FOCUSSED RESEARCH REVIEW



CCR5 in recruitment and activation of myeloid-derived suppressor cells in melanoma

Viktor Umansky^{1,2} \cdot Carolin Blattner^{1,2} \cdot Christoffer Gebhardt^{1,2} \cdot Jochen Utikal^{1,2}

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Abstract Malignant melanoma is characterized by the development of chronic inflammation in the tumor microenvironment, leading to the accumulation of myeloidderived suppressor cells (MDSCs). Using ret transgenic mouse melanoma model, we found a significant migration of MDSCs expressing C-C chemokine receptor (CCR)5 into primary tumors and metastatic lymph nodes, which was correlated with tumor progression. An increased CCR5 expression on MDSCs was associated with elevated concentrations of CCR5 ligands in melanoma microenvironment. In vitro experiments showed that the upregulation of CCR5 expression on CD11b⁺Gr1⁺ immature myeloid cells was induced by CCR5 ligands, IL-6, GM-CSF, and other inflammatory factors. Furthermore, CCR5⁺ MDSCs infiltrating melanoma lesions displayed a stronger immunosuppressive pattern than their CCR5⁻ counterparts. Targeting CCR5/CCR5 ligand signaling via a fusion protein mCCR5-Ig, which selectively binds and neutralizes all three CCR5 ligands, increased the survival of tumor-bearing mice. This

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Viktor Umansky V.Umansky@dkfz-heidelberg.de

- ¹ Skin Cancer Unit (G300), German Cancer Research Center (DKFZ), Im Neuenheimer Feld 280, 69120 Heidelberg, Germany
- ² Department of Dermatology, Venereology and Allergology, University Medical Center Mannheim, Ruprecht Karl University of Heidelberg, Mannheim, Germany

was associated with a reduced migration and immunosuppressive potential of tumor MDSCs. In melanoma patients, circulating CCR5⁺ MDSCs were increased as compared to healthy donors. Like in melanoma-bearing mice, we observed an enrichment of these cells and CCR5 ligands in tumors as compared to the peripheral blood. Our findings define a critical role for CCR5 not only in the recruitment but also in the activation of MDSCs in tumor lesions, suggesting that novel strategies of melanoma treatment could be based on blocking CCR5/CCR5 ligand interactions.

Keywords Myeloid-derived suppressor cells ·

Chemokine receptors · Chemokines · Immunosuppression · Melanoma · Regulatory myeloid suppressor cells

Abbreviations

ARG	Arginase
BM	Bone marrow
CCL	C-C motif ligand
CCR	C-C motif receptor
CXCL	C-X-C motif ligand
CXCR	C-X-C motif receptor
DCs	Dendritic cells
GM-CSF	Granulocyte-macrophage colony-stimulating
	factor
HIF	Hypoxia-inducible factor
IFN	Interferon
IL	Interleukin
М	Monocytic
MDSCs	Myeloid-derived suppressor cells
NF-ĸB	Nuclear factor-ĸB
NO	Nitric oxide
PD-1	Programmed death receptor
PD-L1	Programmed death-ligand 1
PMN	Polymorphonuclear

ROS	Reactive oxygen species
TGF	Transforming growth factor
TNF	Tumor necrosis factor
Tregs	Regulatory T cells
VEGF	Vascular endothelial growth factor

Introduction

Metastasizing malignant melanoma remains a disease with a rapid progression and dismal prognosis despite recent therapeutic improvements [1, 2]. Well-documented melanoma immunogenicity makes this tumor a preferred target for the application of different immunotherapeutic strategies in the last years, dealing with tumor antigen-specific and -nonspecific immunostimulation or adoptive transfer of melanoma-specific activated T cells [3, 4]. Moreover, recently approved novel treatments involving the blockade of molecules inducing T cell anergy (so called negative check points) has brought optimism into the field of melanoma immunotherapy. Antibodies against CTLA-4 (ipilimumab) or programmed death (PD)-1 receptor (pembrolizumab and nivolumab) have been demonstrated to induce durable responses with long-term survival in patients with metastatic malignant melanoma [5, 6]. However, such beneficial outcome could be achieved only in a subset of patients due to the ability of the tumor to "strike back" and induce the immunosuppression in non-responding cancer patients [7, 8].

