlrp3^{-/-} mice⁸². However, colorectal tumorigenesis induced by AOM in the presence of a high-cholesterol diet is mediated by NLRP3 inflammasome activation⁹⁶. Could these contrasting roles be explained to a certain extent by the differences in the gut microbiota between different animal facilities or the use of littermate versus non-littermate controls? It is important to note that genetically modified mice carrying the gain-of-function mutation *Nlrp3*^{R258W} [G], which is homologous to the human *NLRP3*^{R260W} mutation, are strongly resistant to experimental colitis and CRC. In these mice, enhanced IL-1β production in colon reshapes intestinal microbiota which in turn supports the development of Treg-cells to restrict gut inflammation⁹⁷. Furthermore, increased production of IL-1β by ASC-dependent inflammasome activation in the absence of PTPN2 in myeloid cells protects against CRC. In this particular model, more colitis in the mice lacking PTPN2 is associated with decreased tumorigenesis⁹⁸. Injection of recombinant IL-1β into NIrp1b^{-/-} mice mediates protection against colitis⁷⁷. This suggests that IL-1β plays an important role in inflammasomemediated protection against colitis. In contrast, a previous study has shown that $II1r^{-/-}$ mice

suffer similar susceptibility as WT to CRC⁸⁸, which might be due to a nullified outcome of differential IL-1R signaling in different tissues. Indeed, a recent study has elegantly demonstrated opposing roles of cell-type specific IL-1R signaling in CRC. The protumorigenic roles of IL-1R in epithelial and T-cells are counteracted by its effects on myeloid cells, particularly neutrophils, where IL-1R signaling contributes to deter tumor-infiltrating bacteria and dampen CRC promoting inflammation⁹⁹. A similar approach has been studied for the role of ASC in skin tumorigenesis, where inflammasome activation driven by ASC in myeloid cells favors epithelial skin tumorigenesis, whereas ASC in keratinocytes serves to limit proliferation, possibly through p53 activation in an inflammasome-independent manner¹⁰⁰. Thus, inflammasome signaling elicits cell-type specific responses, which altogether, determine the propensity for tumorigenesis.

Inflammasome-independent protection in colorectal cancer

The ability of inflammasome sensors to provide protection against cancer does not always rely on the effector cytokines. The protective role of NLRC4 in the development of CRC is associated with its intrinsic ability to restrict the proliferation and drive apoptosis of epithelial cells in both steady-state and the early phase of tumorigenesis⁸² (FIG. 3c). Apart from CRC, NLRC4 amplifies inflammatory signaling pathways in macrophages independently of inflammasome assembly and potentiates the production of IFN- γ in CD4⁺ and CD8⁺ T-cells to suppress melanoma growth in mice¹⁰¹ (FIG. 3d). Although mouse NAIP1–6 are components of the NLRC4 inflammasome, NAIP-mediated protection against CRC is related to their ability to inhibit hyperactivation of the transcription factor STAT3 and the expression of genes encoding anti-apoptotic and proliferation-related molecules, an NLRC4 inflammasome–independent and epithelium-intrinsic function of NAIPs¹⁰² (FIG. 3c). Furthermore, simultaneous recognition of flagellin in tumor cell lines by NAIPs and TLR5 induces tumor cell clearance by innate immune cells and activation of tumor-specific T-cell responses in mice¹⁰³.

An inflammasome-autonomous function of AIM2 in inhibiting inflammation-induced and spontaneous colorectal tumorigenesis has been suggested by two independent studies ^{80,81}. AIM2 interacts with the DNA-dependent protein kinase to limit PI3K/AKT activation ^{80,104}, thereby suppressing overt proliferation of colonic stem cells and inducing cell death ^{81,104} (FIG. 3c). A similar negative regulatory effect of the putative inflammasome sensor NLRC3 on PI3K-AKT signaling in limiting mTOR activation has been described to inhibit cellular proliferation ¹⁰⁵. Although the specific ligand that AIM2 senses in the colon has yet to be determined, host-DNA released after intestinal injury or DNA derived from the gut microbiota might activate AIM2 ¹⁰⁶. Indeed, AIM2 localizes to DNA in the nucleus of intestinal epithelial cells and bone marrow cells in response to dsDNA breaks caused by ionizing radiation or chemotherapeutic agents ¹⁰⁷. Whether the DNA-sensing property of AIM2 is required for its tumor suppressive function is not known. Another mechanism by which AIM2 restricts tumorigenesis is through antagonizing NF-κB activity to induce apoptosis, as shown in breast cancer cells ^{108,109}.

 $NLRP6^{110-112}$ and $NLRP12^{113}$ are potential inflammasome sensors. NLRP6-dependent secretion of mucin 2 **[G]** (MUC2) in the intestinal epithelium (FIG. 4) is required to clear

colitogenic bacteria. However, MUC2 secretion can be either dependent or independent of the inflammasome 111,114 . Likewise, despite of its ability to form inflammasomes, the protective function of NLRP12 against colitis and associated tumorigenesis is attributed to the negative regulation of inflammation via suppression of NF- κ B pathways 115,116 (FIG. 3c).

Inflammasome-microbiota-diet axis.

The composition of symbiotic microorganisms that live in our gut, the so-called gut microbiome, is one of the principal environmental factors that contributes to immune homeostasis in the intestine ¹¹⁷. Disturbance in the microbial ecology results in the development and progression of CRC, which can be modulated by the use of broadspectrum antibiotics¹¹⁸. In addition to their conventional role as a guardian of cellular integrity, inflammasomes can serve as a surveillance system, regulating the host/microbiota crosstalk in health and disease. The contrasting phenotypic outcomes in mice with identical genetic deficiencies are intriguing and can largely be attributed to different microbial composition across mice. The notion of inflammasomes regulating the gut microbial landscape emerged from a study that found that a 'colitogenic' gut microbial community, defined by an increased or decreased relative abundance of Prevotellaceae or Lactobacillus, respectively, predisposes NIrp6^{-/-} mice to exacerbated DSS-induced colitis and tumorigenesis or low-grade intestinal inflammation 110. Dysbiosis has also been reported in mice that are deficient in inflammasome components AIM2, NLRP3, ASC, caspase-1, and IL-18^{110,119,120}. The distinct microbiota profile characterized by an increased relative abundance of Lactobacillus murinus, and decreased abundance of colitogenic bacteria, Akkermensia muciniphila, is associated with decreased gut inflammation and CRC in *Nlrp3*^{R258W} mice⁹⁷. The colitogenic gut microbiota can be transmissible, as suggested by altered susceptibility of mice lacking NLRP6, AIM2, or NLRP12 following reciprocal exchange of gut microbiota with WT mice^{106,110,121}. Dysbiosis driven by NLRP6 deficiency elevates the production of CCL5, a chemokine that recruits immune cells in the intestinal lamina propria and mediates the secretion of IL-6, which in turn acts on epithelial cells to drive a pro-tumorigenic response⁸³ (FIG. 4). Consistently, CCL5 deficiency prevents dysbiosis-induced colitis and tumorigenesis, suggesting that CCL5 mediates immune dysregulation downstream of the microbial community^{83,110}. Furthermore, metabolites produced by gut microbiota may influence inflammasome-mediated disease outcome. The microbiota-derived metabolite taurine promotes the production of IL-18 in an NLRP6dependent manner, whereas histamine and spermine inhibit NLRP6¹²² (FIG. 4). An additional mechanism that NLRP6 employs to protect against tumorigenesis is to induce the secretion of MUC2 in sentinel goblet cells that expels intruding bacteria from the inner mucous layer^{111,114} (FIG. 4). This phenotype is unaffected by microbiota transfer, highlighting that certain biological functions of NLRP6 are not influenced by gut microbiota.

