

The Immune Mechanisms Involved in the Pathogenesis and Pathophysiology of Myelodysplastic Syndromes and Immunotherapeutic Strategies

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Abstract

Recent clinical and molecular studies of Myelodysplastic Syndrome (MDS) showed the contribution of abnormal activation of innate immune signals and associated inflammation to the pathogenesis of MDS. The presence of abnormal levels of cytokines, chemokines and growth factors (tumor necrosis factor alpha /TNF- α /, interferon gamma /IFN- γ /, transforming growth factor beta, myeloid growth factors /G-CSF and GM-CSF/, interleukin (IL)-6, IL-8) in the peripheral blood and in bone marrow of MDS patients has been described. These levels depend on analyzed MDS subtypes. Toll-Like Receptors (TLRs) and multiple downstream signaling mediators are overexpressed in MDS. NF- κ B transcription factors are activated in response to inflammatory cytokines, pathogenic antigens, oxidative stress, DNA damage and the activation of pattern recognition receptors. Mesenchymal Stem Cells (MSCs) are primitive, non-hematopoietic stem cells that give rise to all of the various types of stromal cells that form bone marrow microenvironment (niche). The immunosuppressive capacity of MSCs is decreased in cells from low risk MDS. MDS-derived MSCs and bone marrow stromal cells are determinants of the fate of hematopoietic progenitors and have an important role in pathogenesis of MDS. Myeloid-Derived Suppressor Cells (MDSCs) are inflammatory and immunosuppressive effectors localized to the bone marrow that express the immune receptor CD33. MDS patients have increased numbers of MDSCs and they induce defects in myeloid and erythroid differentiation. Although hematopoietic cell transplantation can be curative, additional therapies are needed. Investigating CD33-targeted therapies in MDS and Chronic Myelomonocytic Leukemia (CMML) patients is justified by high frequency of CD33 expression. Blockade of immune checkpoints (programmed death-1 and its two ligands and cytotoxic T-lymphocyte associated antigen 4) can be a potential therapy in MDS and CMML patients. Bispecific Killer Cell Engager (BIKE) targeting CD16 expressed on effector natural killer cells and CD33 is able to facilitate elimination CD33+ MDS targets and immunosuppressive MDSC targets.

Keywords: Immunotherapies; Innate immune signaling; MDS; Microenvironment; NF- κ B; Toll-like receptors

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Chronic Myelomonocytic Leukemia (CMML) has long been recognized as a distinct clinico-pathological entity with features of both myelodysplastic and myeloproliferative syndromes resulting in different clinical presentations [12,13]. FAB group system classified CMML as part of MDS, given the morphologic evidence of dysplastic hematopoiesis. The FAB Group later proposed a reclassification of CMML patients into two subtypes based on White Blood Cell (WBC) count at diagnosis [14]. Patients with WBC counts of $< 13 \times 10^9/L$ were considered to have myelodysplastic CMML (MD-CMML) and those with $> 13 \times 10^9/L$ were considered to have myeloproliferative CMML (MPO-CMML). However, the two groups have overlapping features. Voglova et al., [15] analyzed 69 patients with CMML, 31 (45%) classified as MD-CMML and 38 (55%) classified as MP-CMML. Cytogenetic abnormalities were more frequent among MP-CMML patients. The median Overall Survival (OS) was significantly longer in the MD-CMML patients than in the MP-CMML group (30 vs. 16 months, respectively; p value < 0.01) and there was no significant difference in leukemic transformation. Over the course of disease, WBC count in 24 MD-CMML patients increased to more than $13 \times 10^9/L$. Therefore, MD-CMML and MP-CMML should be considered as different stages of the same disease. World Health Organization (WHO) in 2002 recognized CMML as a distinct entity and moved it to a new category called MDS/MPD [16]. WHO classification differentiates CMML-1 and CMML-2 according to blast percentages and more recently also CMML-0 with less than 5% medullary blasts [17].

