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Targeting the bone marrow microenvironment in multiple myeloma

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Acknowledgements

This work was supported in part by the R01CA181683 and The Leukemia & Lymphoma Society. There are no conflicts of interest associated with this review.

This article is part of a series of reviews covering Hematologic Malignancies appearing in Volume 263 of *Immunological Reviews*.

Summary: Multiple myeloma (MM) is characterized by clonal expansion of malignant plasma cells in the bone marrow (BM). Despite the significant advances in treatment, MM is still a fatal malignancy. This is mainly due to the supportive role of the BM microenvironment in differentiation, migration, proliferation, survival, and drug resistance of the malignant plasma cells. The BM microenvironment is composed of a cellular compartment (stromal cells, osteoblasts, osteoclasts, endothelial cells, and immune cells) and a non-cellular compartment. In this review, we discuss the interaction between the malignant plasma cell and the BM microenvironment and the strategy to target them.

Keywords: myeloma, bone marrow, immune cells, BMSCs, vessel formation

Introduction

Multiple myeloma (MM) is characterized by clonal expansion of malignant plasma cells in the bone marrow (BM) leading to multiple bone lytic lesions, anemia, and immunodeficiency at the time of diagnosis (1). It is the second most common hematologic malignancy in the United States (2). MM is almost always preceded by a premalignant disease well known as monoclonal gammopathy of undetermined significance (MGUS). MGUS is found in approximately 2% of the general population aged 50 years and in 5% of those older than 70, and it progresses to MM at a rate of 1% per year (3). The response rate and overall survival (OS) of MM have significantly improved due to the introduction of novel agents such as thalidomide, lenalidomide, and bortezomib, and autologous stem cell transplantation (4). However MM continues to be a mostly incurable disease. Therefore, there is an urgent need for the development of other therapeutic agents that not only target the tumor clone but its permissive microenvironment.

MM cells grow and expand almost exclusively within the BM, thus suggesting the importance of the BM microenvironment in supporting MM cell growth and survival. The clonal plasma cell trafficking in and out of the BM allows the progression or ‘metastasis’ of the disease to new BM sites (5). The BM microenvironment consists of a cellular compartment and a non-cellular compartment. The cellular compartment can be subdivided into hematopoietic cell types including myeloid cells, T lymphocytes, B lymphocytes, NK cells, and osteoclasts, while non-hematopoietic cells include bone marrow stromal cells (BMSCs), fibroblasts, osteoblasts, endothelial cells, and blood vessels. The non-cellular compartment includes the extracellular matrix (ECM), oxygen concentration, and the liquid milieu (cytokines, growth factors, and chemokines), which are produced and/or affected by the cellular compartment within the bone marrow microenvironment. These microenvironment compartments exert differential effects on MM cell progression and may also work synergistically. In this

review, we discuss how each BM microenvironment compartment supports MM cell growth and disease progression, as well as how to target the environment to prevent MM progression (Fig. 1).

The immune microenvironment in MM

An important step in the progression of tumors is evasion and suppression of the host immune system (6, 7). The role for the immune system in suppressing tumor growth was demonstrated *in vivo* using immunodeficient mouse models. For instance, Rag2^{-/-} mice and SCID (severe combined immunodeficiency) mice, which lack both B and T cells, develop spontaneous adenocarcinomas (8) or T-cell lymphomas (9), respectively. In the normal microenvironment the effector cells, mainly the natural killer (NK) cells and cytotoxic T lymphocytes (CTLs), are capable of driving potent anti-tumor responses. However, tumor cells often induce an immunosuppressive microenvironment, which favors the expansion of immunosuppressive cell populations,