The effects of the inflammasome—gut microbiota axis have been extended from the gut to systemic metabolic and inflammatory processes. Microbiota composition influences the susceptibility of mice lacking NLRP3 to non-alcoholic steatohepatitis, which can progress to hepatocellular carcinoma¹²³. However, more recent studies argue that dysbiosis observed in

inflammasome-deficient mice is dependent on the facilities used to house the animals 124,125. Diet and the aseptic techniques used by different facilities may affect the ecology of gut microbiota, which in turn affects the activation status of inflammasomes. Indeed, mice fed with high-fat diet (HFD) have different microbial communities than those fed a normal diet or low-fat diet¹²⁶. Dietary cholesterol and dietary-derived deoxycholic acid [G] serve as endogenous danger signals that activate the NLRP3 inflammasome and contribute to HFDrelated colonic inflammation and CRC^{96,127}. On the other hand, NLRP3 activation by shortchain fatty acids or inhibition by omega-3 fatty acids prevent inflammation 128,129. Lastly, obesity is a risk factor in numerous cancers, and recent evidence presents inflammasome involvement as one link between this form of metabolic dysregulation and tumor-sustaining angiogenesis. Tumorigenesis in HFD-fed mice following orthotopic implantation of breast cancer cells is mediated by NLRC4 inflammasome activation. There is increased gene expression of NLRC4 in the obese TME of humans and mice. Immune cells with pronounced NLRC4 inflammasome activation are recruited in the TME of obese mice, leading to IL-1β release, which acts on adipocytes to promote VEGF production ¹³⁰. Metabolites of HFD or the alteration of gut microbiota in HFD-fed mice may activate the NLRC4 inflammasome ^{122,126}. These studies highlight a dynamic and emerging association among diet, microbiota, and inflammasome activation, indicating that dysbiosis influenced by inflammasomes should be revisited and interpreted with care.

Inflammasomes in human cancer

Evidence presented above from studies of murine models highlights the multifaceted roles of inflammasomes in cancer. Inflammasome signaling in human cancer is controlled by a combination of genetic factors, such as inherited genomic variations and acquired somatic mutations, and environmental factors that can affect epigenetics, gene expression, and ultimately provide stimulation for activation. Our understanding of the significance of inflammasomes in human cancer susceptibility has been enhanced by investigations of the genotype—phenotype correlations and gene expression profiling in cancers.

Gene polymorphisms and mutations

Polymorphisms in the genes encoding inflammasome components are associated with increased predisposition to multiple cancers. Several single-nucleotide polymorphisms (SNPs) in the *NLRP3* region are associated with susceptibility to Crohn's disease [G] 131,132, which is a strong risk factor for CRC. Among those SNPs, the gain-of-function *NLRP3* (Q705K) is associated with poorer survival in advanced-stage CRC¹³³. The same *NLRP3* variant is a risk allele for melanoma in Swedish males¹³⁴. Individuals with polymorphisms in *NLRP3*, *NLRP12*, and *CASP1* have a greater risk of gastric cancer when they are infected with *Helicobacter pylori*, displaying the interplay between genetic and environmental factors in tumorigenesis¹³⁵. A hyperactive *NLRP1* mutation causes spontaneous skin inflammation and a predisposition to skin cancer¹³⁶. However, other reports on the association of *NLRP1* polymorphisms with asbestos-associated mesothelioma^{137,138} are controversial. The *AIM2* gene contains a site for microsatellite instability that results in frequent gene mutation in CRC and small bowel cancers^{139,140}. In addition, *AIM2* is a potential oncogenic driver in endometrial cancer, though most

microsatellite-containing genes are bystander genes¹⁴¹. Altogether, SNP associations provide clues for determining which inflammasome components are important for the pathogenesis of specific cancer types. Going further, it would be helpful to examine the functional outcome of individual SNPs, such as alterations in inflammasome function or changes in expression levels.

Although inflammation is associated with a higher risk of cancer, it might be protective in some cases. Patients with familial Mediterranean fever [G] suffer from autoinflammation due to hyperactive Pyrin inflammasome, however, have a lower combined incidence of cancer than the general population¹⁴². It could be that pyrin inflammasome activation is beneficial in inhibiting tumorigenesis, but these results should be interpreted with caution, as the drugs used to treat FMF patients have anti-tumor effects. Further studies are needed to define the relation between genetic polymorphisms in inflammasomes and general cancer incidence or susceptibility to certain cancers.

Differential expression

Gene-expression profiling in many cancers has revealed differential gene expression of inflammasomes, which imply that inflammasome signaling is altered in cancer. In certain types of cancer, expression of inflammasome components are upregulated. Components of NLRP3 and AIM2 inflammasomes are highly expressed in nasopharyngeal and lung cancer tissues, compared with normal tissue, and this molecular signature is correlated with improved probability of survival of nasopharyngeal cancer 143,144. On the other hand, the NLRP3 inflammasome is overexpressed in oral SCC tissue and is associated with unfavorable pathology. In oral SCC tissue, enhanced expression of ASC is an independent predictor of poor prognosis¹⁴⁵. The discrepancy in the role of NLRP3 in cancer of anatomically adjacent oral and nasopharyngeal epithelia could be due to the distinct etiology of cancers in these tissues. While oral SCC is more attributed to chronic exposure of carcinogens such as tobacco, nasopharyngeal carcinoma is strongly linked with Epstein-Barr Virus infection. Therefore, it would be interesting to check whether inflammasome may have a protective role in other virus-associated cancers. The NLRP3 inflammasome is associated with the development of lymphoproliferative malignancy secondary to Sjogren syndrome [G]. Patients who later develop non-Hodgkin lymphoma express higher levels of NLRP3 inflammasome at the time of diagnosis ¹⁴⁶. Inflammasome activity also has a crucial role in drug resistance in acute lymphoblastic leukemia. Due to hypomethylation, CASP1 and NLRP3 expression is higher in glucocorticoid-resistant cells and cells at relapse. In vitro inhibition of caspase-1 blocks glucocorticoid receptor cleavage, thereby restoring sensitivity to treatment ¹⁴⁷. NLRP3 and NAIP expression is increased in urine sediments of patients diagnosed with bladder cancer. Combination of NAIP along with the established marker CK20 results in greater sensitivity for predicting the histological outcome of bladder cancer, suggesting that inflammasome genes could be useful as non-invasive diagnostic tools for bladder cancer ¹⁴⁸. Also, NLRP12 is highly expressed in prostate cancer epithelium compared to that of adjacent benign tissues. Despite high expression of pro-IL-1β and pro-IL-18, mature IL-1β or IL-18 are not detected in malignant prostate cancer cells, implying that NLRP12 may promote progression of prostate cancer independently of inflammasome activity¹⁴⁹.