The immune escape of melanomas is mediated by different mechanisms dealing with structural and functional changes both in tumor and stroma cells, leading finally to the inability of even activated effector immune cells to reject the tumor. One of these mechanisms has been recently shown to involve a rapid recruitment, expansion, and activation of MDSCs, representing a heterogeneous population of immature myeloid cells that fail to complete their differentiation under chronic inflammatory conditions that are typical for the tumor microenvironment and strongly accelerate tumor progression [9–12]. These cells are known to express in mice CD11b and Gr1 surface markers and are divided into two subsets: polymorphonuclear Ly6G⁺Ly6C^{lo} (PMN) and monocytic Ly6G⁻Ly6C^{hi} (M) cells [9, 10, 13]. In humans, MDSCs can be characterized as Lin⁻HLA-DR^{-/lo}CD33⁺ or Lin⁻HLA-DR^{-/lo}CD11b⁺CD 14⁻CD15⁺CD33⁺ PMN-MDSCs and CD14⁺HLA-DR^{neg/lo} orLin⁻HLA-DR^{neg/lo}CD11b⁺CD14⁺CD15⁻M-MDSCs[13–15]. Both mouse and human MDSCs are able to inhibit the antitumor reactivity of T and NK cells due to different mechanisms, in particular, via reactive oxygen species (ROS), nitric oxide (NO), programmed death-ligand 1 (PD-L1), and arginase (ARG)-1 [9, 10, 13-16]. A long-term secretion of various chronic inflammatory mediators, including granulocyte–macrophage colony-stimulating factor (GM-CSF), vascular endothelial growth factor (VEGF), transforming growth factor (TGF- β), interleukin (IL)-1 β , IL-6, tumor necrosis factor (TNF- α), interferon (IFN)- γ , and chemokines (C-C motif) ligand (CCL) 2, CCL3, CCL4, and CCL5 produced by tumor and stroma cells has been reported to promote the generation, recruitment, and activation of MDSCs in tumor lesions [9–12].

Chemokines are small (8-14 kDa), structurally related chemotactic cytokines, which regulate the trafficking of lymphocytes and myeloid cells through interactions with specific transmembrane, G protein-coupled C-C chemokine receptors (CCR) [17]. Although CCR share a high degree of homology with up to 75% in case of CCR5 and CCR2 [18], they bind to different ligands. Few of the chemokines can bind more than one receptor. Chemokines are considered to be key drivers in the development of inflammatory diseases and cancer [17]. Chemokines are secreted by tumor and host cells to attract immune cells through binding onto their receptors, resulting in the signaling through the heterotrimeric G proteins [17]. Different chemokines were suggested to be involved in MDSC recruitment to melanoma microenvironment, however, the role of CCR5 and its ligands in such mobilization and in MDSC activation is poorly understood. In this review, we discuss the role of CCR5/CCR5 ligand interactions in the trafficking, expansion, and activation of MDSCs during tumor progression based on the data obtained in transgenic mouse melanoma model and in melanoma patients.

Chemokines and MDSC recruitment to the tumor site

The pattern of chemokines involved in MDSC migration to the tumor microenvironment seems to be dependent on the MDSC subset (monocytic or polymorphonuclear) and on the tumor model. The role of CCL2 and its receptors in the attraction of M-MDSCs has been well described. In particular, it has been reported that the trafficking of M-MDSCs in several mouse tumor models occurred via an interaction between CCL2 and its receptors CCR2, CCR4, and CCR5 [19]. Moreover, melanoma-infiltrating M-MDSCs have been shown to display CCR2-dependent immunosuppressive activities in the presence of GM-CSF [19]. In contrast, the enhanced production of C-X-C motif receptor (CXCR) 2 ligands supported the migration of PMN-MDSCs to the tumor site [20]. In the transplantable prostate cancer mouse model, it has been recently demonstrated using generated soluble CCR2-Ig fusion protein [21] that CCL2/CCR2 interaction plays a pivotal role in the recruitment of bone marrow-derived myeloid cells to the peripheral blood and their subsequent migration to the tumor site [22, 23]. Moreover, the targeting of CCL2/CCR2 axis with antibody carlumab showed a therapeutic activity in patients with metastatic, castration-resistant prostate cancer [24].

