

# Chapter 13

## Arginine Metabolism, a Major Pathway for the Suppressive Function of Myeloid-Derived Suppressor Cells

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**Abstract** Various mutations in cancer create a microenvironment surrounding the tumor, characterized by the presence of a chronic inflammatory infiltrate which facilitates the growth of the tumor cells, enhances angiogenesis and more importantly, inhibits any protective immune response. One of the most prominent inflammatory cells are the so-called myeloid-derived suppressor cells (MDSCs), a heterogeneous population of immature myeloid cells that are potent inhibitors of T cell, NK cell, and dendritic cell functions. Recent findings in tumor-bearing mice and patients with cancer indicated that the increased metabolism of the nonessential amino acid L-Arginine by MDSC-producing Arginase I inhibits T-cell-lymphocyte responses. Here, we discuss some of the most recent concepts of how MDSC expressing Arginase I may regulate T-cell function in cancer and suggest possible therapeutic interventions to overcome this inhibitory effect. In addition, we discuss how metabolic limitation of L-Arginine can be used as a novel therapy to downmodulate T-cell responses in several diseases. Altogether, this chapter emphasizes the importance of the metabolism of the amino acid L-Arginine as a regulator of inflammation-linked diseases and also suggests the potential use of this pathway as a therapy to control unbalanced T-cell responses in autoimmunity and transplantations.

**Keywords** Arginine · Myeloid-derived suppressor cells · Immune response · L-Arg starvation · Arginase I expression · tumors-infiltrating MDSCs · Hematopoietic progenitors · Molecular mechanisms · MDSCs in vivo

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## 1 Introduction

Current concepts in cancer development and progression have convincingly demonstrated that malignant tumors create a chronic inflammatory microenvironment that promotes their growth and invasive properties. Until recently, the presence of this inflammatory response was poorly understood. The bands of inflammatory cells and fibrotic tissues seen surrounding many solid tumors were thought to be the remains of a failed attempt by the immune system to control the growth of the malignant cells. Similarly, the high numbers of granulocytes found in the peripheral blood of some cancer patients without an active infection were classified as leukemoid reactions and were primarily considered to be a nonspecific effect of the continued tumor growth. Research during the past two decades has instead shown that these inflammatory cells are induced by tumors and play an important role in supporting carcinogenesis and their growth, invasion, and metastatic spread. The heterogeneous population of cells that make up this chronic inflammatory microenvironment is composed primarily of CD11b<sup>+</sup> myeloid cells that are highly suppressive of antitumor T-cell responses. However, they also promote angiogenesis, induce regulatory T cells, and even protect tumor cells from the effects of chemotherapy and radiation therapy. The molecular mechanisms used by these cells to suppress T-cell function include depletion of amino acids arginine, tryptophan, and cysteine, the production of reactive nitrogen species such as nitric oxide (NO) and peroxynitrites (NOO<sup>-</sup>), and the production of reactive oxygen species (ROS). Here, we discuss the most recent data on how myeloid-derived suppressor cells (MDSCs) metabolizing L-arginine (L-Arg) may regulate the production of reactive nitrogen species and ROS and suppress T-cell function in cancer and other diseases.

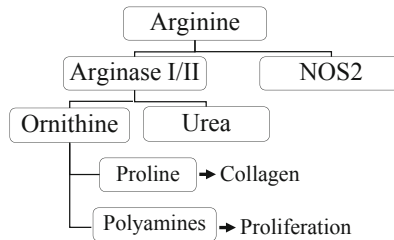
## 2 Alterations of the Immune Response in Cancer

A dysfunctional immune response in cancer patients manifested by the loss of delayed-type hypersensitivity was demonstrated several decades ago, but the underlying mechanisms were unknown [62], [63], [110], [109]. Initial hypotheses included the presence of “blocking antibodies,” the production of suppressor factors by tumor cells, and the generation of suppressor macrophages [31], [32], [107]. Murine models also showed that tumor growth was associated with a progressive decrease in T-cell function that could be reestablished through the use of prostaglandin inhibitors or low-dose chemotherapy [28], [29], [56]. These concepts were incorporated early into the immunotherapy trials where low-dose cyclophosphamide or local radiation was used as a preconditioning regimen preceding adoptive cellular therapy. However, early immunotherapy trials in human patients failed to reproduce the therapeutic successes seen in murine models (with 3–5-day-old tumors) (reviewed in [26]). In fact, several vaccine trials demonstrated that tumors were able to progress even in the presence of a strong T-cell response [102].