Reduced expression of inflammasome components in certain tumors may be indicative of their tumor suppressor function. For instance, histone methyltransferase G9A mediates invasion and migration of lung cancer cells through repressing CASP1 expression. CASP1 is downregulated in lung adenocarcinoma compared to normal tissue, and reduced CASP1 expression is associated with poor survival, indicating that CASP1 may serve as a prognostic marker in lung cancer¹⁵⁰. The level of AIM2 expression is lower in CRC tumors than in adjacent normal tissue. The lack of AIM2 expression is correlated with higher tumor grade and is associated with poorer survival¹⁵¹. This finding is supported by gene expression analysis from the TCGA database showing lower levels of NLRP1, NLRP3, NLRC4 and AIM2 expression in CRC than in healthy controls, but results vary when different databases are used for the analysis ¹⁵². Evaluation of inflammasome expression in hepatocellular carcinoma reveals a dynamic pattern during the progression of the disease: NLRP3 and AIM2 inflammasomes are upregulated in cirrhotic tissue but then are lost in cancer. Moreover, lower expression of these inflammasome components correlates with advanced clinicopathological features of HCC. These results are not straightforward but may provide insight into how chronic inflammation fosters malignant transformation. Cells proliferating in the presence of persistent inflammation and inflammasome activation may accumulate mutations, lose expression of tumor-suppressive NLRP3, ultimately leading to cancer progression ¹⁵³. Although not well-studied as an inflammasome sensor, NLRC5 is a key transcriptional coactivator of MHC class I genes. Reduced NLRC5 expression is associated with impaired CD8⁺ T-cell activation and immune evasion in cancers. Lower NLRC5 expression corelates with reduced survival in melanoma, bladder and cervical cancers, suggesting that NLRC5 may be used as a prognostic marker for multiple cancers ¹⁵⁴.

Therapeutic approaches

Therapeutics targeting inflammasome activity have been shown effective for autoinflammatory periodic fever syndromes and used experimentally for treating inflammation-driven neurodegenerative diseases and metabolic disorders. Although there is ample evidence that inappropriate inflammasome regulation contributes to the pathogenesis of human cancers, where and how inflammasome therapy is applicable in cancer should be evaluated critically. One emerging approach could be modulating inflammasome activation while administering chemotherapeutics or cell therapeutics to maximize their efficacy. Prospectively, cytokine blockade may prove useful in various clinical settings, ranging from preventive regimens for individuals predisposed to chronic inflammation, to therapeutic intervention to restrict tumor progression in precancerous settings, and to palliative or adjuvant treatment for advanced cancers.

Inflammasome signaling during therapy

Recent findings address the interactions between chemotherapeutic agents and inflammasome activation. Cancer chemotherapeutics, such as anthracyclines and platinum-based drugs, elicit cytotoxicity against malignant cells. This is achieved in part, by inducing immunogenic cell death which can be modulated by inflammasome signaling ¹⁵⁵. The observation that caspase activity augments antitumor immune responses induced by anthracyclin ¹⁵⁶ led to the discovery that NLRP3 inflammasome activation is required for

effective cancer chemotherapy 157 . The release of various DAMPs, including ATP, HMGB1, and IL-1 α from dying tumor cells activates the NLRP3 inflammasome in dendritic cells (DC) to release IL-1 β , which is crucial for priming IFN- γ producing CD8⁺ T-cells and activating NK-cells 157 (FIG. 5). Furthermore, a loss-of-function polymorphism in the purinergic receptor P2RX7 in patients with breast cancer who were treated with anthracyclines, has been correlated with more metastasis 157 . On the other hand, gemcitabine and 5-fluorouracil (5-FU) activate NLRP3 inflammasome via cathepsin B release in MDSCs, thereby producing IL-1 β levels insufficient for CD8⁺ T-cell priming but sufficient to drive IL-17-producing CD4⁺ T cells 158 (FIG. 5). Likewise, NLRP3 inflammasome mediates resistance to 5-FU treatment for oral SCC 159 , and reduces the efficacy of DC-derived anti-tumor vaccines against grafted tumor cells 47 .

A recent study showed that AIM2 inflammasome activation by antibody-dependent cellular phagocytosis of tumor DNA into macrophages following monoclonal antibody-based cancer treatment suppresses anti-tumor immunity by upregulating PD-L1 and indoleamine 2,3-dioxygenase¹⁶⁰ This finding suggests that the use of immune checkpoint blockade in combination with antibody treatment may be beneficial to boost treatment efficacy.

Although IL-1 β signaling enhances the efficacy of doxorubicin against breast adenocarcinomas and fibrosarcomas ¹⁶¹, the efficacy of cisplatin against malignant mesothelioma tumor cells is increased by concomitant use of IL-1Ra¹⁶². Also, impaired doxorubicin efficacy towards breast cancer cells in the presence of IL-18 suggests a role of IL-18 in the development of chemotherapy resistance¹⁶³. Eradicating large solid tumors at advanced stages remains challenging, and new attempts have been made to harness inflammasome signaling for better treatments. Adoptive therapy with chimeric antigen receptor–redirected T-cells engineered with inducible IL-18 release mounts acute inflammation and reduces the number of repressor cells, resulting in an augmented immune attack against large established pancreatic tumors¹⁶⁴.

In general, GSDMD has been viewed as an executioner of pyroptosis downstream of caspase-1 and caspase-11. However, a recent study has demonstrated that apoptosis-inducing chemotherapies are capable of inducing pyroptosis by activating gasdermin E (GSDME) in a caspase-3 dependent manner¹⁶⁵. Based on this finding, it would be expected that chemotherapy would be more effective in GSDME–expressing cancers. It is worth to investigate whether GSDME mediated pyroptosis is a preferred mode of cell death that subsequently activates inflammasome in neighboring cancer cells.

Inflammasome-targeting therapy

Multiple approaches can be used to target inflammasome activity, including abrogation of upstream signaling pathways, inhibition of inflammasome components, and antagonism of end-products of inflammasome activation (TABLE 2). Pharmacological inhibition of the NLRP3 inflammasome has been widely implemented in laboratory studies, which have been reviewed elsewhere ^{166,167}. In clinical studies, cytokine blockade is the most successful approach, and evidence of the effectiveness of IL-1 inhibition in anticancer treatment is just emerging. A Phase II clinical trial investigating the effect of IL-1Ra anakinra in patients with early-stage multiple myeloma indicates that IL-1Ra suppresses markers of disease

progression 168,169 . IL-1Ra blocks signaling induced by both IL-1 α and IL-1 β . While the production of the latter cytokine is virtually inflammasome-dependent, studies have shown IL-1 α release can be either dependent or independent of inflammasome activation 170 . A Phase III trial of MABp1 (a monoclonal antibody targeting IL-1 α) treatment in refractory CRC has shown clinical benefit, and an increase in median survival 171 . This suggests that the efficacy of anakinra in cancer treatment may in part come from the inhibition of IL-1 α .