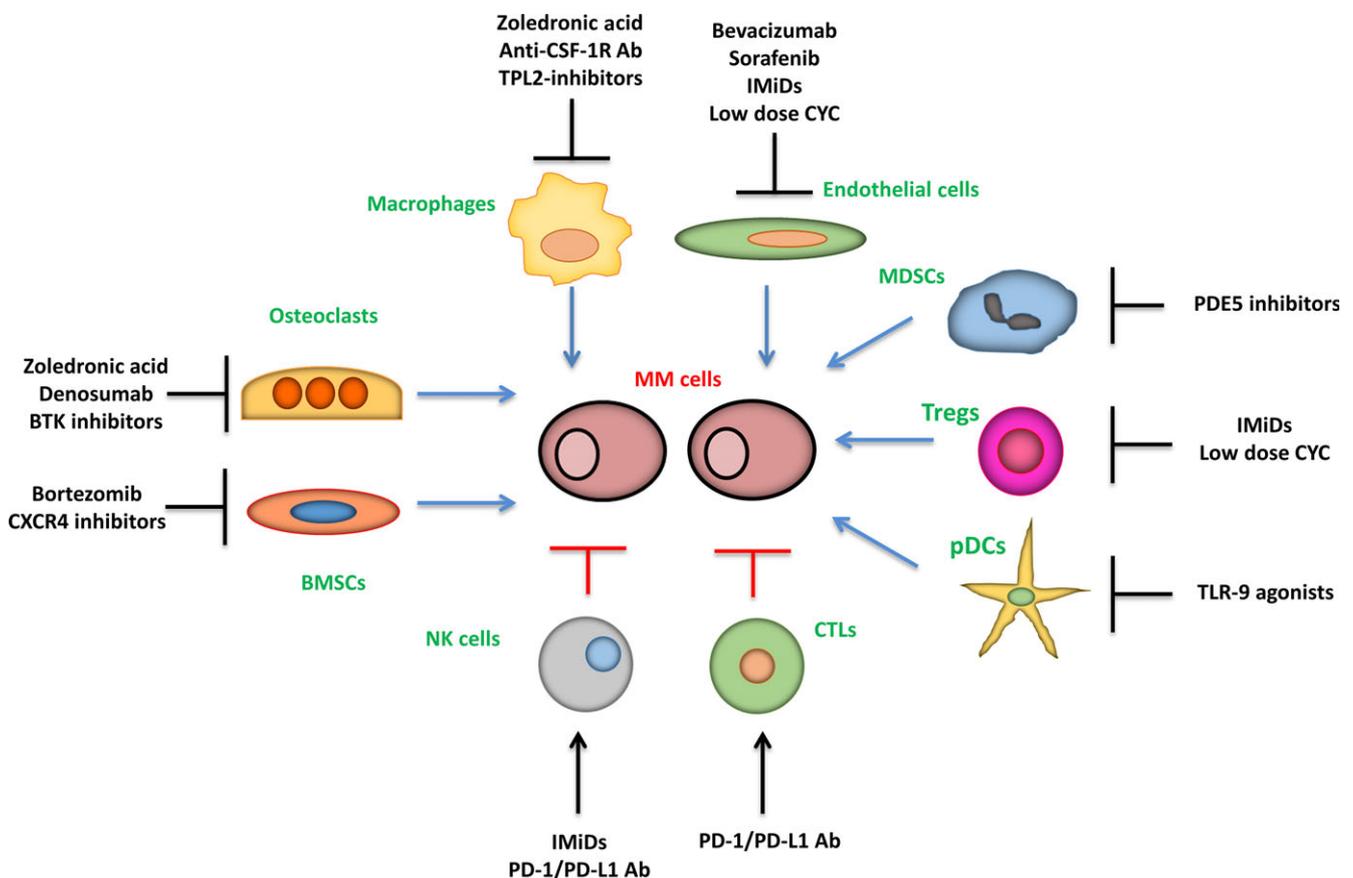


Fig. 1. Targeting the cellular compartment of the bone marrow (BM) microenvironment in multiple myeloma (MM). Treatments suppressing the functions of myeloid derived suppressor cells (MDSCs), Tregs, plasmacytoid dendritic cells (pDCs), macrophages, bone marrow stromal cells (BMSCs), osteoclasts, and endothelial cells in MM microenvironment are under development, while IMiDs and PD-1 and PD-L1 antibody (PD-1/PD-L1 Ab) induce NK cell and cytotoxic T-lymphocyte (CTL) functions.

such as myeloid derived suppressor cells (MDSCs) and regulatory T cells (Tregs). MM is associated with both cellular and humoral immune deficiencies (10–12), indicating that the evolution of disease in MM is associated with an immunosuppressive milieu that fosters immune escape and tumor growth.

Myeloid derived suppressor cells (MDSCs)

MDSCs are a heterogeneous population of immature myeloid cells that differentiate into macrophages, granulocytes, or dendritic cells under normal conditions. However, under pathological conditions such as cancer, differentiation of immature myeloid cells is inhibited, resulting in accumulation of MDSCs (13). In cancer patients and tumor models, MDSCs accumulate in the tumor microenvironment due to release of soluble factors by tumor cells or cells in the microenvironment (14, 15). Previous reports showed that cancer patients with higher MDSC levels have shorter survival compared to patients with lower MDSC levels (16, 17). Depletion of MDSCs in tumor-bearing mice using Gr-1 antibody inhibited tumor outgrowth (18, 19), suggesting that MDSCs may be a target of anti-tumor treatment. There are two main subsets of MDSCs, granulocytic MDSC (G-MDSC) and monocytic MDSC (Mo-MDSC). In mice, G-MDSCs are identified as $CD11b^+ Ly6G^{hi} Ly6C^{low}$ and Mo-MDSCs as $CD11b^+ Ly6G^- Ly6C^{high}$, while in humans G-MDSCs are $CD11b^+ CD33^+ HLA-DR^{-/low} CD14b^-$ and Mo-MDSCs are $CD11b^+ CD33^+ HLA-DR^{-/low} CD14^+$. In tumor-bearing mice, G-MDSCs are the main MDSC subset to be expanded in the peripheral lymphoid organs (20). MDSCs can suppress T-cell proliferation through expression of immune suppressive factors, such as arginase, reactive oxygen species (ROS), and nitric oxide (NO). G-MDSCs have increased levels of ROS and low levels of NO, whereas Mo-MDSCs have increased level of NO but low levels of ROS (20, 21). It is also reported that MDSCs can induce the development of Tregs *in vivo*, which are anergic and suppressive (22).