The production of CCL2, chemokine (C-X-C motif) ligand (CXCL) 8 (also known as IL-8), and CXCL12 can be induced by prostaglandin E2 resulting in a strong enrichment of MDSCs in ovarian and gastric cancer microenvironment [25]. In contrast, the expression of CXCL12 has been demonstrated to decrease MDSC accumulation in a mouse model of breast cancer [26]. Other investigators, however, reported a dominating role of CXCL1, CCL5, and CCL7 but not CCL2 in the MDSC migration into mouse tumors [27].

The chemokine CCL5 has been recently described to activate hypoxia-inducible factor (HIF)-1a signaling cascades, leading to the upregulation of the VEGF expression [28]. Importantly, both HIF-1 α and VEGF are considered to play a key role in MDSC generation and activation [9, 10]. It has been published that CCL5 supported the tumor growth, invasion, angiogenesis, as well as immune cell recruitment to the tumor microenvironment via the interaction with CCR5 [29]. This receptor is a member of the trimeric guanine nucleotide-binding-protein-coupled seven-transmembrane receptor superfamily that acts via G proteins. It is composed of 352 amino acids and has a molecular mass of 40.6 kDa [18]. Besides CCL5, CCR5 can bind chemokines CCL3 and CCL4 that are secreted by tumor cells, T cells, monocytes/macrophages, dendritic cells (DCs), and MDSCs [17]. CCR5 is mainly expressed on fibroblasts, myeloid cells, T cells, and vascular cells [18].

CCR5 in cancer progression

CCR5 has been found to be a key receptor for the entry of HIV. Interestingly, individuals, exhibiting a 32 pb deletion in the CCR5 gene (CCR5 Δ 32), produce a non-functional protein and are therefore resistant to HIV infection [30]. In addition, males bearing this functional mutation in CCR5 acquired resistance to the development of prostate cancer that indicates an importance of this chemokine receptor for cancer progression [31].

Mouse studies showed that CCR5 expression both in tumor cells and various host cells was important for tumor progression. Thus, breast cancer cells that express a functional CCR5 could display increased cell migration and invasiveness [32]. Furthermore, CCR5 deficiency caused apoptosis of melanoma cells through the inhibition of nuclear factor- κ B (NF- κ B) and upregulation of IL-1Ra [33]. Blocking CCR5 expression was reported to reduce the potential for gastric cancer cell dissemination [34], to suppress bone metastasis of prostate cancer cells [35] and to inhibit the proliferation and invasion of cervical cancer cells regulated by microRNA-107 [36]. Other publications demonstrated that CCR5 expression on stromal cells is necessary for the spread of melanoma cells to the lungs in a transplantable B16 melanoma model [37], and that CCR5deficient mice displayed a delayed B16 melanoma growth and a better response to cancer vaccines [38, 39]. Furthermore, delayed growth of colon cancer and melanoma in CCR5 knockout mice was described to be associated with reduced tumor infiltration with regulatory T cells (Tregs) as compared to wild-type mice [40, 41].

Therefore, it was suggested that CCR5–CCR5 ligand interactions may favor tumor development in multiple ways: acting as growth factors, stimulating angiogenesis, modulating the extracellular matrix, inducing the recruitment of additional stromal and inflammatory cells, and taking part in immune evasion mechanisms [39].

To address the question whether MDSCs could be recruited to the melanoma microenvironment through CCR5 in more clinically relevant conditions, we used the ret transgenic mouse model of spontaneous skin melanoma, which resembles human melanoma with respect to histopathology and clinical development ensuring natural tumor-stroma interactions [42]. We found an increased frequency of CCR5⁺ MDSCs among total MDSCs in melanoma lesions (primary skin tumors and metastatic lymph nodes) as compared to the BM and peripheral blood. Furthermore, the frequency of CCR5⁺ MDSCs was significantly elevated in melanoma lesions in the course of melanoma progression. Interestingly, it has been recently described that a subset of CCR5⁺ breast cancer cells showed increased invasion and migration capacity, promoting breast cancer metastasis [32].