In the early 1990s, the identification of several discrete but specific alterations in T cells from mice or patients with cancer, such as a decreased expression of the T-cell receptor  $\zeta$  chain (CD3 $\zeta$ ), a diminished level of the tyrosine kinases p56<sup>lck</sup> and p59<sup>lyn</sup>, and the inability to upregulate Jak-3 and to translocate nuclear factor kappa B (NF- $\kappa$ B)-p65 [19], [45], [55], [62], [64], [114], [115], provided the first molecular mechanisms to explain the decreased T-cell response in cancer. Almost simultaneously, investigators developed cellular and molecular models that provided important insights into the multiple mechanisms by which cancer and chronic inflammatory diseases could selectively inhibit T-cell responses [41], [81], [101]. These models facilitated the discovery of immunoregulatory mechanisms such as the expression of checkpoint molecules on T cells and antigen-presenting cells (APCs) [18], [43], [48–50], the development of regulatory T cells [60], [61], and the accumulation of tumor-induced MDSCs [7], [20], [80], [93].

Using cocultures of activated murine peritoneal macrophages and T cells, Otsuji et al. [77] and Kono et al. [45], [46] first demonstrated that activated peritoneal macrophages cocultured with T cells induced the loss of the CD3 $\zeta$  chain of the T-cell receptor and suppressed T-cell responses *in vitro*. This effect was blocked by the use of oxygen radical scavengers, suggesting that it was, in part, mediated by ROS [14]. Soon after, Schmielau et al. described the presence of an increased number of activated neutrophils in the peripheral blood of patients with advanced pancreatic and breast cancer who also showed a diminished expression of the CD3 $\zeta$  chain [91]. Changes in the expression of the CD3 $\zeta$  chain were also found in patients with metastatic renal cell carcinoma [117] where increased granulocyte counts were found to be associated with a poor outcome [82]. In addition, Zea et al. and Baniyash et al. [6], [115], [118] demonstrated that the changes in T cells were also found in infectious diseases such as tuberculosis and leprosy, suggesting that the chronic inflammatory microenvironment rather than the tumor cells were responsible for the induction of T-cell dysfunction.

Which tumor factors lead to the activation and/or accumulation of MDSCs? Gabrilovich et al. [113] and Bronte et al. [17] demonstrated that the vascular endothelial growth factor (VEGF), granulocytic colony-stimulating factor (G-CSF), and granulocytic–monocytic colony-stimulating factor (GM-CSF) produced by tumor cells arrested the differentiation of myeloid cells, resulting in the accumulation of immature myeloid cells (iMCs) that, in turn, suppressed T-cell function. These suppressive myeloid cells were found to be increased in patients with head and neck, breast, and lung cancer [2], [3] and were initially thought to block T-cell responses by producing interleukin-10 (IL-10), transforming growth factor beta (TGF- $\beta$ ), and prostaglandin E<sub>2</sub> (PGE<sub>2</sub>). However, it soon became apparent that MDSCs had additional and more potent inhibitory mechanisms that had not previously been described.

