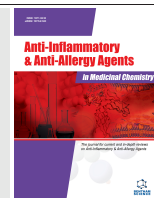


## REVIEW ARTICLE

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SCIENCE

# The Trinity of Matrix Metalloproteinases, Inflammation, and Cancer: A Literature Review of Recent Updates

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**Abstract:** The critical link between cancer and inflammation has been known for many years. This complex network was further complexed by revealing the association of the matrix metalloproteinase family members with inflammatory cytokines, which were previously known to be responsible for the development of metastasis. This article summarizes the current studies which evaluate the relationship between cancer and inflammatory microenvironment as well as the roles of MMPs on invasion and metastasis together.

**Keywords:** Cancer, cytokine, inflammation, matrix metalloproteinase, TIMP, inhibitors.

## 1. INTRODUCTION

Matrix metalloproteinases (MMPs) are a zinc-dependent endopeptidase family mainly responsible for tissue remodeling in various physiological and pathological processes [1]. They play a significant role in degrading extracellular matrix (ECM) through their proteolytic functions which is crucial in providing a convenient environment for cell growth and morphogenesis [2]. Up to date, 24 members of MMPs have been identified in humans [3]. All of them are expressed in their latent forms and require subsequent activation to perform their proteolytic activity against ECM. They are regulated mainly by tissue inhibitor of metalloproteinases (TIMP) [4, 5].

Altered regulation of MMPs can result in various diseases such as cancer, arthritis, nephritis, atherosclerosis, and ulcers [6, 7]. A large body of literature confirmed that in cancer, MMPs contribute to many tumorigenic processes such as angiogenesis, proliferation, metastasis, and invasion [8].

For instance, the MMP-2 expression level was measured in epithelial ovarian cancer cells (EOC) and a direct relation was found between MMP-2 levels and the degree of invasiveness along with metastasis of the cells [9]. Similar results were found in another study performed on the EOC where the expression level of MMP-2 and MMP-14 were investigated. The results showed that both MMPs were highly expressed in these cells compared to healthy tissues [10]. MMP-1 is also observed to be up-regulated in a wide range of advanced cancers where the majority of the cases revealed a significant negative correlation between its expression and patient survival [11]. On the other hand, MMP-12 has been observed to be overexpressed in non-small cell lung cancer exhibiting a positive correlation with metastasis [12] as well as in esophageal squamous cell carcinoma with lymph node metastasis [13]. Several studies demonstrated MMP-9 overexpression in many cancer types including breast cancer, lung cancer [14], osteosarcoma [15], colorectal cancer [16], and cervical cancer [17]. Furthermore, MMP-7 expression has been positively correlated with the aggressiveness of oral and cutaneous squamous cell carcinomas [18].

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Numerous compounds targeting MMPs, both natural and synthetic, have been tried in cancer studies in an attempt to inhibit tumour growth and metastasis. Those that were effective in suppressing the expression of MMPs also prevented cancer cells from growing and proliferating which shows the undeniable significance of these enzymes in cancer progression [19].

The aim of this review is to discuss the role of inflammation and its mediators in cancer microenvironment as well as their contribution to invasion and metastasis through MMP-related pathways.

### 1.1. The Link Between Inflammation and Cancer

For decades, researchers have put an enormous effort into understanding the mechanism of cancer growth and progression. Over the years it has become evident that cancer is not all about a pile of overly proliferated cells but rather an entire system involving blood vessels, immune cells, inflammatory mediators, and many other factors that help cells constantly grow and spread. Hence it is crucial to explore and decipher the roles of a tumour microenvironment along with its components and how they contribute to cancer progression, in order to come up with an effective approach in therapy. In this section, a number of inflammatory mediators and their functions in cancer will be discussed.

Cancer and inflammation were linked in 1863 by Rudolf Virchow for the first time, after finding immune cells in tumours. But it was not considered to be an indicator of cancer until after it became evident that inflammation causes genetic instability and downregulation of DNA repair pathways [20].