The Canakinumab Anti-inflammatory Thrombosis Outcomes Study [G] (CANTOS) was a clinical trial to determine whether IL-1 β inhibition prevents cardiovascular events in patients who had high markers of inflammation after a myocardial infarction. In a secondary analysis, it was found that canakinumab reduced lung cancer incidence and mortality but did not affect other types of cancer¹⁷². The results are encouraging for cancers in which inflammation is highly involved in cancer development and progression. In a Phase II trial for metastatic CRC, co-administration of anakinra with 5-FU and bevacizumab has shown a favorable median survival similar to that of other palliative therapies¹⁷³. Therefore, targeted therapy against inflammasome activation could be useful in adjuvant or palliative therapies for cancer.

Conclusion

Understanding how inflammasome signaling affects tumor initiation and progression has been one of the most intriguing questions in the field. Inflammasomes exhibit distinct and sometimes conflicting roles in multiple facets of tumorigenesis. The influence of the inflammasome in tumor promotion ranges from suppressing antitumor immunity and cell death to fostering proliferation, angiogenesis, and metastasis. The relative expression of inflammasome components differs in various cell types⁴, which suggests that inflammasomes perform distinct functions in different cellular compartments. The tumor-suppressive function of the inflammasome is largely reflected in its preventive role in colitis and colon cancer, which is achieved by tumor immunosurveillance, maintaining epithelial integrity, mucus production, and suppressing the proliferation of intestinal epithelial cells. Regardless of whether the dysregulated inflammasome signaling is a result of dysbiosis or vice versa, which has not been conclusively investigated yet, both affect intestinal inflammation and cancer development. In addition to genetic factors, environmental factors (e.g., diet) and experimental conditions associated with animal models influence the ecology of gut microbiota and, in turn, inflammasome activation.

Given that the outcomes of inflammasome signaling are diverse across tumor types, gaining insight about how to manage this diversity will be an important area for future investigations. Clinical trials that specifically inhibit inflammasome components in human cancers are yet to be performed (Table 2). Although a major clinical trial on inhibiting the downstream effector molecule IL-1 β has recently yielded promising results¹⁷², blocking IL-1 β or IL-18 individually is not the same as caspase-1 inhibition. Caspase-1 blockade can inhibit global inflammatory responses regulated by both inflammasome-dependent cytokines and pyroptosis. In addition, inhibition of a specific inflammasome like NLRP3 by MCC950 can block pathological effects of NLRP3 without compromising beneficial effects from other inflammasomes. Indeed, the development of highly specific NLRP3 inhibitors, such as

MCC950, and caspase-1 inhibitors have opened exciting new avenues for translational research with the potential for therapeutic targeting of tumorigenesis. The studies highlighted in this Review outline a roadmap to developing specific anticancer therapy by modulating inflammasome signaling, which could set the stage for the concept of "tumor immunoediting" by inflammasome signaling.

Acknowledgements

Research studies from our laboratory are supported by the U.S. National Institutes of Health (AR056296, CA163507, AI124346, and AI101935 to T.-D.K.), the American Lebanese Syrian Associated Charities (to T.-D.K.). We apologize to our colleagues whose work was not cited due to space limitation.

Glossary

Gut microbiota

Ecological community of microorganisms that harbors in gastrointestinal tract

Pyroptosis

An inflammatory and lytic form of cell death mediated by inflammatory caspases

gp130^{F/F} mice

Mice are generated using a phenylalanine knock-in substitution at tyrosine 757 in the cytoplasmic domain of the IL-6 receptor β -chain Gp130. They rapidly develop tumors in the epithelium of the glandular stomach and highlight a key role for STAT3 signaling in gastric tumorigenesis

Tumor microenvironment

Cellular and molecular environment where tumor cells interact with infiltrating immune cells, fibroblasts, blood vessels and extracellular matrix

Tumor associated macrophages

A class of mostly abundant immune cells present in the tumor microenvironment. They have tumor-promoting phenotype via modulating tumor cell proliferation, tumor angiogenesis, invasion and metastasis

Alarmins

Damage-associated molecular patterns such as HMGB1 or IL-1 α released by damaged or necrotic cells

Plasmacytoid dendritic cells

Type I interferon–producing subset of dendritic cells with antigen presenting potential

Hepatic sinusoidal endothelial cells

A special type of endothelial cells which represent the interface between blood cells on the one side and hepatocytes and hepatic stellate cells on the other side

Epithelial to mesenchymal transition

A process by which epithelial cells lose their motility and cell-cell adhesion properties and acquire mesenchymal fibroblast like properties

Matrix metalloproteinases

A family of endopeptidases capable of degrading extracellular matrix components, influencing multiple cellular processes such as migration and adhesion

Azoxymethane

A potent carcinogen which is used to induce colon carcinoma in mice and rats. It is metabolized to methyl-azoxymethanol in the liver and then reaches to the colon via the blood stream rather than the bile

Nlrp3R258W mice

Genetically modified mice carrying R258W mutation in the *Nlrp3* gene, which corresponds to R260W mutation in the *NLRP3* gene in human. These mice develop severe cutaneous lesions, including erythema, scaling and the thickening of both epidermis and dermis, symptoms that recapitulate urticaria-like skin lesions reported in Muckle-Wells syndrome patients

Mucin 2

A glycoprotein which is particularly prominent in the gut and is secreted from goblet cells in the epithelial lining into the lumen of the large intestine

Deoxycholic acid

A bile-acid which emulsifies and solubilizes dietary fats in the intestine

Crohn's disease

An inflammatory bowel disease that involves chronic inflammation of digestive tract

Familial Mediterranean fever (FMF)

Mutations in gene encoding pyrin (MEFV) are associated with FMF, which is an autosomal-recessive, autoinflammatory disorder characterized by episodic fever and neutrophil-mediated inflammation of serosal tissues

Sjogren syndrome

An autoimmune disease that mostly affects the salivary and lacrimal glands, resulting in dry mouth and dry eyes

Canakinumab Anti-inflammatory Thrombosis Outcomes Study

A randomized, double blinded, placebo-controlled trial to evaluate the effect of canakinumab, a human monoclonal antibody that selectively neutralizes IL-1 β , in the prevention of recurrent vascular events in patients with previous myocardial infarction