Previous reports have shown an increase in the number of MDSCs in the peripheral blood (PB) (23, 24) and BM (25) of MM patients compared to healthy donors. MDSCs induce MM growth by suppressing T-cell-mediated immune responses, while MM cells induce the development of MDSCs from healthy donor peripheral blood mononuclear cells, confirming a bidirectional interaction between MDSCs and MM cells and immune effector cells (24). A recent report showed that purified MDSCs from patients with MM

was able to induce more Treg development than MDSCs from age-matched controls (26). Interestingly, MDSCs from 5TGM1 murine MM mice displayed a significantly high potential to differentiate into mature and functional osteoclasts than those from non-tumor controls, which indicates that tumor-induced MDSCs exacerbate cancer-associated bone destruction by directly serving as osteoclast precursors (27).

Given that novel agents such as the immunomodulatory drug lenalidomide and the proteasome inhibitor bortezomib target both MM cells and the BM microenvironment (28), the effect of these drugs against MDSCs was studied. However, neither bortezomib nor lenalidomide were able to alter the suppressive activity of MDSCs (24). This indicates that additional strategies are needed to target MDSCs in the MM microenvironment. Phosphodiesterase-5 (PDE5) inhibitors reduced the suppressive machinery of tumor recruited MDSCs through downregulation of arginase 1 and nitric oxide synthase-2 expression in murine tumor models (18, 29, 30). Noonan et al. (31) recently reported that PDE5 inhibitor, tadalafil, reduced MDSC function in a relapsed/refractory MM patient. The strategy targeting MDSCs in MM with PDE5 inhibitors may represent a novel approach that can augment the efficacy of tumor-directed therapies.

Regulatory T cells (Tregs)

Among the T cells recruited to the tumor sites that have immunosuppressive functions are Tregs. T-cell infiltration has been shown to occur within the tumor microenvironment due to microenvironment-secreted chemokines/cytokines (32). Tregs are a subset of $CD4^+$ T lymphocytes that suppress functions of antigen-presenting cells (APCs) and effector T cells by direct contact or by release of anti-inflammatory cytokines (IL-10 and TGF- β); they are characterized by the expression of transcription factor FOXP3 (33). These cells accumulate in the tumor microenvironment and the peripheral blood of patients with cancer (34, 35). The increased frequency of Tregs has been generally considered as a marker of poor prognosis due to Treg-mediated suppression of anti-tumor immunity (36, 37). It has been shown by using the diphtheria toxin inducible 'depletion of regulatory T cell' (DEREG) mice (38) that Treg depletion induces regression of solid tumors, which was associated with an increased intratumoral accumulation of activated $CD8^+$ cytotoxic T cells (39, 40). These data indicate that targeting Tregs in cancer can be a potential anti-tumor strategy.

Many groups have reported an increase of functional Tregs in MM patient's PB compared to healthy donors (23, 41–44). A positive association of Treg frequency with international staging system (ISS) and paraprotein level was observed (42). The correlation between increased numbers of functional Tregs and disease progression was also shown in a MM mouse model (45). MM patients with higher percentage of Tregs in the peripheral blood are shown to have shorter time to progression (44) and shorter overall survival (43). Beyer et al. (41) showed that Tregs from MM patients express increased levels of IL-10 and TGF- β compared to healthy controls, indicating a more suppressive function of MM patients derived Tregs. However, there are some conflicting results (46, 47). The mechanism of how MM cells induce Tregs is not well understood. Feyler et al. (48) showed in an *in vitro* experimental model that MM cells can directly induce Tregs in an APC-independent manner mediated, at least in part, through MM expression of ICOS-L. These data showing the association of Tregs with MM progression suggest that Tregs could be targeted along with the tumor cells in MM.

Low-dose cyclophosphamide (CYC) has been shown to reduce the numbers and function of Tregs, and to induce anti-tumor, immune-mediated effects (49, 50). In a MM mouse model, low-dose CYC showed a transient depletion of Tregs resulting in reduced occurrence of MM and improved survival rate (51). Lenalidomide and pomalidomide, which are immunomodulatory drugs (IMiDS) used as anti-MM treatment, are reported to inhibit expansion and function of Tregs (52). However, for more specific and effective targeting of Tregs, it is vital to understand how Treg development, homeostasis, and effector function are controlled at the molecular level.