Inflammation is an immune response of organisms to cellular stress, tissue injury, and infections. It helps restore tissue functions through several repair mechanisms [21]. A large number of factors are involved in this process and it includes various crosstalks between immune and non-immune cells like endothelial cells, epithelial cells, and fibroblasts. Contrary to healthy tissues, cancerous cells develop a mechanism that constantly triggers inflammatory reactions leading to chronic inflammation [22]. Because, as tumour cells grow bigger

and proliferate rapidly, they start demanding urgent oxygen and nutrition supply for their survival. As a consequence, they release various chemical signals that draw immune cells such as macrophages and granulocytes into the tumour site. Following this infiltration, molecules called cytokines are produced by the immune cells which trigger angiogenesis to provide necessary oxygen and nutrients. On the other hand, several other chemicals are produced to create an escape route for the tumour and also reactive oxygen species are released by the inflammatory cells, causing further damage in their DNA.

In almost every cancer, inflammation can be observed [23] and the inflammatory environment of a tumour consequently leads to metastasis [24]. Several studies highlighted the anti-cancer activity of anti-inflammatory drugs which clearly shows the importance of inflammation in cancer [25].

Chronic inflammation is known to be one of the major indicators of cancer [23]. It induces neoplastic transformation of tissues and helps tumours develop further. Two pathways can be mentioned as underlying factors of inflammation in cancer: An intrinsic pathway which is related to genetic mutations that result in oncogene activation and tumor suppressor gene inactivation, an extrinsic pathway where inflammatory conditions are present, eventually causing cancer. Both of these pathways lead to the activation of various transcription factors such as NF- $\kappa$ B, STAT3, HIF1 $\alpha$  in tumor cells which result in the expression of several chemokines, cytokines (such as IL-1 $\beta$ , IL-6, IL-23, and TNF- $\alpha$ ), and prostaglandins. These factors are produced by immune system cells in the extrinsic pathway such as macrophages and by neoplastic cells in the intrinsic pathway which trigger inflammation further through the recruitment of leukocytes to the site of tumours. Following the activation of this inflammatory process, a vicious circle is created where reactive factors such as reactive oxygen species (ROS) cause tissue injury and persistent stimuli for regeneration [26].

Constant inflammatory signals trigger a developing tumour invasion with an alteration in tissue homeostasis. Additionally, cell stress molecules as well as apoptotic/necrotic compounds of both tumour and healthy cells -such as damage-associated

molecular patterns (DAMPs)- initiate the stimulation of macrophages and M2 polarization (alternatively activated macrophages) as well as fibroblast recruitment [27-29]. Other factors such as glucose concentrations, iNOS, hypoxia, TGF- $\beta$  also cooperate in fibroblast recruitment and the activation of the fibrotic process which takes part in the progression of tumour microenvironment composition [30, 31].

Damage-associated molecular patterns (DAMPs) are endogenous molecules secreted by stressed cells undergoing necrosis and by extracellular matrix upon tissue damage. These molecules act as a danger signal that promotes an inflammatory response. Elevated levels of DAMPs are found to be linked with various inflammatory diseases such as arthritis and cancer [32].

In the tumour microenvironment, not only tumour cells but also infiltrated immune cells play a significant role in the progression of the disease. The interaction between DAMPs and Toll-like-receptors (TLRs) alters the regulation of cytokines [33]. And because the core of a tumour mass lacks oxygen and nutrition, cells undergo necrosis and constantly produce DAMPs. They are also produced upon immunogenic cell death and ECM degradation. These molecules interact with TLRs as well as macrophages and endothelial cells leading to the secretion of several cytokines that participate in tumour growth and metastasis [34]. Secretion of DAMPs activates TLRs further, causing more secretion of DAMPs and cytokines including several interleukins as well as TNF- $\alpha$  and TGF- $\beta$  [35-37].

TLRs are membrane bound receptors and they recognise a wide range of DAMP molecules such as heat shock protein-60 (HSP60), MMP-2, and high mobility group box protein (HMGB1) which leads to the secretion of various pro-inflammatory mediators [33]. HMGB1 is the most abundantly produced DAMP molecule by dying tumour cells and it has a significant role in malignancies. It interacts with TLR4 in the oxidated state causing the secretion of cytokines. On the other hand, when it is in a reduced state, it binds to CXCL12 triggering chemotaxis *via* CXCR4 [38]. The significance of CXC receptors in cancer will be discussed in the next section.