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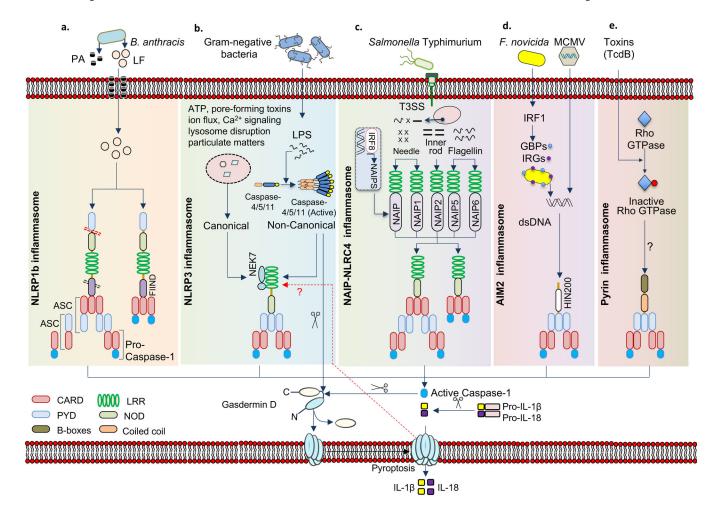


Fig. 1 |. Diverse mechanisms of inflammasome activation.

a Bacillus anthracis toxin, which contains protective antigen (PA) and lethal factor (LF), activates NLRP1 inflammasome by inducing cleavage at the N-terminal linker region (red dotted line). PA forms pores in the host cell membrane which is used by LF to enter the cell. Auto-proteolytic cleavage at the FIIND domain (black dotted line) has also been observed. Caspase-1 is recruited into the complex via ASC- or by direct association with NLRP1 through CARD-CARD interactions. b NLRP3 inflammasome is activated by various pathogen associated molecular patterns (PAMPs) and damage associated molecular patterns (DAMPs). NEK7 is an upstream activator of NLRP3 inflammasome assembly. Noncanonical NLRP3 inflammsome activation induced by cytosolic LPS is caspase-4/5/11 dependent. Caspase 11 cleaves the N-terminal domain of gasdermin-D to induce pyroptosis. c Bacterial type 3 secretion system (T3SS) components (needle and inner rod) and flagellin are sensed by NAIPs to assemble and activate NLRC4 inflammsome. The basal transcription of NAIPs is regulated by IRF8. NLRC4 enables ASC-dependent or ASC-independent CARD-CARD interaction for casapse-1 activation. d AIM2 is activated by host or pathogen-derived dsDNA. During Francisella tularensis infection, interferon regulatory factor 1 (IRF1) transcriptionally regulate the expression of GBPs and IRGs to liberate bacterial dsDNA which is recognized by AIM2. e Pyrin inflammasome is activated when

Pyrin senses the modification of Rho induced by Rho-inactivating toxins. Inflammasome activation results in activated caspase 1 inducing pyroptosis via cleavage of the N-terminal domain of gasdermin-D that generates pores on the host plasma membrane, which leads to the release of bioactive IL-1 β and IL-18.

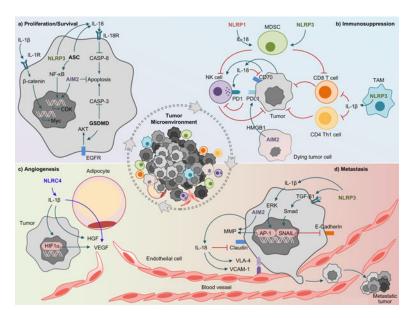


Fig. 2 |. Protumorigenic roles of inflammasome components.

a Proliferation. NLRP3-mediated release of IL-18 or IL-1 β activates β -catenin which induces the oncogene c-Myc, that enhances proliferation of lymphoma cells. ASC in gastric epithelial cancer cells induces IL-18 production and NF-KB activation that leads to cellular proliferation. Gasdermin-D (GSDMD) promotes epidermal growth factor receptor-mediated protein kinase B (AKT) signaling in non-small cell lung cancer. b Immunosuppression. NLRP1-mediated IL-18 production in multiple myeloma enhances the generation of myeloid-derived suppressor cells (MDSCs) in the immune niche that leads to tumorigenesis via inhibiting CD8⁺ T-cells and natural killer (NK)-cells. NLRP3-mediated IL-1β in tumor associated macrophages (TAMs) inhibits anti-tumor immunity of CD4⁺ Th1 cells and CD8⁺ T-cells. High mobility group box 1 (HMGB1) released from the disrupted mitochondrial iron metabolism in an AIM2-dependent manner promotes the upregulation of the immune checkpoint programmed death-ligand 1 (PDL1) in pancreatic ductal adenocarcinoma. IL-18 facilitates immune escape of gastric cancer cells by upregulating programmed cell death protein 1 (PD1) on NK-cells and downregulating CD70 on tumor cells. CD70 increases the cytotoxicity of NK-cells and induces tumor-specific T-cell memory. c Angiogenesis. NLRC4 inflammasome mediated release of IL-1β acts on adipocytes to induce the production of vascular endothelial growth factor (VEGF). In tumor cells, IL-1β stimulates the secretion of hepatocyte growth factor (HGF) and induces hypoxia-inducible factor-1 (HIF1α) in tumor cells to transcriptionally regulate VEGF production. **d**| Metastasis. NLRP3 promotes epithelial-mesenchymal transition (EMT) by enhancing transforming growth factor beta 1 (TGF-β1) mediated Smad signaling that induces Snail expression which downregulates E-cadherin in squamous cell carcinoma and gastric carcinoma. AIM2 enhances the production of matrix-metalloproteinases (MMPs) that leads to the invasion of cutaneous squamous cell carcinoma. IL-1β increases the transcriptional activity of activator protein (AP-1) that induces MMPs increasing the invasiveness of breast ductal cancer cells. Tumor-derived IL-18 induces vascular cell adhesion molecule-1 (VCAM-1) expression in hepatic sinusoidal endothelial cells (HSECs) and very late antigen 4 (VLA-4) in melanoma cells that facilitates VCAM-1 dependent melanoma cell adhesion to HSECs.

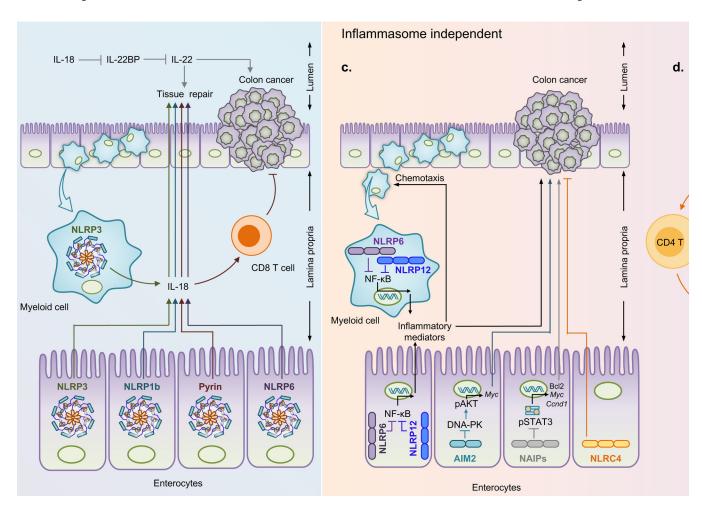


Fig. 3 |. Protective roles of inflammasomes in cancer.