Dendritic cells (DCs)

Dendritic cells (DCs) are BM-derived professional APCs that present self and non-self antigens to T cells and promote immunity or tolerance (53). Antigen presentation by DCs induces naive T cells to differentiate into effector and memory T cells, but it can also lead to different forms of T-cell tolerance, depending on the functional status of the DCs. Myeloid DCs (mDCs) and Plasmacytoid DCs (pDCs) are the two major DC subsets that have been identified based on their origin, phenotype, and function (54). Several studies have documented an increase of DCs in human tumor sites, which often correlated with adverse prognosis (55–57). Indeed, loss of immune function of tumor-infiltrating DCs

has been linked to the suppressive effects of the tumor microenvironment mediated by various cytokines (58). Recent findings have demonstrated that tumor-infiltrating pDCs from solid tumors express high levels of ICOS-L, which explains their ability to induce Tregs (59, 60). It was also shown that TGF- β secreted by DCs from breast cancer patients was partially associated with induction of Tregs (61). Similar findings of induction of Tregs by DCs were observed in MM patients (62).

DCs play an important role in normal plasma cell differentiation and survival (63, 64). However, the frequency and function of DCs in MM patients compared to healthy individuals is still controversial (65, 66). Chauhan et al. (67) showed that pDCs are increased in MM patient's BM compared to healthy controls and pDCs confer growth, survival, chemotaxis, and drug resistance against MM cells. Targeting Toll-like receptors with CpG oligodeoxynucleotides both restores pDC immune function and abrogates pDC-induced MM cell growth. Toll-like receptor 9 (TLR-9) agonist inhibited pDC-induced MM cell growth through Interferon secretion and activation of TLR9/MyD88 signaling axis (68). Kukreja et al. (69) reported that DCs enhanced clonogenic growth of MM cell lines and primary tumor cells from MM patients. This effect was inhibited by blockade of the RANK–RANK ligand and BAFF–APRIL-mediated interactions. These data suggest that MM–DC interactions may directly impact the biology of MM and may be a target for therapeutic intervention.

Natural killer cells (NK cells)

NK cells represent a heterogeneous lymphocyte population with cytotoxic anti-tumor capacity and multiple immunoregulatory properties. One of the NK cell activating receptors is Natural Killer group 2D (NKG2D) which recognizes various proteins expressed on the surface of target cells in response to several forms of cellular stress. MHC class I polypeptide-related sequence A (MICA) is one of the ligands for NKG2D. Target tumor cells ectopically expressing MICA are efficiently killed via NKG2D despite the expression of MHC class I molecules (70).

NK cells in MM patients are increased in the PB (71, 72) and BM (73, 74) compared to healthy individuals. However, the expansion of NK cells in MM patients is not associated with their activation. It is reported that the NKG2D expression on the surface of NK cells from MM patients is decreased (75, 76), which may lead to the escape of MM from immunosurveillance. One of the mechanisms proposed

is the increased levels of soluble MICA in the circulation of MM patients, which triggers the downregulation of NKG2D and impaired lymphocyte cytotoxicity (75). The functional defect of NK cells in MM patients can also be explained by the expression of programmed cell death 1 (PD-1) on NK cells of MM patients (77). Engagement of PD-1 with their ligand PD-L1, which is expressed on MM cells, can down-modulate the NK cell versus MM effect.

In MM, the therapeutic efficacy of IMiDs is known to originate, at least in part, from the activation of NK cells. IMiDs are able to stimulate T cells to produce IFN- γ and IL-2 leading to NK cell activation (78, 79). Lenalidomide upregulates CD16, CD40L, and LFA1 on NK cells, thereby facilitating ADCC against MM cells (80). Salvage therapy with lenalidomide after allogenic stem cell transplantation for MM leads to an increase of activated NKp44⁺ NK cells (81). Also the proteasome inhibitor bortezomib has been shown to promote NK cell activation by increasing the levels of MICA on the surface of MM cells (75). These results show that, at least in part, the efficacy of novel anti-MM agents is associated with NK cell activation.

Macrophages

Cells of the monocyte–macrophage lineage are one of the major components of the leukocyte infiltration in tumors. There is strong evidence that these cells promote inflammatory circuits that ultimately lead to tumor progression, tumor-cell invasion, and metastasis (82).

Zheng *et al.* (83) first showed that physical interaction between macrophages and MM cells activates signaling pathways that protect MM cells from apoptosis induced by drug treatment, thereby contributing to MM development of drug resistance. A subsequent study (84) found that the interactions between P-selectin glycoprotein ligand 1 (PSGL-1) and intercellular adhesion molecule-1 (ICAM-1) on myeloma cells and E/P selectins and CD18 on macrophages, respectively, allowed macrophages to protect myeloma cells from drug-induced apoptosis through stimulation of SRC, ERK1/2 kinases, and c-MYC and suppression of drug-induced caspase activation. However, macrophages are also able to protect myeloma cells from apoptosis through non-contact-mediated mechanisms (85), suggesting that macrophages promote myeloma cell survival through both a contact-mediated and non-contact-mediated mechanisms.