It is well established that in a tumour microenvironment, many non-tumour cells are present along with cancer cells. Among these, macrophages are the major inflammatory components. When they are infiltrated into the tumour bed, they become tumour-associated macrophages or TAMs in short [29]. Researches have shown that TAMs are closely linked with tumour progression and angiogenesis. They express TLRs and are activated by DAMPs indicating their contribution to cancer cell invasion and metastasis [26, 39, 40]. It is thought that TAMs are derived from the circulating monocytes present in the blood. When a tumour develops, these monocytes relocate to its site first. Afterwards, they transform into TAMs and construct the largest immune population. In this process, T-cells with anti-tumour properties are also recalled which can destroy cancer cells. However, settled tumours manage to block their anti-tumour activities by enforcing a suppressive environment. On the other hand, macrophages encounter a similar fate. While they exhibit cytotoxic activities under normal circumstances, they become strongly possessed by cancerous cells in tumour bed leading to a complete differentiation in their functions. Consequently, they develop immuno-suppressive activity and participate in tumour progression [41]. Various studies reported a significant correlation between high levels of TAMs and aggressive tumours [39, 42, 43]. For instance, they produce growth factors like EGF, VGF, VEGF which help cancer cells proliferate directly and cytokines that activate certain pathways controlling cell apoptosis such as the STAT3 pathway by IL-6 [44, 45].

Under hypoxic conditions of cancerous tumours, macrophages produce various pro-angiogenic factors including CXCL8 (precursor of IL-8), PlGF (placental growth factor), Bv8 (prokineticin), and VEGF [46]. On the other hand, IL-10 and TGF- $\beta$  are some of the other cytokines that show immuno-suppressive activity inhibiting anti-tumour properties of T cells [47, 48] even though TGF- $\beta$  can also display migration inhibiting activity in some cancers as will be discussed in the next section.

The chaotic circumstances that a tumour microenvironment generates influence even some of the healthy cells' functions including immune system cells, endothelial cells, and fibroblasts as well as

the compounds they express. Various studies confirmed that in tumour progression and metastasis, proteolytic enzymes and the extracellular matrix (ECM) components play a major role together with immune cells through building the inflammatory environment [49, 50].

The inflammation in the tumour bed also produces mutagenic factors that help develop tumour formation [24]. It is a major source for cell survival and growth along with pro-angiogenic factors and extracellular matrix remodeling enzymes that support invasion, metastasis, and angiogenesis [26].

Macrophages play a significant role in remodeling extracellular matrix through the production of certain enzymes such as MMPs and cathepsins. Remodeling of ECM along with ECM binding cytokines triggers inflammatory cell infiltration, angiogenesis, and tumour invasion. For instance, cathepsin B and S produced by TAMs can induce cancer spread and angiogenesis [51]. Furthermore, MMP-9 produced by TAMs plays an important role in skin cancer progression [52]. Experiments have shown that MMP-2 and -9 modulate the ECM *via* releasing VEGF that induces angiogenesis in pancreatic cancer [53, 54].

Immune cells have been a major focus of inflammation-related studies. It has been reported that mesenchymal stem cells (MSCs) and fibroblasts are crucial for the regulation of inflammatory response [55, 56]. MSCs exhibit strong suppressive activities through various mechanisms. One of these mechanisms involves ECM remodeling where MSCs trigger tumour progression through MMPs. One study reported that in ovarian cancer, MMP-2 and -9 produced by MSCs promote tumour invasion [57].

There are numerous other inflammatory factors and hundreds of articles published on their relations with different cancer types. In the next section, some of the major mediators and their activity on triggering MMP overexpression in cancer will be discussed.

## 1.2. Inflammation, MMPs, and Cancer

There is sufficient evidence indicating an important link between cancer and chronic inflamma-

tion. When exposed to infectious agents, tissues are infiltrated by immune cells, chemokines, cytokines, and growth factors that contribute to the metastasis of cancer cells [58, 59]. The participation of MMPs in inflammatory processes includes regulation of physical barriers, modulation of inflammatory mediators such as chemokines and cytokines, helping chemokines form a gradient in damaged tissues that recall leukocytes to the infectious or injured area [60, 61].