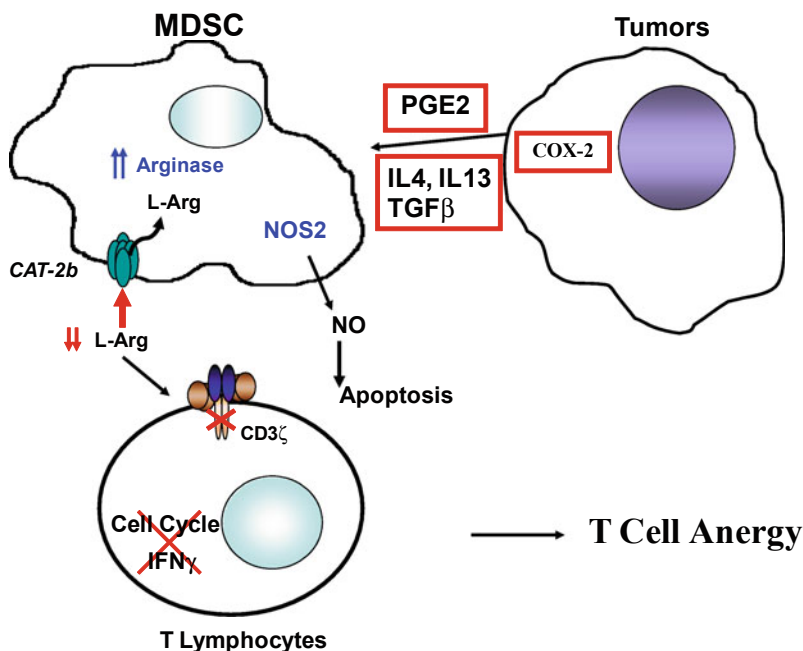


**Fig. 13.1 L-Arginine metabolism in myeloid cells.** L-Arginine is metabolized in myeloid cells through arginase I and II and nitric oxide synthase 2 (NOS2). L-Arginine hydrolysis through arginase I and II results in the production of urea and ornithine, the later being a major precursor for the synthesis of polyamines and collagen.

### 3 Metabolism of L-Arg by Myeloid Cells

In addition to the production of immunosuppressive cytokines, MDSCs were found to rapidly deplete the amino acid L-Arg from the microenvironment. L-Arg is the substrate for at least four enzymes that exist as multiple isoforms in MDSCs: nitric oxide synthases (NOS1, NOS2, and NOS3), arginases (arginase I and II), arginine glycine amidinotransferase (AGAT), and L-Arg decarboxylase (ADC) [66]. The normal serum concentration of L-Arg is maintained through a combination of dietary intake and de novo synthesis. Dietary L-Arg is taken up by intestinal epithelial cells and traverses the plasma membrane via the  $\gamma^+$  system of cationic amino acid transporters (CATs) [13]. De novo synthesis of L-Arg occurs primarily in the kidney as a result of recycling of citrulline produced in the intestine [65]. Once L-Arg is transported into the cytoplasm, its metabolism depends on the type of cell. In myeloid cells, L-Arg is primarily metabolized by the inducible NOS (iNOS) or by arginase I or II (Figs. 13.1 and 13.2). iNOS metabolizes L-Arg to produce citrulline and nitric oxide, the latter of which plays an important role in cytotoxic mechanisms in myeloid cells and vasodilatation in endothelial cells [4], [34]. Alternatively, arginase I and arginase II metabolize L-Arg to L-ornithine and urea, the first being the precursor for the production of polyamines essential for cell proliferation and an important mechanism for detoxification of protein degradation in hepatocytes [65]. Two other enzymes, ADC and AGAT, convert L-Arg to agmatine, which, in turn, is converted to putrescine and urea by agmatinase [66]. Mammalian ADC is highly expressed in the brain [39], [120], while AGAT is expressed in the brain and heart [15], [37]. ADC and AGAT appear to be less important in the immune response.