The migration of CCR5⁺ MDSCs to the tumor sites could be mediated by CCR5 ligands CCL3, CCL4, and CCL5 since we demonstrated that their concentrations were significantly increased in the lysates of primary tumors and metastatic lymph nodes as compared to serum in the same mice. These findings confirmed other reports demonstrating that melanoma and other tumors produced elevated amounts of CCR5 ligands [9, 39, 43, 44]. Interestingly, MDSCs infiltrating mouse melanoma may produce CCR5 ligands by themselves and attract high numbers of CCR5 expressing Tregs in vitro and in vivo [41]. However, the amount of tumor cells producing CCR5 ligands is much higher than that of infiltrating MDSCs, leading to an elevated ligand production in melanoma lesions as compared to the peripheral blood. Moreover, it has been found that these chemokines may not only induce trafficking of CCR5⁺ cells but also upregulate the CCR5 expression on their surface [45]. In our in vitro experiments, CCR5 ligands were shown to enhance the trafficking of CD11b⁺Gr1⁺ immature myeloid cells in the transwell assay that could provide an explanation for a profound accumulation of CCR5⁺ MDSCs in skin tumors and metastatic lymph nodes.

Earlier we demonstrated that melanoma lesions from ret transgenic mice contained also elevated amounts of numerous cytokines and growth factors, including IL-6, GM-CSF, VEGF, IL-1 β , and IFN- γ that were associated with the accumulation of tumor-infiltrating MDSCs and fast tumor progression [46, 47]. To address their potential effects on CCR5 expression, we incubated bone marrow (BM)-derived CD11b⁺Gr1⁺ immature myeloid cells with some of these factors alone or in combination with CCR5 ligands and found a strong stimulation of CCR5 expression. This suggests that not only CCR5 ligands but also other chronic inflammatory factors could mediate CCR5 upregulation and recruitment of MDSCs into melanoma lesions (Fig. 1). Other groups have recently presented similar observation on increased CCR5 expression induced by tumor-derived colony-stimulating factors and HIF-1 α in breast cancer [48, 49].

Role of CCR5 in MDSC activation

Having shown that trafficking of CCR5⁺ MDSCs into the tumor site was mediated by CCR5 ligands and other inflammatory factors, we addressed the question of their functionality. To this end, we analyzed the immunosuppressive pattern of CCR5⁺ and CCR5⁻ MDSC subsets in various lymphoid organs and melanoma lesions from the same tumor-bearing mice. In CCR5⁺ MDSCs, we observed a significantly higher expression of ARG-1, ROS, PD-L1, and NO known to mediate MDSC immunosuppressive functions [9-16] than in their CCR5⁻ counterparts. Importantly, this difference was especially pronounced between these MDSC subpopulations infiltrating skin tumors and metastatic lymph nodes. Moreover, an increasing production of all four immunosuppressive molecules by tumorinfiltrating CCR5⁺ MDSCs (in contrast to CCR5⁻ subpopulation) was shown to be significantly correlated with melanoma progression. In addition, in vitro incubation of BM-derived CD11b⁺Gr1⁺ immature myeloid cells with factors enriched in the tumor microenvironment (such as IL-6, GM-CSF, IL-1β, IFN-γ, IL-10, and CCR5 ligands) induced a significant upregulation of PD-L1 and ARG-1 expression on CCR5⁺ MDSC. When investigating the impact of CCR5 expression on MDSC immunosuppressive activity, we observed that CCR5⁺ MDSC isolated from the BM of tumor-bearing mice showed a tendency for stronger inhibition of T cell proliferation than their CCR5⁻ counterparts. We had to use in this functional assay CCR5⁺ and CCR5⁻ MDSCs sorted from the BM due to insufficient numbers of these cells infiltrating tumors, which demonstrated stronger differences in the immunosuppressive pattern.