Both, WHO classification and criteria for MDS are shown in Table 1 [18]. Using the International Prognostic Scoring System (IPSS), MDS is classified into low, intermediate-1, intermediate-2 and high-risk for progression towards AML [19]. Despite increasing insight into the tumor biology of MDS, the etiology of these syndromes remains undetermined. However, there is increasing evidence that cytopenia in MDS may, at least in part, be due to

Introduction

Myelodysplastic Syndromes (MDS) are a heterogeneous group of clonal Hematopoietic Stem Cell (HSC) disorders characterized by ineffective hematopoiesis, peripheral cytopenias, frequent karyotypic abnormalities and risk of transformation to Acute Myeloid Leukemia (AML) [1-10]. The first MDS classification, the French-American-British (FAB) classification, published 33 years ago allowed scientific research of this disease [11]. FAB group system was modified and further defined to recognize and classify distinct sub-categories of MDS based on genetic features.

lymphocyte-mediated myelosuppression suggesting that dysregulated immune mechanisms may be involved in the pathogenesis of MDS [20]. This hypothesis is supported by frequent association of MDS and CMML with clinical manifestations of Autoimmune Disorders (AD) and inflammatory response of the immune system [12,20,21-53]. Epidemiologic studies demonstrated that AD patients (suffering from rheumatoid arthritis, Sjögren syndrome, lupus erythematosus, seronegative arthritis, panarteritis nodosa, autoimmune hemolysis and pernicious anemia) have a higher risk to develop MDS or AML compared to general population [45].

Classification	Blood findings	Bone marrow findings
Refractory cytopenia with unilineage of dysplasia (RCUD)	Unicytopenia or bicytopenia, No or rare blasts (<1%)	Unilineage dysplasia: >10% cells in one myeloid lineage
Refractory anemia (RA), refractory neutropenia (RN), refractory thrombocytopenia (RT)		<5% blasts; <15% of erythroid precursors are ring sideroblasts
Refractory anemia with ring sideroblasts (RARS) <5% blasts	Anemia, No blasts	> 15% of erythroid precursors are ring sideroblasts Erythroid dysplasia only
Refractory cytopenia with multilineage dysplasia (RCMD) lineages <1x10 ⁹ /L monocytes	Cytopenia(s), No or rare blasts (<1%) No Auer rods	Dysplasia in >10% of the cells in two or more myeloid <5% blasts in marrow ± 15% ring sideroblasts No Auer rods
Refractory anemia with excess blasts-1 (RAEB-1) <1 x 10 ⁹ /L monocytes	Cytopenia(s), <5% blasts No Auer rods	Unilineage or multilineage dysplasia; 5%-9% blasts No Auer rods
Refractory anemia with excess blasts-2 (RAEB-2) <1 x 10 ⁹ /L monocytes	Cytopenia(s), 5%-19% blasts Auer rods±	Unilineage or multilineage dysplasia; 10%-19% blasts Auer rods±
Myelodysplastic syndrome -unclassified (MDS-U) cell lineswhen accompanied by a cytogenetic abnormality considered as presumptive evidence for a diagnosis of MDS <5% blasts	Cytopenias <1% blasts	Unequivocal dysplasia in <10% of cells in one or more myeloid
MDS associated with isolated del(5q) platelet count Isolated del(5q) cytogenetic abnormality No Auer rods	Anemia Usually normal or increased hypolobated nuclei, No or rare blasts (<1%)	Normal to increased megakaryocytes with <5% blasts

Table 1: World Health Organization MDS Classification and Criteria (2008). Adapted according Nybakken and Bagg [18]

The Immune System Defects in Myelodysplastic Syndromes

Aberrant immunity, including abnormal immune cells and molecules, contributes to the development of MDS. Various immune molecules, including Interferon-γ (IFN-γ), Tumour Necrosis Factor-α (TNF-α) and Interleukins (ILs), produced by Antigen-Presenting Cells (APCs) and T lymphocytes generate a cytokine milieu that can lead to the destruction of HSCs. The excessive apoptosis was largely cytokine mediated with a number of proinflammatory and proapoptotic cytokines such as TNF-α, Transforming Growth Factor- β (TGF-β), and Interleukin 1β (IL1β) being overexpressed in the marrows of

MDS patients. Stem/progenitor cells are impaired by these factors and exhibit marked deficiencies in proliferation and differentiation, high levels of apoptosis and dysfunctional responses to growth factor stimulation [42,54-56]. Overexpression of immune-related genes is widely reported in MDS [52]. Hyperactivation of innate immune/Toll-Like Receptor (TLR) signaling was described in MDS [50,53,57-60]. The innate immunity system is a conserved host defence mechanism that detects and eliminates pathogens [61,62]. Signals are mediated via downstream signaling mediators and eventually lead to activation of key intracellular molecular effectors such as transcription factor NF-κB and Mitogen-Activated Protein Kinases (MAPK). The resulting immune responses, including release of inflammatory cytokines, cause elimination of pathogens. Innate immunity responses are mediated by phagocytes such as macrophages and dendritic cells. However, TLR on hematopoietic progenitor cells stimulate innate immune system replenishment [63,64] and may be involved in the pathogenesis of MDS [50,53,65-69].