The expression of arginase I and NOS2 in murine macrophages is differentially regulated by Th1 and Th2 cytokines [33], [68] with interferon gamma (IFN- $\gamma$ ) up-regulating NOS2 exclusively and IL-4, IL-10, and IL-13 inducing arginase I [67], [89]. The mitochondrial isoform arginase II is not significantly modulated by Th1 or Th2 cytokines [83]. In turn, arginase I and NOS2 appear to modulate each other's expression. The inhibition of arginase I leads to an increased NOS2 expression and, consequently, increases the production of NO [12]. Moreover, the upregulation of



**Fig. 13.2 T cell dysfunction induced by arginase I.** Tumor cells expressing COX-2 and releasing PGE<sub>2</sub>, and high levels of different mediators present in the tumor microenvironment including TGF- $\beta$ , IL-4, and IL-13 induces the expression of arginase I and CAT-2B in MDSC. This leads to a reduction of extra cellular levels of L-Arginine, which finally activates GCN2 and blocks the expression of multiple genes including CD3 z, IFN $\gamma$ , cyclin D3 and cdk4. A similar reduction occurs in patients with cancer, but through the release of arginase into the extracellular environment. Furthermore, MDSC release NO, which is implicated in low recognition of antigens and direct induction of apoptosis in T cells.

arginase I inhibits NOS activity and contributes to the pathophysiology of several diseases including vascular dysfunction and asthma [119]. The mechanism of inhibition of NOS2 expression by arginase I appears to be mediated by L-Arg depletion, which blocks the translation of NOS2 [57]. In addition, low levels of nitric oxide induce nitrosylation of cysteine residues of arginase I which increases its biological activity, further reducing L-Arg [90].

The expression of arginase I or NOS2 also has effects on the extracellular levels of L-Arg. Peritoneal macrophages stimulated with IL-4 plus IL-13 increase the expression of arginase I and CAT-2B, which results in a rapid increase in the uptake of extracellular L-Arg with the consequent reduction of L-Arg in the microenvironment. In contrast, macrophages stimulated with IFN- $\gamma$  that preferentially increase the expression of NOS2 do not increase CAT-2B expression and do not deplete L-Arg from the microenvironment [83]. Results from the arginase I and arginase II knockout mice confirm that only arginase I is able to deplete serum levels of L-Arg [16], [38]. Coculture experiments of macrophages producing arginase I and activated T cells

resulted in the loss of CD3 $\zeta$ , an arrest in T-cell proliferation, and the inability of T cells to produce IFN- $\gamma$  (but not IL-2). The addition of arginase inhibitors or exogenous L-Arg reversed the CD3 $\zeta$  loss and reestablished T-cell proliferation [83]. These results were confirmed with macrophages from arginase I-conditional knockout mice (unpublished findings). In contrast, T cells cocultured with macrophages expressing NOS2 did not develop these alterations.

## 4 Effects of L-Arg Starvation on T Cells

The association between an increased expression of arginase I, a decrease in L-Arg levels, and changes in T-cell responses was first suggested by experiments showing that mice undergoing extensive surgery developed thymic involution and a decrease in splenic T cells. This effect was prevented by the injection of L-Arg [5]. Our initial experiments demonstrated that culturing T cells in a tissue culture medium with L-Arg levels < 50  $\mu$ M resulted in a significant decrease in cell proliferation [104]. In addition, T cells activated in an L-Arg-free environment developed all the alterations previously described in tumor-bearing mice and cancer patients, i.e., the decreased expression of CD3 $\zeta$ , an inability to upregulate Jak-3, a decreased translocation of NF- $\kappa$ B-p65, and the inability to produce IFN- $\gamma$  [116]. More importantly, Rodríguez et al. also showed that the absence of L-Arg arrested T cells in the G<sub>0</sub>-G<sub>1</sub> phase of the cell cycle, while T cells cultured with L-Arg progressed easily through the S and G<sub>2</sub>-M phases [86]. This arrest in cell cycle progression was caused by a selective inability to upregulate cyclin D3 and cdk4, which did not affect other cyclin proteins [86]. In fact, silencing cyclin D3 in T cells resulted in a similar inhibition of proliferation as that caused by the absence of L-Arg. Additional research showed that L-Arg starvation impaired the expression of cyclin D3 and cdk4 in T cells through a decreased mRNA stability and diminished rate of translation [86], [88].