Taken together, we observed that CCR5⁺ MDSCs could not only accumulate in melanoma lesions but also displayed an enhanced immunosuppressive capacity (Fig. 2). Recently, it has been reported that CCR5^{high} Tregs infiltrating human colorectal tumors displayed stronger immunosuppressive activity than their CCR5^{low} counterparts [50]. In addition, the blockade of CCR5 signaling could reduce the migration of Tregs into tumors in mouse colon

Fig. 1 Chemokines induce MDSC trafficking into melanoma microenvironment. Chemokines, including CCL2, CXCL1, CXCL8, and CCR5 ligands (CCL3, CCL4, and CCL5), stimulate migration of MDSCs from the bone marrow to peripheral blood and further to the tumor site. CCR5 ligands upregulate the expression of CCR5 on MDSCs, infiltrating tumor lesions



Fig. 2 Induction of CCR5 expression on MDSCs is associated with their activation. CCR5 ligands and other inflammatory factors (such as GM-CSF, IL-1β, IL-6, TNF-α, IL-10, IFN-γ) stimulate CCR5 expression on MDSCs. They displayed significantly stronger immunosuppressive pattern than their CCR5-negative counterparts reflected by higher expression ROS, ARG-1, NO, and PD-L1, allowing the inhibition of effector T cells (Th1 and CTL) and stimulation of Treg



carcinoma model and impair their *in vivo* suppression ability [40]. However, exact molecular mechanisms responsible for the stronger immunosuppression mediated by CCR5⁺ MDSCs are not described and need to be investigated.

Targeting CCR5/CCR5 ligand interactions

Given a critical importance of CCR5 for cell migration and activation, this receptor and its ligands were considered as therapeutic targets. Human small molecular antagonist of CCR5, Maraviroc, which binds to CCR5, thereby blocking the receptor-ligand interaction, has been approved for the treatment of patients with HIV infection, acting by inhibition of viral entry through the CCR5 receptor [51]. However, it failed to show any activity against murine CCR5 [52]. Studies on cancer patients demonstrated that Maraviroc-mediated cytotoxic and apoptotic effects in colorectal cancer cells [53], reduced the potential for gastric cancer cell dissemination [34] and inhibited metastatic potential of prostate and breast cancer cells [32, 35]. Furthermore, the blockade of CCR5 by Maraviroc has been recently reported to induce the repolarization of tumor-associated macrophages and to result in beneficial clinical responses in colorectal cancer patients with liver metastases [54].

Another possibility includes an application of receptorbased fusion proteins or neutralizing antibodies to CCR5 or its ligands. In mice, CCR5 blockade with anti-CCR5 antibody has been recently reported to lead to the inhibition of B16 melanoma growth and MDSC accumulation in tumor tissues [55]. Furthermore, targeting of chemokine CCL5 could decrease apoptosis of tumor-infiltrated CD8⁺ T cells in mouse colon tumor model [56] and reduce the immunosuppression activity of MDSCs in mouse mammary carcinoma [49], leading in both tumor models to the inhibition of tumor progression.

In our experiments in ret transgenic melanoma-bearing mice, we used a soluble receptor-based fusion protein mCCR5-Ig that was previously reported to selectively bind and neutralize all three CCR5 ligands (CCL3, CCL4, and CCL5) simultaneously [57]. We demonstrated that mice treated with the fusion protein displayed a significantly prolonged survival as compared to animals injected with nonrelated anti-mouse IgG (control group). Moreover, 25% of mice remained alive after 100 days of the treatment without any signs of tumor progression. Importantly, systemic injections of mCCR5-Ig resulted in a significant reduction in MDSC frequency among leukocytes and in the proportion of CCR5⁺ subpopulation within total MDSCs infiltrating skin tumors as compared to the control group. In addition, tumor MDSCs from the mice treated with mCCR5-Ig displayed reduced immunosuppressive pattern reflected by a lower NO production than in MDSCs from control tumor-bearing mice. We observed also an inhibitory effect of mCCR5-Ig on the recruitment of Tregs that are also characterized by the high expression of CCR5 [40, 41, 50]. Importantly, we failed to demonstrate a decreased accumulation of conventional CD4⁺ and CD8⁺ T cells in melanoma lesions since the expression of CCR5 on these cells was found to be significantly lower than on Tregs. This suggests that effector CD4⁺ and CD8⁺ T cells could use other chemokine receptors for their trafficking to the tumor microenvironment and were not negatively influenced by blocking CCR5/CCR5 ligand interactions.