a IL-18 released from Kupffer cells in an NLRP3 inflammasome dependent manner controls liver metastasis of colon carcinoma by enhancing Fas ligand (FasL) expression on natural killer (NK) cells, promoting their tumoricidal function. b NLRP3, NLRP1b, Pyrin, and NLRP6 inflammasomes mediate the production of IL-18 that enhances the barrier function and regenerates epithelial cells to protect against colorectal cancer (CRC). IL-18 modulates the bioavailability of IL-22 which has dual effects in CRC. Pyrin-mediated release of IL-18 promotes CD8+ T-cells to inhibit CRC. c| NLRP6 and NLRP12 function in both the myeloid cells and enterocytes to negatively regulate the expression of NF-κBmediated inflammatory cytokines and chemokines. These inflammatory mediators induce the chemotaxis of immune cells into the lamina propria during colitis. AIM2 inhibits DNAdependent protein kinase (DNA-PK)-mediated phosphorylation of AKT and cMyc induction to inhibit overt proliferation of intestinal stem cells. NAIPs inhibit signal transducer and activator of transcription 3 (STAT3) hyperactivation and cellular proliferation to prevent CRC, whereas NLRC4 restricts proliferation and drives apoptosis of epithelial cells. d NLRC4 in myeloid cells releases chemokines which potentiate the production of IFN- γ from CD4⁺ and CD8⁺ T-cells to suppress melanoma growth.

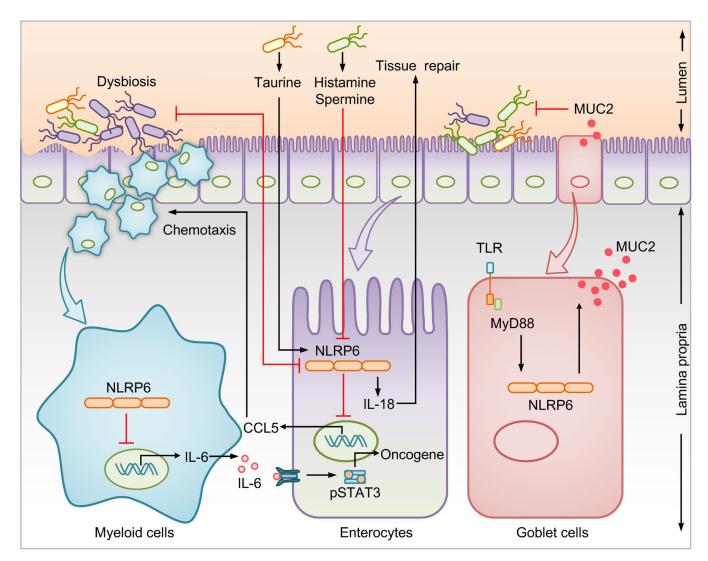


Fig. 4 |. Inflammasome-microbiota axis in intestinal homeostasis.

Several immune mechanisms work in concert with the intestinal microbiota to maintain intestinal homeostasis and provide protection against colorectal cancer (CRC). Dysbiosis inhibits NLRP6 inflammasome activation in enterocytes. Conversely, NLRP6 in enterocytes inhibits intestinal dysbiosis and CCL5-mediated recruitment of immune cells into the lamina propria. Increased IL-6 production from myeloid cells in the absence of NLRP6 acts on neighboring enterocytes, to activate the oncogenic transcription factor signal transducer and activator of transcription 3 (STAT3). The microbial metabolite taurine activates, whereas histamine and spermine suppress NLRP6– mediated IL-18 secretion. NLRP6 in sentinel goblet cells induces the secretion of mucin 2 (MUC2) which expels intruding bacteria found in the inner mucous layer providing protection against CRC.

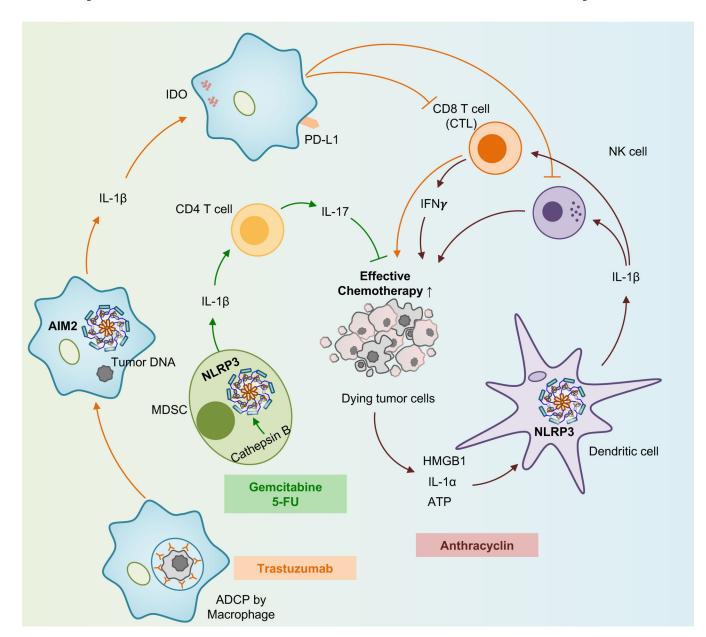


Fig. 5 |. Inflammasome signaling during chemotherapy.

Gemcitabine and 5-fluorouracil (5-FU) activate NLRP3 inflammasome in myeloid-derived suppressor cells (MDSCs) to produce IL-1 β , which primes CD4⁺ T-cells to release IL-17. High mobility group box 1 (HMGB1), IL-1 α , and adenosine triphosphate (ATP) released from dying tumor cells activate NLRP3 inflammasome in dendritic cells (DCs) to release IL-1 β which is crucial for activating natural-killer (NK) cells and priming CD8⁺ T-cells to produce IFN- γ . Antibody-dependent cellular phagocytosis of tumor cells by macrophages leads to AIM2 inflammasome activation. IL-1 β upregulates the expression of programmed death-ligand 1 (PD-L1) and indoleamine 2,3-dioxygenase (IDO) in macrophages that inhibit NK cell and cytotoxic T lymphocyte (CTL)-mediated cytotoxicity.

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Table 1.