How does the depletion of one amino acid, L-Arg, leads to the specific molecular changes that result in T-cell anergy? Previous work had shown that amino acid starvation leads to the accumulation of empty aminoacyl-transfer RNAs (aminoacyl-tRNAs), which leads to the activation of general control nonrepressed 2 (GCN2) kinase that, in turn, phosphorylates the translation initiation factor eukaryotic initiation factor 2 alpha (eIF2 $\alpha$ ). The phosphorylated form of eIF2 $\alpha$  binds with high affinity to eIF2 $\beta$ , blocking its ability to exchange guanosine diphosphate (GDP) with guanosine triphosphate (GTP), which inhibits the binding of the eIF2 complex to methionine-aminoacyl-tRNA. This results in a decreased initiation of global protein synthesis. Our results show that T cells cultured in a medium without L-Arg have high levels of phospho-eIF2 $\alpha$  and a decreased global protein translation that preferentially impairs the synthesis and expression of the RNA-binding protein HuR, which confers stability to messenger RNA (mRNA) containing AUUA-rich elements such as cyclin D3 [86], [88]).

## 5 Arginase I Expression in Tumors-Infiltrating MDSCs

Some tumor cell lines including non-small lung carcinoma and breast carcinoma have been shown to express arginase [10], [95], [103]. This was thought to be a mechanism for the production of polyamines needed to sustain the rapid proliferation of tumor cells. Our results suggest instead that arginase I is primarily expressed in MDSCs infiltrating tumors, which inhibits T-cell function and represents a potent mechanism for stromal remodeling and for tumor evasion [84].

Two major subsets of MDSCs have been reported: granulocytic MDSCs (G-MDSCs) that are CD11b<sup>+</sup> LY6G<sup>+</sup> LY6C<sup>low</sup> and monocytic MDSCs (M-MDSCs) that are CD11b<sup>+</sup> LY6G<sup>-</sup> LY6C<sup>high</sup> [111]. However, several reports have also shown the presence of tumor-infiltrating MDSCs that express CD11b<sup>+</sup> LY6G<sup>-</sup> LY6C<sup>-</sup>, a phenotype reminiscent of alternatively activated macrophages [17], [84]. In addition, granulocytic and monocytic subpopulations of iMCs can be found in the bone marrow of healthy mice, but these do not appear to suppress T-cell function [8], [53], [97]. These variations in MDSC phenotype appear to be the result of the different combinations of soluble factors produced by different tumor types. The balance between G-MDSCs and M-MDSCs, their biology, and the mechanisms that lead to their accumulation is still a matter of significant research. Recent data suggest that M-MDSCs may be precursors of G-MDSCs [112]. G-MDSCs are the major source of arginase I in tumor-bearing hosts and are significantly more potent inhibitors of T-cell function *in vitro* [84], whereas tumor-associated M-MDSCs primarily metabolize L-Arg through NOS2 [111]. In addition, recent publications demonstrate that MDSCs promote angiogenesis and create a “pre-metastatic niche” for circulating tumor cells [27].

In spite of the phenotypic differences, researchers have shown that the depletion of both G- and M-MDSCs using antibodies against the myeloid differentiation antigen GR-1 (anti-GR-1) antibodies induces an antitumor effect mediated by CD8<sup>+</sup> T cells [35], [80], [93].