MDS are characterized not only by abnormal HSCs and immune system defects but also by changes in the hematopoietic microenvironment (niche) [70-74]. The pathogenesis of MDS likely depends on the interaction between aberrant hematopoietic cells and their microenvironment. Chronic immune stimulation in combination with senescence –dependent changes was observed in both, Hematopoietic Stem/Progenitor Cells (HSPC) and niche and seems to be critical to the pathogenesis of the disease. Inflammatory processes are regulatory stimulus promoting the proliferation and apoptotic death of hematopoietic progenitors in MDS. Immune system dysregulation, as a key driver of the pathological evolution of MDS, includes cytokine milieu abnormalities and inflammatory alterations in natural killer cells, T cells, and Myeloid-Derived Suppressor Cells (MDSC).

A detailed understanding of these mechanisms, which contribute to the pathogenesis of MDS, may help to find and to define novel targets for diagnosis and therapy in this disease.

The Association between Autoimmune Diseases and Myelodysplastic Syndromes

Immune and autoimmune biological anomalies have also been reported in MDS, such as the presence of antinuclear antibodies, antimitochondrial autoantibodies, Antineutrophil Cytoplasmic Autoantibodies (ANCA), autoantibodies rheumatoid factor, and cryoglobulins [32,75,76]. Approximately 10-30% of patients with MDS or CMML are associated with AD (Table 2), the most frequent being vasculitis, seronegative polyarthritis and specific skin lesions (Sweet’s syndrome, pyoderma gangrenosum) [21,23,26,43,76-84]. Distribution of AD among MDS subtypes is controversial [45]. It seems that is more involved in Refractory Anemia with Excess Blasts (RAEB), a MDS subtype characterized by increased myeloblasts or the presence of Auer rods, where in one study 86% MDS patients is associated with AD and 52% MDS patients is without AD. In a series of 235 MDS patients, 46 (19.6%) patients displayed features of AD [85]. In this study, distribution of MDS subtypes was similar between MDS cohorts with and without AD. MDS patients with AD are mostly male (up to 70%) and of older age (mean 78-83% years), which may be somewhat different from AD observed in general population, that

predominate in females and in younger patients. Apart from trisomy 8 in patients with Behcet’s disease, frequently associated with MDS [81-83], there seems to be no significant association between karyotype and MDS associated with AD [45]. Distribution of MDS subtypes with del(5q) and del(7q)/ monosomy 7 are similar in association with AD or without AD. Association of MDS with vasculitis may independently predict adverse outcome [86]. Other AD

Type of autoimmune manifestation in MDS	Examples
Systemic vasculitis	Giant-cell arteritis Aortitis Medium- and small sized Vessel vasculitis
Isolated autoimmune disorders	Cutaneous vasculitis Polyarthritits Polyneuropathy
Classical connective tissue disorders	Systemic lupus erythematosus Raynaud’s disease Polymyalgia rheumatic
Autoimmune hematological disorder	Autoimmune hemolytic anemia Immune thrombocytopenia
Asymptomatic immunological serological abnormalities	Positive antineutrophil antibody Positive rheumatoid factor

Table 2: Autoimmune diseases associated with MDS.

Adapted according Oostvogels et al., [87]

do not influence outcome of MDS patients when associated with MDS [45].

A causal relationship is yet to be established between MDS and autoimmunity. The exact mechanism(s) underlying MDS and AD are not well established and are supposed to be related to immune dysfunction induced by MDS or by immunosuppressive therapy. Immune deregulation and synthesis of autoantibodies due to abnormalities in T and B cells with production of cytokines, defective macrophage clearance and neutrophil function, with subsequent prolonged circulation of immune complexes and activation of inflammatory mediators, reduced CD4 count, immature natural killer cells and impaired function of monocytes and dendritic cells with abnormal antigen presentation are observed. All these features may result from abnormal stimulation by dysplastic bone marrow stem cells [32,88-90]. Treatment options include treating both diseases concomitantly with 5-azacitidine [91,92].