Chemokine receptors belong to the G protein-coupled receptor superfamily and display several functions in cancer progression [62]. One of these receptors known as C-C motif chemokine receptor-10 (CCR10) is produced by plasma cells, melanocytes, and skin-resident T cells [63]. It can be stimulated by CCL27 and CCL28 chemokines [64]. The interaction between CCR10 and CCL27 is involved in T-cell mediated skin inflammation [65]. Several studies highlighted the contribution of CCR10 to cell growth and migration in many tumours such as melanoma [66], glioblastoma [67], and squamous cell carcinoma [68]. One recent study performed on multiple breast cancer cell lines (MCF-7, BT-474, and MDA-MB-231) investigated the influence of CCR10-CCL27 interaction on cell migration and its mechanism. Results indicated that CCR10 is highly expressed in all these cell lines and it is associated with capsular invasion as well as lymph node metastasis. Additionally, stimulation of CCL27 dose-dependently led to the activation of the ERK1/2 pathway and therefore overexpression of MMP-7 resulting in cell invasion and migration [69].

CXC chemokine receptors belong to a G-protein superfamily known as chemokine receptors. They can induce chemotaxis which contributes to the progression of various diseases. Among these receptors, CXCR3 has been found in many tumours. It can be activated by several chemokines such as CXCL9, 10, 11, and 14 [70]. Studies reported the involvement of CXCR3 in colorectal cancer [71], basal cell carcinoma [72], and breast cancer [73, 74]. Additionally, its overexpression has been found closely related to renal cell carcinoma metastasis [75] as well as lymph node metastasis of lung adenocarcinoma [76]. Furthermore, a recent study demonstrated that in gastric cancer, CXCR3 activated by CXCL10 triggers cell inva-

sion and migration *via* PI3K/Akt pathway activation and upregulation of MMP-2 and MMP-9 [77].

Supporting evidence revealed that immune responses can be modulated by neutrophils in the tumour microenvironment which can lead to tumour development [78]. Neutrophils can interact with cells, cytotoxic mediators, ECM as well as the release of MMPs. Among these, MMP-9 significantly contributes to tissue damage and inflammation through proteolytic cleavages leading to ECM degradation and cytokines/chemokines activation. Previous studies demonstrated that collagen breakdown by MMP-8 and 9 and the cleavage of a prolyl endopeptidase afterwards, generate a tripeptide known as N-acetyl-proline-glycine-prolyline (ac-PGP) [79, 80]. This tripeptide has been shown to bind CXCR2, a receptor of IL-8 and a powerful neutrophil chemotactic factor. This process triggers the chemotaxis of inflammatory cells to the site of tumour [81, 82]. One study conducted on non-small cell lung cancer tissues revealed a correlation between CXCR2 expression and tumour inflammation as well as angiogenesis [83]. Additionally, it has been reported that in breast cancer cells, CXCR2 plays a significant role in tumour invasion and metastasis to lung tissues [84]. However, CXCR2 is not only expressed by neutrophils. It is also produced by a wide range of tumours including ovarian, pancreatic, lung, melanoma tissues which indicates a potential role of ac-PGP tripeptide in tumour cell chemoattraction [83, 85].

In a recent study, the role of inflammation-generated extracellular matrix fragments (ac-PGP) on tumor cells disseminating to lung parenchyma was investigated in mice with mammary and melanoma tumours. Exposure to cigarette smoke and lipopolysaccharide led to neutrophil accumulation in the lungs causing a high level of MMP-9 expression and therefore allowing the release of ac-PGP tripeptides which attracted tumour cells to the lung parenchyma. On the other hand, MMP-9 negative mice exhibited a decreased level of ac-PGP. Additionally, silencing CXCR2 on tumour cells indicated that the chemoattractant effect of ac-PGP is dependent on the presence of CXCR2 as well. These results show a significant role of MMP-9 in cancer metastasis with the contribution of inflammatory mediators [86].

Experimental evidence revealed that CXCL12–CXCR4 interaction elevated active MMP-9 expression in several human cancer cell lines including colorectal cancer cells, head and neck squamous cell carcinoma cells as well as nasopharyngeal carcinoma cells [87-89]. Researchers also investigated the correlation between tumour progression in breast cancer and the expression of CXCR4, VEGF, and MMP-9. They discovered that the expression of CXCR4 was 61% higher than in normal tissues while VEGF expression was higher by 68% and MMP-9 by 63% and each of these markers correlates with tumour progression. Moreover, combined elevated expression of any two of these markers was observed to be highly associated with lymph node metastasis in breast cancer [90].