## 6 Molecular Mechanisms of Tolerance Induced by MDSCs

The mechanisms by which MDSCs induce T-cell tolerance include the production of arginase I, peroxynitrites, or ROS (H<sub>2</sub>O<sub>2</sub>). The effect of arginase I does not require cell-to-cell contact, while peroxynitrites and H<sub>2</sub>O<sub>2</sub> require close proximity of MDSCs and T cells. Our data suggest that the depletion of extracellular L-Arg by arginase I represents one of the primary mechanisms for the induction of T-cell tolerance [83]–[85]. In fact, the depletion of L-Arg through these mechanisms is not limited to the tumor microenvironment but can also be measured in the depletion of L-Arg levels in the plasma of patients with renal cell carcinoma [87], [117]. Furthermore, the addition of arginase I inhibitors nor-N(omega)-hydroxy-L-arginine (nor-NOHA) or NOHA *in vitro*, or its injection in tumor-bearing mice, prevents the loss of T-cell function and results in an immune-mediated antitumor response which inhibits tumor growth in a dose-dependent manner [84].

Peroxynitrites and  $H_2O_2$  also produced by MDSCs cause T-cell tolerance through cell-to-cell contact. This mechanism appears to require the coexpression of arginase I and NOS2 [7], as shown by the fact that the addition of NOS2 and arginase inhibitors to cocultures of MDSCs and activated T cells completely reestablishes T-cell function [9]. It is possible that this cell–cell suppression of T-cell function is primarily mediated by the production of peroxynitrites. Under limiting amounts of L-Arg, NOS2 preferentially produces peroxynitrites ( $ONOO^-$ ) instead of nitric oxide (NO).  $ONOO^-$  are highly reactive oxidizing agents that nitrate proteins and induce T-cell apoptosis [42]. Ntyosylation also appears to affect the conformational flexibility of the T-cell antigen receptor and its interaction with the major histocompatibility complex (MHC) in  $CD8^+$  cells. Therefore, MDSCs can directly disrupt the binding of specific peptides on MHC to  $CD8^+$  T cells [58], [73]. MDSCs coexpressing arginase I and NOS2 can also impair  $CD8^+$  T-cell function by blocking their ability to secrete  $IFN-\gamma$  when stimulated with specific antigens [23], [51], [53], [84], [97], [106]. This suppression requires the production of IL-13 and  $IFN-\gamma$  [25], [96], [97] and signaling through the STAT1 transcription factor [51]. In addition, MDSCs have been shown to induce regulatory T cells by producing high levels of stem cell factor (SCF) [36], [79].

## 7 MDSCs in Human Tumors

Human MDSC phenotypes vary significantly ranging from iMCs [94], [100] to activated granulocytes [87]. In cancer patients, M-MDSCs have been characterized as expressing either  $CD14^+HLA-DR^{lo}$  or  $CD11b^+CD14^-CD33^+CD15^-$ , while G-MDSCs express  $CD11b^+CD14^-CD33^+CD15^+CD66b^+$  [24], [30]. A study of 117 patients with metastatic renal cell carcinoma (RCC) demonstrated a six- to ten-fold increase in arginase activity in the peripheral blood mononuclear cells (PBMCs), as compared to normal controls [117]. Separation of the different subpopulations of MDSCs demonstrated that the major source of arginase were G-MDSC which separated with the PBMCs when centrifuged over Ficoll–Hypaque [87]. These cells suppressed the ability of T cells to proliferate and produce  $IFN-\gamma$  *in vitro*.

Human MDSCs differ in several ways from murine MDSCs. Normal human granulocytes constitutively express arginase I as a potent antibacterial and antiviral mechanism. Arginase I expression in mature human granulocytes does not appear to be up-regulated by cytokines such as IL-4, IL-13, or TGF- $\beta$ . However, hematopoietic stem cells can be induced to express high levels of arginase I when cultured in a medium with GM-CSF, G-CSF, and IL-6 [59]. Human MDSCs also differ from murine MDSCs in their mechanism of arginine depletion. Human MDSCs do not uptake L-Arg (as murine MDSCs do). Instead, arginase I is stored in primary [69] or gelatinase granules [40] and is released into the microenvironment at the time of degranulation, depleting the local levels of L-Arg. T cells stimulated in this L-Arg-depleted microenvironment develop a loss of the CD3 $\zeta$  chain expression and are unable to produce  $IFN-\gamma$  and to proliferate [47], [70], [117]. In fact, the high levels



of arginase I released in the sera of renal cell carcinoma patients result in a decrease of L-Arg to  $< 50 \mu\text{M}$  (normal control levels are  $50\text{--}150 \mu\text{M}$ ) and a significant increase in ornithine levels, a result of arginine metabolism by arginase I. Therefore, high arginase I levels have a systemic metabolic effect (L-Arg depletion) and block the protective T-cell responses [117].