T-cell and B-cell Abnormalities in MDS

The existence of functionally polarized human T cell responses based on their profile of cytokine secretion in both the CD4+ T helper (Th) and the CD8+ T cytotoxic cell subset has been established. Human Th1 and Th2 cells not only produce a different set of cytokines but also exhibit distinct functional properties. Deviation of type I and type II T cells and its negative effect on hematopoiesis in MDS *in vitro* was described [93]. In MDS, autologous T lymphocytes suppress both erythroid (CFU-E) and granulocytic (CFU-GM) progenitor cell growth *in vitro* [94,95]. CD8+ cells mediated this inhibition of hematopoiesis through the Major Histocompatibility Complex (MHC) class I molecules on target marrow cells. Removal of T cells from bone marrow often enhances colony formation [96,97]. Successful treatment with Anti-Thymocyte Globulin (ATG) eliminates or reduces the myelosuppressive effect of these autologous T cells [98]. The decline of CD8+ cells in high-risk MDS is related to the expression of the negative co-stimulatory T-cell receptor

Programmed Death-1 (PD-1) and its ligand PDL-1. Higher levels of PD-1/PDL-1 in bone marrow cells are associated with resistance to therapy and with a poorer prognosis. It has recently been shown that T cell expression of the immunoinhibitory receptor PD-1 is regulated by DNA methylation. The hypomethylating agents (azacitidine and decitabine; HMAs) induced PD-1 expression on T cells in the MDS microenvironment, thereby likely hampering the immune response against the MDS blasts. Combination therapy using HMAs with a PD-1 pathway inhibitor can solve this problem.

Oligoclonal expansion of T cells in MDS was reported using flow cytometry and spectratyping [99-101]. Cukrova et al. [38] questioned the auto-reactivity of T-cells in MDS and found a defective *in vitro* cytotoxicity of these cells. The frequencies of activated T-cells were not related to characteristics of MDS patients [102]. However, the absolute lymphocyte count at diagnosis showed the adverse prognostic impact in a large cohort of MDS patients suggesting an influence of the host immunity on the disease in MDS patients [103].

More than 50% of early stage MDS patients have anti-erythroid autoantibodies in their bone marrow cultures. These autoantibodies are mainly directed against autologous erythroblasts and correlated with increased apoptosis [35].

The Involvement of Regulatory T-cells (Treg) in the MDS Pathogenesis

Treg are known to influence both the autoimmunity and tumour progression [104]. Kordasti et al. [105] evaluated the absolute number of both CD4+ and CD8+ Treg in the peripheral blood of 52 MDS patients. A significant correlation was shown between increased number of CD4+ Treg and several markers of disease aggressiveness (number of blasts in bone marrow, disease progression). None of these correlations was found for CD8+ Treg [105]. Kotsiniadis et al. [106] confirmed the effect of Treg on antitumour immunity in course of MDS. They found different Treg pattern in early and late stage of MDS. Treg were impaired in function and also in bone marrow homing in early stage MDS. However, Treg retained their function in late stage disease but were expanded [106]. In a retrospective study, Mailloux et al., [107] investigated the phenotypic features of Treg subsets including naive, central memory and effector memory cells, in association with MDS progression. They found a significant shift from a central memory phenotype toward an effector phenotype connected with a higher percentage of abnormal bone marrow myeloblasts. The analysis of effector memory Tregs using flow cytometry may be a simple and useful method to predict an early immune escape in MDS patients [108]. Moreover, Treg were significantly reduced in MDS patients responding to treatment. The recruitment of CD8+ cytotoxic T-cells, the degree of dyserythropoiesis and the need for erythropoietin treatment were inversely related with the levels of Treg in the bone marrow of MDS patients [109].

Natural Killer Cells in MDS

Natural Killer (NK) cells interact with clonal cells. NK cytolytic function against different tumour targets was reduced in MDS patients in relation with increased risk of MDS, higher IPSS, abnormal karyotype and excess of blasts [110]. The percentage of NK cells was similar in MDS patients and in healthy controls. However, NK cells of MDS patients expressed increased levels of granzyme B and were

mediators of cytotoxicity against dysplastic hematopoietic precursors [111]. Marcondes et al. [112] explored the relationship between NK function and IL-32 expression. NK cells from 48 MDS patients displayed impaired NK function utilizing distinct receptor-ligand interactions compared to healthy controls [111]. Reduced NK function showed global defects in NK receptor signaling. NK cell receptor proteins G2D (NKG2D), DNAX-Accessory Molecule-1 (DNAM-1) and natural cytotoxicity receptor NKp30 are involved in activation of NK cells. CD226 (Cluster of Differentiation 226), PTA1 (platelet and T cell activation antigen 1) or DNAM-1 is a protein that in humans is encoded by the *CD226* gene which is located on chromosome 18q22.3. Reduced expression of all these activating receptors were associated with impaired NK function in MDS [111,113,114]. NK cells from MDS patients fail to exhibit appropriate effector response. Based on low levels of IL-32 in CMML and high levels in MDS but suppressed cytotoxicity function in both diseases, IL-32 levels did not correlate with cytotoxic function. Abnormal stroma in MDS may play an inhibitory role in NK cell differentiation and development. Loss of immunosurveillance may then lead to the accumulation of cells with DNA damage in the intermediate stages of MDS progression. NK cells become more dysfunctional as MDS progresses. However, the direct cause and effect are unknown.