In a recent study (86), the role of macrophages in MM has been further investigated, and interesting findings have clarified molecular mechanisms of activation of MM-associated

macrophages. Human myeloma-associated monocytes/macrophages (MAM), but not MM cells, were found to be the predominant source of interleukin-1 β (IL-1 β), IL-10, and tumor necrosis factor- α , whereas IL-6 originates from both stromal cells and macrophages consistent with previous results. TLR2 and TLR6 expression on human myeloma BM CD14⁺ monocytic cells correlated with local processing of versican, a proteoglycan TLR2/6 agonist, suggesting that the versican-TLR2/6-mitogen-activated protein 3 (MAP3) kinase, TPL2 (Cot/MAP3K8) pathway may ultimately activate MM-associated macrophages. Indeed, ablation of TPL2 in the genetically engineered *in vivo* myeloma model, Vk*MYC, led to prolonged disease latency associated with plasma cell growth defect through the abrogation of the ‘inflammatory switch’ of MM macrophages associated with development of MM. Interestingly, pharmacologic TPL2 inhibition in human monocytes led to dose-dependent attenuation of IL-1 β induction/secretion in response to TLR2 stimulation, suggesting that this may represent a new therapeutic target in MM, acting on the microenvironment and not on MM cells (86).

Tumor-associated macrophages are also a rich source of potent proangiogenic cytokines and growth factors, such as vascular endothelial growth factor, IL-8, and fibroblast growth factor-2, and express a broad array of angiogenesis modulating enzymes including matrix metalloproteinases, cyclooxygenase-2, and colony-stimulating factor-1 (87). Neo-vessel formation and angiogenesis are important pathogenic mechanisms associated with MM progression (discussed later); these observations support the hypothesis that macrophages may also support MM growth indirectly through the paracrine stimulation of MM-associated neoangiogenesis.

Interestingly, MM-associated macrophages are also able to participate directly, through vessel incorporation (vasculogenic mimicry), to the formation of MM-associated neovessels (88). Thus, macrophages seem to greatly contribute to MM-associated neovascularization through both the paracrine secretion of angiogenic factors (angiogenic pathway) and a vasculogenic pathway, and may therefore represent an important target for designing novel anti-neovessel drugs in MM.

PD-1/PD-L1 pathway as a target of modifying the MM immune microenvironment

PD-1 is a type I transmembrane protein which belongs to the CD28 family (89). PD-1 is expressed on activated and exhausted T and B cells and has two ligands, PD-L1 and

PD-L2. PD-L1 is not expressed on normal epithelial tissues but it is aberrantly expressed on a variety of solid tumors (90). Binding of PD-L1 to PD-1 reduces cytokine production and activation of the target T cells, leading to an immunosuppressive microenvironment.

It is reported that PD-L1 is not expressed on normal plasma cells, while it is expressed on primary MM cells (91). *In vitro* analysis has shown that cytokines (91) and BMSCs (92) increase PD-L1 expression on MM cells, indicating that the BM microenvironment plays a role in the activation of the PD-1/PD-L1 pathway. It has been demonstrated that PD-1 expression is upregulated on T cells (93) and NK cells (77) isolated from patients with MM compared to healthy donors, likely leading to an inhibition of anti-tumor immunity through the expression of PD-L1.

Clinical trials targeting PD-1/PD-L1 pathway to overcome tumor-associated immune suppression have shown promising results for a variety of solid tumors. Some groups have reported the efficacy of inhibiting the PD-1/PD-L1 pathway in preclinical studies of MM. Rosenblatt *et al.* (93) showed that CT-011, an anti-PD1 antibody, enhanced activated T-cell responses after DC/tumor fusion stimulation in MM. Hallet *et al.* (94) showed that PD-L1 blockade combined with stem cell transplant and whole-cell vaccination increased the survival of myeloma-bearing mice. Kearl *et al.* (95) showed that PD-L1 antibody improves survival of murine MM when combined with whole body irradiation. Considering the elevation of PD-1 and its ligand in the MM microenvironment, inhibition of the PD-1/PD-L1 pathway has the potential to change the strategy of the microenvironment targeted therapy in MM.