## 8 Generation of MDSCs from Hematopoietic Progenitors

The process of myelopoiesis and commitment to a myeloid-cell lineage is tightly regulated. Accumulating evidence however indicates that tumor-derived factors alter this process and result in an increased number of iMCs, the majority of which are MDSCs [24]. Different cytokines including VEGF and GM-CSF participate in the recruitment of MDSCs from the bone marrow, [17]. In fact, reports by Ohm and Carbone show that serum levels of VEGF directly correlated with numbers of MDSCs in the blood and spleen and are associated with poor prognosis in cancer patients [74]–[76]. Tumor-derived VEGF has been previously associated with an arrest in dendritic cell maturation through the inhibition of NF- $\kappa$ B signaling [22], [78]. Treatment of MDSCs with all-*trans* retinoic acid appears to counter the inhibition of NF- $\kappa$ B signaling and promote MDSC differentiation into mature APCs [52]. Interestingly, however, treatment of patients with IL-2 and the VEGF-R inhibitor, bevacizumab, resulted in an increase in MDSCs [87].

Increased levels of GM-CSF have also been associated with MDSC-dependent suppression which was reversed by the use of neutralizing antibodies to GM-CSF [8]. Similar effects on MDSCs have been suggested with other growth factors including Fms-like tyrosine kinase 3 (Flt3) ligand [99], stem cell factor (SCF) [79], and S100 calcium-binding protein A9 (S100A9) [11]. In a recent study, Youn et al. demonstrated in a series of elegant experiments that M-MDSCs from tumor-bearing mice were able to acquire a granulocytic morphology in the presence of tumor cell-conditioned medium in vitro or after the adoptive transfer to tumor-bearing recipients, effectively converting into G-MDSCs. This process appeared to be controlled by epigenetic silencing of the retinoblastoma gene through modifications mediated by histone deacetylase 2 (HDAC-2) [112]. Another study suggested instead that G-CSF, GM-CSF, and IL-6 are the central mediators of the maturation of hematopoietic progenitors into MDSCs [59]. A complete understanding of these pathways could identify new molecular targets aimed at blocking MDSC maturation.

## 9 Induction of Arginase and Other Suppressive Mechanisms in MDSCs

In vitro studies had shown that murine macrophages cultured with IL-4 + IL-13 (and TGF- $\beta$ ) increased the expression of arginase I and their ability to suppress T cells. We explored whether these factors were being produced by tumors and

whether they induced arginase I in MDSCs *in vivo*. Experiments using 3LL Lewis lung carcinoma and Colon carcinoma cell line MCA-38 however failed to show the production of these cytokines by these cell lines. Instead, what we found was the expression of high levels of cyclooxygenase-2 (COX-2) and the production of high quantities of prostanoids including PGE<sub>2</sub>. COX-2 inhibitors or silencing of COX-2 in tumor cells completely blocked their ability to induce arginase I in MDSCs [85]. Consequently, treatment of tumor-bearing mice with COX-2 inhibitor sc-58125 decreased the expression of arginase I in MDSCs infiltrating the tumor and induced an immune-mediated antitumor effect [85]. Similar results have been reported in mice bearing the 4T1 breast carcinoma [98] and in mice with 1,2-dimethylhydrazine diHCl (1,2-DMH)-induced colon carcinoma [105]. Other factors may also play a role in the induction of arginase in MDSCs including hypoxia-inducible factor 1 (HIF-1) and HIF-2 (reviewed in [92]), IL-4, IL-13, and IFN- $\gamma$  [25] in mice and IL-8 in human MDSCs (Rotondo et al). In addition, CCAAT enhancer-binding protein beta (C/EBP $\beta$ ) [59] and STAT3 [108] have been proposed as molecular regulators of arginase in tumors.