Abnormal Levels of Inflammatory Cytokines and Chemokines in the Peripheral Blood and Bone Marrow of MDS Patients

A variety of immune molecules, including IFN- γ , TNF- α and ILs produced by Antigen-Presenting Cells (APCs) and T lymphocytes generate a cytokine milieu that can lead to destruction of HSCs. The secretion of TNF- α and other related cytokines, such as IFN- γ or IL-6, is higher in low-risk MDS, whereas these and other cytokines are down-regulated in high-risk cases [50]. The overproduction of IFN- γ , TNF- α and ILs is hypothesized to contribute to the pathogenesis of MDS. Elevated amount of these secreted factors impair stem/progenitor cells that exhibit marked deficiencies in proliferation and differentiation, high levels of apoptosis and dysfunctional responses to growth factor stimulation [42,115-123]. IL-17 enhances the production of IFN- γ and TNF- α by bone marrow T lymphocytes from patients with lower risk MDS and may be involved in the pathogenesis of lower risk MDS [124].

Increased rates of intramedullary apoptosis are the main cause of the cytopenias in MDS. Apoptosis is initiated by the death receptor Fas and its specific ligand (Fas-L), which is overexpressed and correlates with the rate of apoptosis in MDS [125-131]. Fas/Apo-1 (CD95) and Fas-L are measured by flow cytometry, quantitative PCR of cDNA generated from mRNA and immunohistochemistry. TNF- α - Related Apoptosis - Inducing Ligand (TRAIL) is a member of the TNF family, which controls apoptosis by binding to agonistic receptors TRAIL-R1 and TRAIL-R2 and decoy receptors TRAIL-R3 and TRAIL-R4. TRAIL is present in normal marrow in negligible amounts, but is constitutively expressed in MDS marrow [119]. Fas-associated death-domain-Like interleukin-1 β -converting enzyme Inhibitory Protein (FLIP) is important in controlling apoptosis in normal cells. Isoforms of FLIP are products of alternative mRNA splicing and have

pro-apoptotic or anti-apoptotic properties. In early MDS, the anti-apoptotic isoform of FLIP downregulated and apoptosis is higher than in MDS with excess blasts, where resistance to apoptosis was described [132]. TNF- α receptor TRAIL-R2, which transmits cytoprotective signals via transcription factor NF- κ B is also increased in late MDS and exerts anti-apoptotic signal through regulation of bcl-2 and bcl-xL [133,134].

However, various cytokines, such as TGF- β , IFN- α and TNF- α itself, activate the p38 Mitogen-Activated Protein Kinase (MAPK) downstream signaling pathway in hematopoietic stem and progenitor cells, that increases apoptotic signaling in MDS bone marrow cells [135-140].

Toll-like Receptor Signaling and its Activation in MDS

The innate immune system is an evolutionarily conserved defense mechanism against pathogens which is implicated in the pathogenesis of MDS [65-68]. The Toll-Like Receptor (TLR) family (10 different TLRs in humans) plays a major role in the initial detection and subsequent elimination of foreign pathogens. This process is achieved through activation of intracellular signaling pathways, such as NF- κ B and MAPK, which initiate a coordinated set of responses. Wei et al., [141] performed a genome-wide Chromatin Immunoprecipitation (CHIP) followed by Sequencing (Seq) analysis of H3K4me3 in MDS. This analysis identified multiple genes marked by increased H3K4me3 in bone marrow CD34⁺ cells. A large majority of the genes identified are known to be involved in TLR-mediated innate immunity signaling and NF- κ B activation [141]. These authors showed in the same study that the histone H3K27me3 demethylase JMJD3/KDM6B containing Jumonji domain 3 (Jmjd3) is significantly overexpressed in MDS bone marrow CD34⁺ cells and has an important role in the regulation of expression of genes involved in innate immunity. Thus JMJD3 demethylase is capable of removing the trimethyl group from histone H3 lysine 27 [142].