Diverse roles of inflammasomes across different cancers

| Cancer Type | Animal Model | In vitro systems |
|---|--|--|
| Lung cancer (implanted tumors) | ■ Rapid growth of LLC cells in mice transduced with human IL-1β–expressing vector⁵⁴. ■ Decreased lung metastases of B16F10 melanoma, RM-1 prostate, and E0771 mammary adenocarcinoma in <i>Nlrp3</i>^{-/-} mice⁶⁶. ■ Decreased lung metastases, and tumor growth of B16 melanoma in <i>II1b</i>^{-/-} mice⁵⁹ or <i>II18r</i>^{-/-} mice⁴². ■ Increased lung metastases of LLC in <i>Casp1</i>^{-/-} <i>Casp11</i>^{-/-} mice⁶³. ■ Reduced tumor growth in nude mice injected with <i>Gsdmd</i>-silenced PC9 cells⁴⁰. | ■ Decreased proliferation and migration of <i>Nlrp3</i> -silenced, CASP1-inhibited, and IL-18BP-added A549 cells ¹⁷⁴ . ■ Augmentation of IL-1α release from AIM2-activated lung tumor—associated pDCs ⁵⁰ . ■ Decreased viability and increased apoptosis in <i>Gsdmd</i> -silenced PC9, H1703, and H1975 cells ⁴⁰ . |
| Breast cancer (implanted tumors) | ■ Reduced tumor growth of Py8119 in <i>IIIb</i>^{-/-} mice¹³⁰. ■ Reduced tumor growth of EO771 or PyT8 or MDA-MB-231 in <i>Casp1</i>^{-/-} and <i>Nlrp3</i>^{-/-} mice⁶⁵. ■ Reduced tumor growth of MDA-MB-435 in mice treated with AIM2/SN2 DNA¹⁰⁸. ■ Reduced tumor progression in 4T1 tumor-bearing mice treated with IL-1R antibody⁴⁹. ■ Retarded tumor growth in E0771 cells—bearing mice treated with anakinra⁴⁹. ■ Reduced tumor growth of Py8119 or EO771 cells in diet-induced obese <i>Casp1</i>^{-/-} <i>Casp11</i>^{-/-} or <i>Nlrc4</i>^{-/-} mice¹³⁰. | ■ Increased migration and invasion of IL-10-treated BT474 cells ⁷³ . ■ Increased migration of IL-18—treated and decreased migration of <i>II18</i> -silenced MCF-7 cells ⁷⁴ . ■ Decreased viability and colonyforming ability of <i>Aim2</i> -overexpressed MCF-7, MDA-MB-231, MDA-MB-435, and MDA-MB-453 cells ^{109,108} . |
| Fibrosarcoma | ■ Reduced MCA-induced tumor incidence in <i>NIrp3</i> ^{-/-} , <i>CaspI</i> ^{-/-} and <i>II1r</i> ^{-/-} mice ⁶⁶ . ■ Reduced tumor growth in IL-18-injected mice after implantation of T241 cells ¹⁷⁵ . | N/A |
| Gastric Cancer | ■ Increased gastric cancer in <i>IL-1B</i> transgenic mice infected with <i>Helicobacter felis</i>³³. ■ Reduced gastric preneoplasia in <i>IIIr</i>^{-/-} mice infected with <i>Helicobacter felis</i>¹⁷⁶. ■ Reduced tumor volume of II18-silenced gastric cancer cells in nude mice⁴³. ■ Reduced tumor incidence in <i>gp136</i>^{F/F} <i>Asc</i>^{-/-} or <i>gp136</i>^{F/F} <i>II18</i>^{-/-} mice³². ■ Decreased tumor growth of <i>Gsdmd</i>-expressing BGC-823 cells in nude mice¹⁷⁷. | ■ Suppressed colony formation of AGS and MKN1 cells treated with II.18 neutralizing antibody ³² . ■ Suppressed colony formation in <i>Asc</i> -/- and <i>Casp1</i> -/- AGS cells ³² . ■ Decreased proliferation and colony formation in <i>Gsdmd</i> -overexpressed BGC-823 cells and increased proliferation in <i>Gsdmd</i> -silenced BGC-823 cells ¹⁷⁷ . |
| Hepatic Cancer (Implanted tumors) | ■ Regression of CT26 tumors in the liver of WT mice after <i>IL-18</i> gene transfer ¹⁷⁸ . ■ Decreased hepatic metastases of B16M cells in mice injected with IL-18BP ⁶² . ■ Reduced tumor incidence in DEN-treated <i>Casp1</i> ^{-/-} and <i>Aim2</i> ^{-/-} mice ¹⁷⁹ . ■ Decreased hepatic metastasis of B16 melanoma in <i>II1b</i> ^{-/-} and <i>Casp1</i> ^{-/-} <i>Casp1</i> ^{-/-} mice ⁵⁸ . ■ Increased metastasis in mice injected with <i>Aim2</i> -silenced HCC cells ¹⁸⁰ . ■ Decreased MC38 metastatic tumors in the liver of <i>Nlrp3</i> ^{-/-} mice ⁶⁴ . ■ Increased MC38 metastatic tumors in the livers of <i>Casp1</i> ^{-/-} <i>Casp1</i> 1 ^{-/-} , <i>Nlrp3</i> ^{-/-} , <i>II18</i> ^{-/-} and <i>II18</i> r ^{-/-} mice ⁶³ . | ■ Increased migration and invasion of <i>Aim2</i> -silenced HCC cells ¹⁸⁰ . |
| Colon Cancer (AOM/DSS) | Increased tumors in the colons of NIrp3 ^{-/-78,79} , Aim2 ^{-/-80,81} , NIrc4 ^{-/-82,83} , Naip1-6 ^{-/-102} , NIrp1b ^{-/-77} , NIrp6 ^{-/-83,181,182} , NIrp12 ^{-/-115,116} , Pyrin ^{-/-84} , Asc -/-77-80,83, Casp1 ^{-/-78} ,82, II18 ^{-/-79,88} and II18r ^{-/-88} mice. Decreased tumors in colons of IL-18 injected Casp1 ^{-/-79} , Pyrin ^{-/-84} or II18 ^{-/-84} mice. Decreased tumor in the colons of Casp1 ^{-/-183} and NIrp3 ^{R258W} mice ⁹⁷ . Decreased tumors in the colons of IL-1Ra-injected WT mice ¹⁸⁴ . Increased tumors in the colons of IL-1β-treated complement deficient mice ¹⁸⁵ . More tumors in the colons of Ptpn2r ^{-/-} mice treated with a vaccine against IL-1β or in Ptpn2 ^{-/-} Asc ^{-/-} mice ⁹⁸ . | ■ Increased proliferation and invasion of HT29, Caco-2, HCA7 and HCT116 cells cocultured with IL-1β-treated normal or cancer-associated fibroblasts ¹⁸⁶ . ■ Decreased survival of AIM2-expressing HCT116 cells ¹⁰⁴ . ■ Decreased migration and invasion of <i>NIrp3</i> -silenced HCT116, HT29 and SW620 cells ⁷⁶ . |
| Prostate Cancer | ■ Decreased metastatic lesions in bones of WT mice injected with <i>Il11b</i> -silenced PC-3 cells and increased metastatic lesions in bones of WT mice injected with IL-1β–overexpressed DU-145 cells ¹⁸⁷ . | ■ Increased migration of IL-1β–stimulated PC-3 cells ¹⁸⁸ . |