## 10 Inhibition of MDSCs *in vivo*

Blocking the accumulation of MDSCs in tumor-bearing hosts has been achieved in animal models or patients with antibodies against Gr-1, CD11b, and CSF1, inhibitors of CSF1 receptor (CSFR1/c-fms), and the multi-targeted receptor tyrosine kinase inhibitor sunitinib. In addition, the use of the antimetabolites gemcitabine (GEM) and 5-fluorouracil (5-FU) has also shown the ability to deplete MDSCs and partially restore T-cell function in tumor-bearing hosts [21], [44], [54], [71], [72], [79]. However, the effects of these anti-MDSC approaches on specific MDSC subpopulations remain unclear. Preliminary data suggest that sunitinib may block the proliferation of M-MDSCs and impair the survival of G-MDSCs [44]. A goal of targeted depletion of selective MDSC subpopulations, or the silencing of specific suppressive mechanisms from MDSCs, may allow us to enhance the efficacy of immunotherapy and other forms of cancer treatment.

## 11 MDSCs: Lessons from Other Diseases and Future Applications

MDSCs are not unique to cancer. Trauma patients and patients with chronic infections including active pulmonary tuberculosis also have increased numbers of MDSCs expressing arginase I that inhibit T-cell function. These data suggest that MDSCs may represent a normal process triggered by tissue damage (danger signal) with the aim of protecting the integrity of the tissues and “healing” the initial injury. This mechanism was described in the late 1980s by Albina et al. studying the healing

of surgical wounds [1]. They described that the tissue surrounding a surgical wound was initially infiltrated by cells expressing iNOS which would most likely eliminate microbial agents contaminating the wound. This surge was followed by cells expressing arginase I which metabolize L-Arg to ornithine, which, in turn, would trigger the synthesis of collagen by fibroblasts, ultimately leading to the healing of the surgical wound. The local depletion of L-Arg would also prevent T cells from infiltrating a healing tissue and cause chronic inflammation at the site. In cancer or chronic infections, tissue damage would also trigger a similar response with the proliferation of fibroblasts producing collagen, aimed at isolating and healing the damaged tissue (i.e., malignant growth). As a matter of fact, many tumors are surrounded by dense fibrous tissue that makes its surgical excision difficult. The major difference between both disease processes (surgical wound vs malignant tumor) is that the surgical wounds heal, thus ending the role for arginase-producing MDSCs. In contrast, malignant tumors do not stop growing and destroying tissue (would not “heal”) promoting instead a chronic inflammatory process mediated by MDSCs. The continuous production of arginase I would ultimately lead to the depletion of L-Arg from the microenvironment and the development of T-cell anergy. Therefore, our working hypothesis has been that tumors “hijack” a normal healing process by promoting the differentiation and activation of MDSCs expressing arginase I, which not only creates a nurturing stroma for the tumor cells but also inhibits any protective antitumor T-cell response. Although this is likely to be an oversimplified version of the complex mechanisms triggered in vivo, it provides a model to understand a complex event in the development of cancer, which could enable the design of new therapeutic approaches to interrupt this dysfunctional response.

In summary, the role of MDSCs in the development of malignant tumors has clearly been demonstrated over the past two decades. The mechanisms that induce these immunosuppressive cells are primarily produced in the tumor microenvironment and include cytokines such as IL-4, IL-13, or TGF- $\beta$ , or prostaglandins (Fig. 13.2). The combination of factors is likely to vary between the different types of tumors. However, understanding how these factors stimulate the maturation of MDSCs and the molecular mechanisms that regulate their function should help develop new targeted therapies to inhibit MDSCs and enhance the efficacy of cancer therapies.

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