Gene expression and mutational analysis of eight human TLRs were performed in a large cohort of MDS [143]. TLR1, TLR2 and TLR6 are significantly overexpressed in MDS bone marrow CD34⁺ cells. TLR1 and TLR6 are known to form functional heterodimers with TLR2. Deep genetic sequencing identified a rare genetic variant of TLR2 (F217S) present in 11% of bone marrow mononuclear cells of patients with MDS where it is associated with NF- κ B activation. The level of this variant is in MDS is significantly higher than in normal population. Inhibition of TLR2 in cultured MDS bone marrow CD34⁺ cells from patients with lower risk of MDS results in increased formation of erythroid colonies. TLR2-mediated innate immune signaling has a role in pathophysiology of MDS and its targeting may have therapeutic potential.

Velegraki et al., [144] demonstrated increased expression of a wide panel of genes involved in TLR4 signaling in bone marrow mononuclear cells. A gene expression microarray showed that TRAF6 is overexpressed in MDS CD34⁺ cells in comparison with healthy controls [145]. Furthermore, DNA arrays revealed the amplification of the TRAF6 locus (chromosome 11p12) and the TIRAP locus (chromosome 11q24.2) in MDS [146,147].

TLR4 is the receptor for Lipopolysaccharide (LPS), which induces the release of critical proinflammatory cytokines that are necessary to activate potent immune responses [148]. LPS/TLR4 signaling has been intensively studied in the past years. Two pathways diverge downstream of TLR4, the Myeloid Differentiation primary response gene 88 (MyD88)-dependent and -independent pathways, resulting in the expression of inflammatory cytokines of IFN-inducible genes. The MyD88-dependent pathway mediates a rapid and acute response, whereas MyD88-independent pathway is responsible for delayed response. MyD88 is a Toll-Interleukin 1 Receptor (TIR) containing adaptor protein that forms a complex on TIR domain of TLR4 (TIRAP). MyD88 recruits IL-1 Receptor Associated Kinase 4 (IRAK4), which then recruits IRAK1, resulting in subsequent autophosphorylation and disassociation from the TLR4-MyD88 complex. This complex then binds to TNF Receptor-Associated Factor (TRAF), key effector of the innate immune signaling complex. E3 ubiquitin ligase TRAF6 plays a key role in downstream activation of NF- κ B. MyD88 is overexpressed in bone marrow progenitors of MDS and is associated with risk stratification and patient survival [60]. Rhyasen et al., [149,150] demonstrated IRAK1 upregulation in MDS bone marrow mononuclear cells and showed that targeting of IRAK1 is a therapeutic approach for MDS.

Bone Marrow Niche and its Involvement in MDS

Hematopoietic stem and progenitor cells reside within the “bone marrow niche”, which is cellular and molecular microenvironment, which maintains and regulates stem cell self-renewal, differentiation and proliferation. Mesenchymal Stem Cells (MSCs) are primitive, non-hematopoietic stem cells that give rise to all of the various types of stromal cells that form bone marrow microenvironment [50,70-74,151-160]. MSCs have important roles in hematopoiesis and immune regulation.

Several studies have indicated that impaired MSCs propagate MDS [50,70-74,151-160]. Among the MSC impairments is altered expression of Aurora Kinase Genes (AURK) with an important role in the regulation of G2/M phase of cell cycle, centrosomes and cytokinesis. The expression of AURK is highly upregulated in MSCs in MDS patients. AURK is also targeted by microRNAs (miR-let-7a and miR-let-7b). Let-7 is a family of tumor suppressor microRNAs that are frequently down-regulated in malignant cells. Let-7 microRNA family members are downregulated in MDS with spliceosome mutations [161]. Dysregulated expression of AURK leads to increased number of centrosomes, gain or loss of chromosomes causing cell death of normal cells and survival of malignant cells.

Hematopoietic stem cells and mesenchymal stem cells undergo changes in response to induction factors like TNF- α , Fas and TGF- β in the bone marrow niche of MDS. However, these stem cells do not originate from the same neoplastic clone and often harbor different chromosomal aberrations, suggesting distinct genetic origin of MDS niche [162].

MDS MSCs release higher amount of IL-6 than normal MSCs [163]. IL6 is secreted by macrophages in MDS bone marrow and induces apoptosis in hematopoietic cells [163]. MDS MSCs inhibit T-cell proliferation *in vitro* and suppress the immune system *in vivo*. MSCs inhibit the proliferation of T-cells in normal healthy controls

through secretion of TGF- β and Hepatocyte Growth Factor (HGF). However, in MDS this secretion is decreased and MSCs may increase the proliferation of T-cells, thereby reducing immunosuppression, which results in increased apoptosis of MDS cells.