Other cellular compartments

Bone marrow stromal cells (BMSCs)

MM cells adhere to BMSCs and ECM into the BM. Adhesion of tumor cells to BMSCs activates many pathways resulting in the upregulation of cell cycle regulating proteins and anti-apoptotic proteins (96). Differences in MM- versus normal BMSCs adhesion molecule expression may facilitate MM cell entrapment in the BM. MM BMSCs express adhesion molecules that bind MM cells inter-cellular adhesion molecule-1 (ICAM-1) and vascular cell adhesion molecule 1 (VCAM-1) at higher levels than normal BMSCs (97, 98). Beta-1 and beta-2 integrin mediated MM cell adhesion may also be stronger to MM BMSCs than to normal BMSCs (99).

The interaction between MM cells and BMSCs triggers NF- κ B signaling pathway and IL-6 secretion in BMSCs. In

turn, IL-6 enhances the production and secretion of vascular endothelial growth factor (VEGF) by MM cells. The existence of this paracrine loop optimizes the BM milieu for MM tumor-cell growth (100). BMSC-MM cell interaction is also mediated through Notch. The interaction of Notch-Notch ligand leads to activate Notch-signaling pathways both in MM cells as well as in BMSCs, with induction of IL-6, VEGF, and insulin-like growth factor (IGF-1) secretion, and is associated with MM cell proliferation and survival (101, 102). Moreover, BMSCs from MM patients expresses several pro-angiogenic molecules such as VEGF, basic-fibroblast growth factor (bFGF), angiopoietin 1 (Ang-1), TGF- β , platelet-derived growth factor (PDGF), hepatocyte growth factor (HGF), and IL-1 (103). Gene-expression profiling data showed that growth differentiation factor 15 (GDF15) is aberrantly secreted by BMSCs in MM (104). GDF15 not only increases survival of stroma-dependent MM cells (105), but also enhances the tumor-initiating potential and self-renewal of MM cells (106). BMSCs in MM seem to support proliferation of the stem-like population of MM cells to a greater extent than normal BMSCs, suggesting that MM BMSCs are more specifically selective for the growth of tumor-initiating cells than normal BMSCs (107).

BMSCs from MM patients have also been shown to release exosomes, which are transferred to MM cells, thereby resulting in modulation of tumor growth *in vivo*. This finding suggests that exosomes might constitute a novel mechanism for intercellular transfer of genetic information in clonal plasma cell disorders (108).

Multiple drugs can also target the BMSC-MM interactions. Bortezomib inhibits MM cell growth triggered by BMSC adhesion, as well as production and secretion of cytokines that mediate MM cell growth and survival (109). In addition, bortezomib directly induces osteoblastic differentiation in BMSCs to combat osteolysis through RUNX-2 (110). The CXCR4 inhibitor AMD3100 enhances sensitivity of MM cell to multiple therapeutic agents by disrupting adhesion of MM cells to BMSCs (111). Novel drug screens using BMSC-MM cell co-cultures may allow the development of therapeutic agents that are clinically relevant to target the BMSCs in MM (112).

Osteoblasts

It has been reported that osteoblasts may contribute to MM pathogenesis by supporting MM cell growth and survival (113). This could potentially result from the ability of osteoblasts to secrete IL-6 in co-culture system with MM

cells. Other mechanisms include the possible role of osteoblasts in stimulating MM cell survival by blocking TRAIL-mediated programmed MM cell death by secreting osteoprotegerin (OPG) (114).

In addition, it is clear that suppression of osteoblast activity is responsible for both osteolytic process and progression of MM tumor burden (115). One of the factors responsible for suppression of osteoblast activity in MM is Dickkopf-1 (DKK1) (116). DKK1 is a Wnt signaling pathway inhibitor, which acts by binding to LRP5/6 preventing Wnt signaling and leading to translocation of β -catenin to the nucleus (117). Elevated DKK1 levels in BM and PB from patients with MM correlated with the gene-expression patterns of DKK1 and were associated with the presence of focal bone lesions (116). Recombinant human DKK1 or BM serum containing an elevated level of DKK1 inhibited the differentiation of osteoblast precursor cells *in vitro* (116). Studies have shown that blocking DKK1 and activating Wnt signaling prevents bone disease in MM, but is also associated with a reduction in tumor burden (118–120). Fulciniti *et al.* (120) showed that the anti-Dkk1 antibody (BHQ880) increases osteoblast differentiation *in vitro* and increases osteoblast number and trabecular bone *in vivo*. Blockade of DKK1 can restore osteoblast activity in MM, which may lead to improvement of MM bone disease.

Proteasome inhibitors have direct effects on osteoblasts to promote osteoblast differentiation and bone formation. Garrett *et al.* showed that proteasome inhibitors regulate bone morphogenetic protein-2 (BMP-2) gene expression of osteoblastic cells in part through inhibiting the proteolytic processing of Gli3 protein (121). Bortezomib increases the number of osteoblasts in a 5T2MM mouse model (122). It was also reported that the serum concentrations of bone-specific alkaline phosphatase (BAP) and osteocalcin, which indicates osteoblast activity, increased significantly in MM patients treated with bortezomib (123). Bone-specific nanoparticles loaded with bortezomib showed increased osteoblastic activity contributing to increased bone volume as well as inhibition in MM growth *in vivo* (124). These results indicate the potential for proteasome inhibitors to increase osteoblastogenesis in the BM microenvironment in MM.