IL-17 is a cytokine family produced by a subgroup of T helper cells (Th17). They play significant roles in inflammatory diseases and cancers [91, 92]. There are six members in this family named IL-17A, -B, -C, -D, -E, and -F. The way in which IL-17 members exhibit their activity is through binding to their receptor family known as IL-17R [93]. Studies revealed that in various tumours, these receptors are overexpressed [94, 95]. One of these receptors, IL-17RB has been observed in several tumours. According to a study conducted on gastric cancer tissues, the expression of IL-17RB increases significantly and it is closely associated with poor prognosis in patients [96]. Additionally, it has been reported that overexpression of IL-17RB plays an important role in the metastasis of pancreatic and prostate cancers [97, 98].

Recent experiments demonstrated that IL-17B can directly stimulate the invasion, growth, and migration of thyroid cancer cells. It can also contribute to tumour invasion and metastasis of thyroid cancer by stimulating the ERK1/2 pathway time- and dose-dependently. Activation of the ERK1/2 pathway promotes the expression of MMP-9 suggesting IL-17B upregulates MMP-9 expression *via* IL-17RB/ERK1/2 pathway [99].

Similarly, IL-17A has been reported to induce overexpression of MMP-9 and therefore cell invasiveness in esophageal adenocarcinoma [100].

Interleukin-1 $\alpha$  (IL-1 $\alpha$ ) is a member of the IL-1 cytokine family that participates in the regulation

of immune and inflammatory responses. It is widely found in the tumour microenvironment with tumour-promoting effects [101, 102]. According to a recent study on pancreatic ductal adenocarcinoma (PDAC), IL-1 $\alpha$  is highly expressed and it plays an important role in cell invasion and migration [103]. Furthermore, MMPs are significantly up-regulated in PDAC by pancreatic stellate cells, a major producer and regulator of the ECM, while their inhibitor TIMP3 is downregulated [104]. As mentioned in the previous part, TGF- $\beta$  is a growth factor with both pro-tumour activity (in the early stages of some cancers) and anti-tumour functions (usually in the late stages). Results obtained revealed that in PDAC, IL-1 $\alpha$  induces a specific MMP/TIMP profile leading to overexpression of MMP-1 and MMP-3 whereas TGF- $\beta$  acts as a migration suppressor through inhibiting MMP overexpression [103].

IL-5 is a T-cell derived cytokine essential for eosinophil activation, differentiation as well as B-cell differentiation [105, 106]. It can induce B-cell proliferation through activating PI3K, Jak2, Btk tyrosine kinases, and HS1 [107]. In a recent study, the roles of IL-5 and its receptor IL-5R $\alpha$  on cell migration in muscle-invasive bladder carcinoma (MIBC) cell lines have been investigated. Results have shown that the expression levels of both IL-5 and IL-5R $\alpha$  are increased compared to healthy cells. Additionally, IL-5 has been observed to induce the expression of MMP-9 *via* activating transcription factors NF- $\kappa$ B and AP-1 causing cell motility and migration of bladder cancer cells. Experiments also revealed that IL-5 induces ERK1/2 signaling which mediates MMP-9 expression [108]. A similar study was conducted on 5637 bladder cancer cells investigating the role of IL-15 which is a key regulator of lymphocyte activation and differentiation. Results revealed that IL-15 promotes the expression of MMP-9 and activates NF- $\kappa$ B through ERK1/2 signaling leading to cell migration and invasion [109].

Arachidonic acid derivatives are known to participate in inflammation, pain, and fever and they are found to be closely linked with tumour development as well. Among those, COX-1 is present on a stable level in nearly all tissues whereas COX-2 is observed highly expressed in hyperplas-

tic tissues such as breast cancer, lung cancer, and gastric cancer [110-112]. In a study conducted on oral squamous cell carcinoma (OSCC), the expression level of COX-2 and MMP-7 were investigated. Experiments revealed that mRNA expressions of both COX-2 and MMP-7 were positively correlated in OSCC indicating a close relationship between these two genes [113].

As mentioned in the previous section, TAMs are transformed monocytes with significant roles in tumour progression. It was reported that TAMs infiltrate into tumour area abundantly which is then associated with metastasis and angiogenesis [114-116]. On the other hand, MMPs are well known to be significant in chronic inflammation, tissue remodeling, and cancer progression. In a study conducted on ovarian cancer cells, the function of TAMs on the expression of MMP-2, MMP-9, and MMP-10 was investigated. Results have shown that TAMs upregulate the production of these three MMPs through activating NF- $\kappa$ B, MAPK signaling, and TLR signaling pathways which indicates the significance of the TAM-MMP relationship in ovarian cancer progression and invasion [117].