CXCL12, a member of the CXC family of chemokines, also known as Stromal Cell Derived Factor 1 (SDF1), is thought to have an important role in cell migration in and out of the bone marrow microenvironment. It is produced by bone marrow stromal cells, including endothelial cells and fibroblasts [152]. CXCL12 expression is lower in normal bone marrow than in MDS bone marrow [71,164]. Upregulated CXCL12 expression increases homing signaling for CXCR4 expressing hematopoietic cells, resulting in their hyperproliferation. This increased CXCL12 may be the reason for hypercellular bone marrow in MDS. CXCR4 high-expression group of MDS patients had a shorter overall survival time and shorter relapse-free survival time compared with those of the low-expression group [165,166]. There are positive correlations between CXCL12 and apoptosis in the low-grade MDS. For the high-grade MDS, there were positive correlations between CXCR4 and VEGF, and between CXCL12 concentration and bone marrow Microvessel Density (MVD). The apoptosis is one of the hallmarks for low-grade MDS and the angiogenesis for high-grade MDS. A refined understanding of the roles that CXCL12/CXCR4 axis and its correlation with angiogenesis and apoptosis play in MDS will fuel the development of therapies that can be targeted to the CXCL12/CXCR4 axis.

Perhaps the most striking evidence that bone marrow MSCs may play an important role in the induction of MDS is based on a study in mice, where selective deletion in osteoprogenitors of Dicer1, a RNaseIII endonuclease, essential for miRNA biogenesis and RNA processing, resulted in development of myelodysplasia and secondary leukemia [167]. Dicer1 was not deleted in hematopoietic stem cells.

As stromal cells in the endosteal niche, osteoblasts have important regulatory role in MDS bone marrow microenvironment. Osteoblasts regulate the maturation and proliferation of osteoclasts that are involved in Hematopoietic Stem Cells (HSCs) support. Strong adhesion between HSCs and osteoblasts maintains HSCs in bone marrow. In response to stress, infection and bleeding, HSCs migrate to vascular niche, resulting in their proliferation and differentiation. Within MDS bone marrow niche, malignant HSCs are found both in vascular niche and endosteal niche.

Induction of Myelodysplasia by Myeloid-Derived Suppressor Cells

Immature Myeloid-Derived Suppressor Cells (MDSCs), known to accumulate in tumor-bearing mice and cancer patients, are site-specific inflammatory and T cell immunosuppressive effector cells that contribute to cancer progression [168-172]. Their suppressive activity is in part driven by inflammation-associated signaling molecules, such as the Danger-Associated Molecular Pattern (DAMP) heterodimer S100A8/S100A9 (also known as myeloid-related protein 8 /MRP8/ and MRP14, respectively), which interact with several innate immune receptors that are involved in the biology of MDSCs activation [46,74,173,174].

Human MDSCs lack most markers of mature immune cells (LIN⁺, HLA-DR⁺) but possess CD33, the prototypical member of

sialic acid-binding immunoglobulin-like super-family of lectins (Siglec) [169,175,176]. CD33 possesses an Immunoreceptor Tyrosine-based Inhibition Motif (ITIM) that is associated with immune suppression [175]. LIN⁻, HLA-DR⁺CD33⁺ MDSCs specifically accumulate in the bone marrow of MDS patients and impair hematopoiesis through a mechanism that involves S100A9 as an endogenous ligand for CD33-initiated signaling. S100A9 protein belongs to the family of S100 calcium-binding proteins that has an important role in inflammation. MDSCs did not expand in the S100A9 protein deficiency [169]. S100A9 protein activation is through the NF- κ B signaling pathway. Therefore, inhibitors of the NF- κ B signaling pathway may reduce MDSCs levels and be useful therapeutic agents in conjunction with active immunotherapy targeted against the cell surface CD33 antigen in MDS patients.

Transmembrane protein CD33 is frequently expressed in cases of MDS and CMML with elevated blast count [177]. In normal individuals, expression of CD33 is associated with myeloid maturation and is present on myeloid but also on some lymphoid cells [178-180]. The CD33 antigen is not expressed in normal hematopoietic stem cells [181,182].