| Cancer Type | Animal Model | In vitro systems |
|----------------------------|---|--|
| Glioblastoma | ■ Reduced growth of 9L cells in WT mice or WT rats inoculated with BMSCs expressing IL-18^{189,190} ■ Increased survival and decreased tumor size in WT rats following injection of IL-18-transduced C6 glioma cells¹⁹¹. ■ Decreased tumor size in SR-B10-injected mice followed by administration of recombinant IL-18¹⁹². ■ Reduced tumor growth of GL261 and U87 cells in <i>Nlrp3</i>-silenced mice following IR-treatment¹⁹³. | ■ Increased proliferation, migration and invasion of IL-1β-treated U87 and U251 cells ¹⁹⁴ . ■ Increased apoptosis of IL-1β-treated hypoxic U87 cells ¹⁹⁵ . ■ Decreased viability and increased apoptosis of 9L glioma cells cocultured with BMSCs expressing IL-18 ^{189,190} . |
| Skin Cancer Melanoma | ■ Delayed tumor onset in 3-MCA-treated II1b^{-/-} mice¹⁹⁶. ■ Reduced tumor growth in mice injected with NIrp1b-silenced 1205Lu cells¹⁹⁷. ■ Reduced tumor incidence in DMBA/TPA-treated II1r^{-/-} and Casp1^{-/-} mice¹⁰⁰. ■ Reduced tumor incidence in LysM-Asc^{-/-} mice and increased tumor incidence in K14-Asc^{-/-} mice after DMBA/TPA treatment¹⁰⁰. ■ Reduced papilloma lesions in NIrp3^{-/-} mice¹⁹⁸. ■ Increased tumor size in NIrc4^{-/-} mice challenged with B16F10 cells¹⁰¹. ■ Reduced B16 tumor growth in chimeric WT mice adoptively transferred with Casp1^{-/-} BMCs¹⁹⁹. | ■ Increased proliferation of IL-18–treated B16M, A375, HMB2, VUP, SK23, MJM melanoma cells ⁶² . ■ Decreased viability and increased apoptosis of <i>Nlrp1b</i> -silenced WM115, 1205Lu and Hs294T cells ¹⁹⁷ . |
| Squamous Cell Carcinoma | ■ Reduced tumor burden in the head and neck of NLRP3 inhibitor (MCC950)-treated <i>Tgfbr1-'-</i> Piten^{-/-} mice²⁰⁰. ■ Delayed onset and smaller tumor area in the tongue of 4-NQO-administered and 5-FU-treated <i>Nlrp3-'</i> and <i>Casp1-'-</i> mice¹⁵⁹. ■ Reduced tumor growth in SCID mice injected with <i>Aim2</i>-silenced UT-SCC7 cells³⁹. ■ Reduced tumor growth in nude mice injected with <i>Nlrp3</i>-silenced WSU-HN6 cells⁶⁹. | ■ More colony formation in LPS +ATP-treated CAL27 cells²00. ■ Reduced viability and increased apoptosis of <i>Nlrp3</i> -silenced WSU-HN6 and CAL27 cells treated with 5-FU¹59. ■ Reduced viability and increased apoptosis of <i>Aim2</i> -silenced UT-SCC7 cells³9. ■ Increased proliferation and migration of IL-1β-treated DOK and TW2.6 cells²01. |
| Pancreatic Cancer | ■ Reduced pancreatic neoplasia and improved survival of <i>Aim2</i>-deficient KC<i>Pink1</i>^{-/-} and KC<i>Park2</i>^{-/-} mice⁵¹. ■ Delayed malignant progression and extended survival in <i>Nlrp3</i>^{-/-} KC mice⁴⁸. ■ Reduced PDA tumor growth in the pancreata of <i>Nlrp3</i>^{-/-}, <i>Asc</i>^{-/-} and <i>Casp1</i>^{-/-} mice⁴⁸. ■ Reduced Panc02 tumor growth in chimeric WT mice adoptively transferred with <i>Casp1</i>^{-/-} BMCs¹⁹⁹. | N/A |
| Hematopoietic neoplasms | ■ Delayed multiple myeloma progression and prolonged survival in <i>Nlrp1</i> ^{-/-} and <i>II18</i> ^{-/-} mice challenged with myeloma cell lines ⁵² . | ■ Enhanced proliferation of IL-18– treated Pfeiffer cells ³⁸ . |
| Malignant Mesothelioma | ■ Delayed onset and reduced tumor incidence in $Asc^{-/-}$ mice ²⁰² . | N/A |

Abbreviations: AOM, azoxymethane; BMCs, bone marrow cells; BMSCs, bone marrow stem cells; DEN, *N*,*N*-diethylnitrosamine; DMBA, dimethylbenz[a]anthracene; DSS, dextran sodium sulfate; HCC, hepatocellular carcinoma; KC, *Pdx1*^{Cre} *Kras* G12D/+; LLC, Lewis lung carcinoma; MCA, methylcholanthrene; N/A, information not available;

NSCLC, non-small cell lung cancer; PDA, pancreatic ductal adenocarcinoma; pDCs, plasmacytoid dendritic cells; SCID, severe combined immunodeficiency; TPA, 12-O-tetradecanoylphorbol-13-acetate; 4-NQO; 4-nitroquinoline 1-oxide; 5-FU, 5-Fluorouracil.

Cell lines: A375, B16F10, HMB2, VUP, SK23, MJM, WM115, 1205Lu, Hs294T: melanoma; RM-1, PC3-ML, DU145: prostate cancer; E0771, Py8119, PyT8, MDA-MB-231, MDA-MB-435, MDA-MB-453, 4T1, BT474, MCF-7: breast cancer; PC, A549, H1703, H1975: lung cancer; T241: fibrosarcoma; BGC-823, AGS, MKN1: gastric cancer; CT26, MC38, HCT116, HPCC, HT29, Caco-2, HCA7, SW620: colon cancer; Hepa1–6: liver cancer; 9L, C6, SR-B10, GL-261, U87, T98G, U251: glioma; UT-SCC7, WSU-HN6, CAL27, DOK, TW2.6: squamous cell carcinoma; Panc02: Pancreatic cancer

Table 2.

Therapeutic targets of inflammasomes in cancer

| Therapy | Inflammasome Target | Cancer type | Clinical trial Phase |
|--------------------|-----------------------------------|---|--|
| Anakinra | IL-1β | Metastatic breast cancer | Phase I/NCT01802970 203 |
| Anakinra | IL-1β | Metastatic CRC | PhaseII/NCT02090101 ¹⁷³ |
| Anakinra | IL-1β | Multiple myeloma Plasma cell neoplasm | PhaseII/NCT00635154 ^{168,169} |
| Canakinumab/Ilaris | IL-1β | CRC, breast cancer, NSCLC, adenocarcinoma | Phase I/NCT02900664 |
| Thalidomide | Caspase-1 | Multiple myeloma ^{204,205} | N/A |
| MCC950/CRID3 | NLRP3 | Head and neck SCC ²⁰⁶ | N/A |
| Glyburide | NLRP3 ²⁰⁷ | N/A | N/A |
| BOT-4-one | NLRP3 | Lymphoma ¹⁶⁷ | N/A |
| IL-18BP | IL-18 ⁹⁰ | N/A | |
| Methylene blue | NLRP3, AIM2, NLRC4 ²⁰⁸ | N/A | N/A |
| CY-09 | NLRP3 ²⁰⁹ | N/A | N/A |

Abbreviations: CRC, colorectal cancer; IL-18BP, IL-18-binding protein, N/A, information not available; NSCLC, non-small cell lung cancer; SCC, squamous cell carcinoma.