Osteoclasts

The balance between bone resorption and bone formation is lost in the majority of cases in MM, resulting in bone destruction and development of osteolytic lesions (125). Several factors are implicated in osteoclast activation,

including RANKL, macrophage inflammatory protein-1a (MIP-1a), IL-3, and IL-6, which are produced by MM cells and play a role to increase osteoclast activity (126).

RANKL is a member of the tumor necrosis factor (TNF) family and plays a major role in the increased osteoclastogenesis implicated in MM bone disease. RANK is a transmembrane signaling receptor expressed by osteoclast cells. MM cell binding to neighboring BMSC within the BM results in increased RANKL expression. This leads to an increase in osteoclast activity through the binding of RANKL to its receptor, on osteoclast precursor cells, which further promotes their differentiation through NF- κ B and JunN-terminal kinase pathway (127). RANKL is also involved in inhibition of osteoclast apoptosis. Blocking RANKL with soluble form of RANK has been shown to modulate not only bone loss, but also tumor burden, in MM *in vivo* models (128). Denosumab is a fully human monoclonal antibody that binds RANKL with high affinity and specificity and inhibits RANKL-RANK interaction, resulting in rapid and sustained suppression of the markers of osteoclastic bone resorption (129).

Bruton's tyrosine kinase (BTK) plays a significant role in B-cell development (130). BTK is highly expressed in MM cells and the BTK inhibitor ibrutinib has been reported to be cytotoxic to MM cells via inhibiting the NF- κ B pathway (131). BTK is also expressed in osteoclasts and implicated in bone resorption by regulating osteoclast differentiation (132). Tai *et al.* showed that ibrutinib blocked RANKL/M-CSF-induced phosphorylation of BTK and downstream PLC- γ 2 in osteoclasts, resulting in reduced bone resorption activity (133). Ibrutinib treatment also significantly inhibited *in vivo* MM cell growth and MM cell-induced osteolysis of implanted human bone chips in SCID mice. These data suggest that BTK can be a target of MM induced osteolytic bone disease.

Endothelial cells and BM vessel formation in MM

It is well established that neovascularization of solid tumors is important for tumor growth and metastasis (134, 135). In the BM, blood vessel circulation is normally induced and maintained by the balanced interplay of cells, cytokines, and growth factors within a complex ecosystem in which endothelial cells and pericytes proliferate in concert with fibroblasts, DCs, inflammatory cells, and hematopoietic stem cells (136). It is now clear that malignant cell growth in the BM upset this balance, leading to increased vascularity and thus tumor progression (136).

The first evidence suggesting that neovascular formation is involved in the MM pathogenesis date back to 1995 (137, 138), when an increase in microvascular density (MVD) was observed in the BM of active MM patients compared to those with inactive MM and MGUS (137). Rajkumar et al. (139) then showed a gradual increase in BM angiogenesis along the disease spectrum of plasma cell disorders from MGUS to smoldering MM, newly diagnosed MM, and relapsed MM, although the expression levels of VEGF, bFGF, and their receptors were similar among MGUS, smoldering MM, and newly diagnosed MM (140). Several other studies have found a significant correlation between BM MVD and clinical parameters of prognosis, including progression free survival (PFS) and overall survival (OS), in MM patients (141).

Increase in PB and BM plasma or serum of the major pro-angiogenic cytokines VEGF, bFGF, HGF, and Syndecan-1 correlate with progression of MM to advanced stage of disease (141). All these observations strongly suggest that BM neovessels and neovessel formation are important pathogenic mechanisms, likely promoting MM progression (142, 143).

Interestingly, endothelial cells (ECs) derived from the BM of MM patients have been shown to be different in terms of transcriptome (144) and proteome (145) profiles from those of MGUS or anemic patients (136). MM derived ECs are endowed of an over-angiogenic phenotype able to support directly the growth, proliferation, and invasion of MM through the direct secretion of several growth factors, including IL-6 (146). For example, a cross-talk between MM cells and ECs has been described, where MM cells secrete VEGF that stimulates ECs to produce IL-6; this cross-talk ultimately determines simultaneous proliferation of both MM cells and ECs (147). MM ECs, but not MGUS ECs, are able to spontaneously secrete several other growth factors, including bFGF and HGF, which also promote MM cell proliferation and survival (148). All these studies show that vessel formation together with functional transformation of BM MM ECs ultimately lead to MM progression in a synergistic way. Although novel anti-MM drugs like thalidomide (148), lenalidomide (145), and bortezomib (149) have anti-angiogenic ability that in part explains their potent anti-MM activity, anti-angiogenic drugs that target the VEGFR2 pathway (such as bevacizumab) have failed to show activity in MM patients (142). This indicates that new and more effective strategies to target MM-associated vasculature are needed to exploit the therapeutic potential of vessel targeting in MM.