Nuclear factor of activated T cell (NFAT) proteins is a family of transcription factors expressed in most immune system cells. They play a crucial role in the transcription of cytokine genes as well as other genes necessary for immune response. They also regulate T cell development and differentiation and bind interleukin-2 (IL-2) promoter in activated T cells [118-121]. However, NFAT genes participate in many other physiological processes as well. Various studies have shown that NFAT genes take part in cancer development and progression *via* regulating cell proliferation, migration, invasion, and angiogenesis [122-125]. The first identified member of this family, NFAT1, has been found highly expressed in several cancers such as breast cancer [126], melanoma [127, 128] and lung cancer [129]. The mechanism through which NFAT1 contributes to tumour growth and metastasis has been reported to be associated with the expression of its target genes including COX-2, MDM-2, IL-8, and MMP-3 [126, 128, 130]. A recent study performed on esophageal squamous cell carcinoma (ESCC) demonstrated that NFAT1

supports metastasis of ESCC cells through regulation of MMP-3 and silencing this gene could prevent cells from migrating [131].

Tumour necrosis factor- $\alpha$  (TNF- $\alpha$ ) is an important pro-inflammatory cytokine. Elevated expression of TNF- $\alpha$  is observed in several autoimmune diseases such as rheumatoid arthritis and multiple sclerosis [132]. It is produced by T-cells and macrophages as a membrane bound protein and is activated by TNF-converting enzymes [133, 134]. Several studies mentioned the significance of TNF- $\alpha$  induced MMPs and their expression in cancer [135, 136]. Multiple pathways can be involved in this process. For instance, in 5637 bladder cancer tissues, experiments showed that TNF- $\alpha$  induces MMP-9 expression through the p38 MAPK pathway [137].

The double-stranded RNA-dependent protein kinase (PKR) is a serine/threonine kinase. It is activated by homodimerization and autophosphorylation and participates in inflammatory responses against infectious factors through inducing NF- $\kappa$ B activation [138]. Furthermore, it has been revealed that PKR mediates the activation of MMP-2 and MMP-9 induced by TNF- $\alpha$  [139] as well as MMP-13 [140]. On the other hand, MMP-13 has been found overly expressed in gastric cancer [141], giant cell tumor (GCT) [142], osteosarcoma [143], and head and neck squamous cell carcinoma [144]. Available data indicate that elevated expression of MMPs mediated by PKR contributes to cancer progression suggesting that PKR could be considered a target in cancer studies.

Even though most MMPs are found overexpressed where inflammation is present, some of them can display anti-inflammatory effects as well. In a study conducted on irreversible pulpitis of mature erupted teeth, treatment with MMP-3 resulted in a decrease in the number of inflammatory cells such as macrophages while it also inhibited IL-6 expression significantly. On the other hand, the inhibition of MMP-3 activity terminated these effects [145]. Furthermore, McMillan *et al.* investigated the role of MMP-9 in allergen-induced airway inflammation *in vivo*. They observed that in the absence of MMP-9, inflammatory cell recruitment significantly increases as well

as the levels of cytokines such as IL-4, IL-13, and macrophage-derived chemokine CCL-22, leading to enhanced pulmonary inflammation [146]. Additionally, MMP-19 deficiency in inflammatory bowel disease caused persistent inflammation and poor recovery in a study conducted by Brauer *et al.* [147]. Similarly, MMP-10 has been observed to restrict the pro-inflammatory activity of macrophages in mice with lung infection [148]. However, there is not enough literature on the anti-inflammatory roles of MMPs in cancer.

## CONCLUSION

Understanding the mechanism of cancer formation and how it develops is the key to finding revolutionary approaches in therapy. The purpose of this review is to enlighten some aspects of the ways through which cancer cells find an escape route using their inflammatory microenvironment with the contribution of MMPs. Overall data have shown a strong relationship between MMP overexpression by inflammatory mediators and cancer progression. Hence, targeting specific molecules involved in this process could be considered as a potential treatment strategy.

## CONSENT FOR PUBLICATION

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## CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

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