CCR5 expression on MDSCs from melanoma patients

Numerous papers published during last years have documented an increase in the frequency of peripheral M-MDSCs and PMN-MDSCs in patients with malignant melanoma [14, 15, 58–60] and other tumors [14, 15, 61] that strongly correlated with tumor load. Furthermore, the frequency of circulating M-MDSCs has been demonstrated to correlate with reduced overall survival and decreased frequency of functionally active antigen-specific T cells in the peripheral blood of patients with advanced melanoma [60]. In addition, elevated amounts of circulating PMN-MDSCs have been reported to correlate with poor prognosis in patients with breast or colorectal cancer [61, 62]. Similar to findings of others, we observed a significant increase in the frequency of M-MDSCs in stage III-IV melanoma patients as compared to age- and gender-matched healthy donors [63]. Importantly, this enrichment was associated with elevated serum levels of chronic inflammatory factors such as IFN- γ , IL-1 β , and CXCL10 that support MDSC accumulation and activation. Moreover, an enrichment of circulating M-MDSCs significantly correlated with a decreased progression-free survival of these patients [63].

Analyzing whether CCR5 could play a critical role for MDSC trafficking in melanoma patients, we detected a significant elevation of the frequency of CCR5⁺ M- and PMN-MDSC subsets in the peripheral blood as compared to their counterparts in age- and gender-matched healthy donors. Interestingly, such increase was observed already in stage I-II patients. Moreover, directly comparing peripheral blood and skin melanoma samples from the same patients, we found a marked elevation of CCR5⁺ M-MDSC frequencies in tumor tissues as compared to the peripheral blood. Similar to observations in tumor-bearing mice, we demonstrated increased concentrations of CCR5 ligands in melanoma lysates as compared to serum samples from the same patients. It has been demonstrated that several chemokines (including CCL5) could be involved in melanoma growth and progression [64]. In addition, the level of chronic inflammatory factors GM-CSF, IFN- γ ,

and IL-1 β was found to be elevated in melanoma lesions that according to our mouse data [46] could create conditions for MDSC migration to the tumor site. Analysis of the immunosuppressive pattern of MDSC subsets from the peripheral blood of melanoma patients revealed higher expression of immunosuppressive molecules (such as ROS, ARG-1, PD-L1, and NO) in circulating CCR5⁺ M-MDSCs and CCR5⁺ PMN-MDSCs than in their CCR5⁻ counterparts. Therefore, like in tumor-bearing *ret* transgenic mice, CCR5⁺ MDSCs were found to be enriched in the peripheral blood and to be further accumulated in the tumor microenvironment of melanoma patients. In addition, they displayed an enhanced immunosuppressive capacity as compared to CCR5⁻ MDSCs.

Conclusion

Taken together, CCR5-CCR5 ligand interactions could play a major role not only in driving MDSCs into the melanoma microenvironment but also in the stimulation of their immunosuppressive functions. Using transgenic mouse melanoma model and human melanoma samples, we demonstrated that melanoma lesions were enriched with CCR5⁺ MDSCs showing enhanced immunosuppressive phenotype and function as compared to CCR5⁻ cells. Importantly, the upregulation of CCR5 expression could be achieved not only by CCR5 ligands but also by other inflammatory factors accumulated in the tumor microenvironment (like GM-CSF, IL-6 etc.). The treatment of melanoma-bearing mice with the fusion protein mCCR5-Ig reduced MDSC migration and immunosuppressive activity, leading to a significant prolongation of mouse survival associated with the decrease in the frequency of MDSCs infiltrating skin tumors. Moreover, tumor MDSCs from the mice treated with mCCR5-Ig displayed reduced immunosuppressive pattern as compared to these cells from control tumor-bearing mice. Importantly, targeting CCR5/CCR5 ligand interactions inhibited the recruitment of Tregs without any changes in the migration of conventional CD4⁺ and CD8⁺ T cells in melanoma lesions. It is plausible that effector T cells use other chemokine receptors for their trafficking to the tumor microenvironment and are not negatively influenced by the treatment. We suggest that blocking CCR5/CCR5 ligand interactions could be combined with other melanoma immunotherapeutic strategies to enhance their efficiency by neutralizing immunosuppression in the tumor microenvironment.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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