The non-cellular compartment

Extracellular matrix

The ECM is a major component of the tumor microenvironment in several cancers, contributing to the regulation of cell survival, proliferation, differentiation, and metastasis (150). Gene-expression profiling has shown that genes encoding for ECM components are dysregulated during tumor progression (151) and in MM ECM components, such as integrins, have been shown to play an important role in drug resistance (152). MM plasma cells directly interact with the ECM via binding of syndecan-1 and very late antigen-4 (VLA-4) to ECM proteins, such as collagen type 1 and fibronectin. These adhesive interactions of MM cells result in upregulation of anti-apoptotic proteins and cell cycle dysregulation (96).

It is increasingly clear, however, that not only does the ECM form an important part of the permissive tumor microenvironment for malignant plasma cells, it also contributes to the premetastatic niche with alterations in the ECM evident at the MGUS phase. A recent proteome profiling study of primary BMSCs from MM patients, MGUS patients, and non-neoplastic control patients revealed a group of ECM proteins, ECM receptors, and ECM-modulating enzymes that are upregulated in a stepwise fashion from MGUS to MM. This includes proteins such as laminin $\alpha 4$, lysyl-hydroxylase 2, integrin $\alpha 5\beta 5$ and matrix metalloproteinase-2 (MMP-2). This indicates that matrix remodeling in MM is already present at the MGUS phase and may provide rationale for ECM directed targeting of the premetastatic niche in MM (153). Preparation of the metastatic niche is potentially mediated by factors such as matrix metalloproteinases and lysyl oxidase, with consequent modulation of collagens and elastins at the premetastatic site. The concept of release of growth factors and cytokines by the tumor cells in preparation for distant site engraftment is now emerging and, for example, bone marrow-derived hematopoietic cells that express VEGFR1 home to tumor specific premetastatic sites and form cellular clusters before the arrival of tumor cells, coincident with the upregulation of fibronectin at these sites providing a permissive niche for arriving tumor cells (154).

As we uncover more about the composition of the ECM in MM and the nature of the complex interactions between MM cells, BMSCs, and ECM components, therapeutic targets are likely to emerge that are not only promising for MM patients, but also for selected targeting of the bone marrow niche in patients with premetastatic disease.

Oxygen concentration

Hypoxia is an imbalance between oxygen supply and consumption that deprives cells or tissues of oxygen. Decrease in oxygen levels are observed in certain types of pathological situations, such as cancer. Hypoxic regions arise in tumors because of rapid cell division and aberrant blood vessel formation (155). In solid tumors, it has been indicated that the hypoxic microenvironment contributes to cancer progression by activating adaptive transcriptional programs, thereby promoting tumor-cell survival, motility, and metastasis leading to worse prognosis (156, 157). It has been shown that the BM of MM mouse models (158, 159) and MM patients (160) are hypoxic compared to healthy controls, so targeting hypoxia niches should be considered as a novel approach for the treatment of MM.

Intratumoral hypoxia promotes metastasis through acquisition of epithelial mesenchymal transition (EMT) features in several models of solid tumors (161–163). Recent studies have suggested that hypoxia activates EMT-related machinery in MM cells, decreases expression of E-cadherin, decreases adhesion of MM cells to the BM, and enhances the egress of MM cells to the circulation (164). In parallel, hypoxia increased the expression of CXCR4, consequently increasing the migration and homing of circulating MM cells to new BM niches. In addition, hypoxia induces

immature and stem cell-like phenotypes in myeloma cell lines *in vitro* (165). These data show that hypoxic conditions change MM cells to a different phenotype, which may lead to changes in treatment sensitivity. TH-302, a 2-nitroimidazole-based nitrogen mustard prodrug, was tested as a hypoxic-activated treatment in the 5T33 MM mouse model. TH-302 induced apoptosis of the MM cells within the bone marrow microenvironment (158) and worked synergistically in combination with bortezomib (166). Therefore, targeting the hypoxic microenvironment in combination with other novel anti-MM agents can be a new anti-MM treatment strategy.

Conclusion

This review shows the advances in the understanding of the association between MM cells and the BM microenvironment. Although the response rate and OS of MM have significantly improved due to the introduction of novel agents, MM is still an incurable disease. As MM pathophysiology is supported by a strong interaction between the clonal plasma cells and the surrounding bone marrow microenvironment, treatment targeting this interaction is necessary for the cure of MM. Further understanding of the MM supportive BM microenvironment and development of new drugs or strategies targeting them are needed.

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