Immunotherapeutic Approaches in MDS

More than 40 years ago the observation that some patients given immunosuppressive conditioning with Antithymocyte Globulin (ATG) followed by bone marrow transplantation sometimes achieved full recovery of their autologous marrow prompted Gluckman et al., [183] to use ATG in patients with severe aplastic anemia. Horse ATG and more recently rabbit ATG have been also used to treat MDS [184-187]. Factors affecting responses included younger age, low IPSS score, and the presence of HLA-DR15 antigens. Complete responses were more common in patients with hypocellular MDS.

The first prospective studies using cyclosporine in patients with MDS was reported by Jonasova et al. [188] who treated 14 cytopenic patients with refractory anemia and variable marrow cellularity. All responders achieved transfusion independence which sustained for up to 30 months. A study in China reported a 62.5% response rate in 32 patients with RA, RARS, and RAEB treated with cyclosporine [189]. Renal failure occurred in a minority and this treatment needs careful followup of renal function.

The CD52 binding monoclonal antibody CAMPATH1 or alemtuzumab has been shown to have efficacy in MDS treatment. Neukirchen et al., [190] reported experience with alemtuzumab in nine MDS RCMD patients. All patients had a hypocellular bone marrow with a blast count <5 % and were classified as intermediate-1 according to the IPSS. We found a response in five patients (60 %); three patients achieved a complete remission 3 and 6 months after the treatment with alemtuzumab, and two patients showed a hematological improvement. Alemtuzumab was administered in a 10-mg dosage for 10 days. Treatment was well tolerated, and no severe side effects were observed. We could confirm the finding that the alemtuzumab is effective and save selected MDS patients. Due to the promising results, further studies, especially with regard to long-term survival and risk of leukemic progression should be initiated.

Gemtuzumab ozogamicin (Mylotarg; CMA-676; Wyeth Laboratories, Philadelphia, PA) is a monoclonal antibody conjugated with the highly potent anthracycline calicheamicin and targeted against the cell surface CD33 antigen [191]. Gemtuzumab binds to the CD33 antigen and is internalized and hydrolyzed. The cytotoxic part of the molecule, calicheamicin, enters the nucleolus, binds DNA strands and causes breaks in DNA, resulting in cell death. US Food and Drug Administration (FDA) approved gemtuzumab ozogamicin for therapy of relapsed AML expressing the CD33 antigen in patients over 60 years of age [192,193]. Raza et al., [194] carried out an open-label, randomized, phase II study to evaluate the safety and efficacy of gemtuzumab ozogamicin monotherapy in patients with the IPSS classification intermediate-2 or high risk MDS. No complete responses or partial responses were observed. Combination therapy with gemtuzumab ozogamicin and Interleukin-11 (IL-11) and gemtuzumab ozogamicin monotherapy were studied in a randomized study conducted at MD Anderson Cancer Center in patients 65 years of age or older with previously untreated AML or high-risk MDS [195]. None of 6 MDS patients randomized to gemtuzumab ozogamicin only arm had complete response. 25% of patients in the combination therapy arm attained complete response. However, this higher complete response did not translate into a survival advantage.

Bispecific Killer Cell Engager (BIKE) targeting CD16 expressed on effector natural killer cells and CD33 is able to facilitate elimination CD33⁺ MDS targets and immunosuppressive MDSC targets and may be therapeutically beneficial for MDS patients [196].

Cytotoxic chemotherapy has non-specific effects due to treatment related toxicities and patients also often relapsed due to residual cancer cells that are inherently resistant to cytotoxic therapy. Cancer immunotherapy has the capacity to overcome these both problems, directing a specific cytotoxic immune response against cancer cells, particularly residual cancer cells. The potential of the immune system to eliminate malignant cells is also demonstrated by allogeneic bone marrow transplantation. Moreover, relapsed disease following allogeneic bone marrow transplantation can be eradicated by the infusion of donor derived lymphocytes [197]. Graft versus host disease remains a major cause of morbidity and mortality following allogeneic transplantation. Allogeneic hematopoietic stem cell transplantation remains the unique curative option for patients with MDS and AML at high risk of relapse.

The development of an effective cancer vaccine requires effective presentation of tumor antigen for effective T cell activation, and the concurrent reversal of the immunosuppressive milieu in order to induce long-term immunity. Dendritic cells are bone marrow derived immune cells with potent antigen presenting abilities capable to induce primary immunity [198]. Dendritic cells are quantitatively and functionally deficient in MDS and AML patients [199]. Dendritic cells are good mediators of antileukemic activity and dendritic cells-vaccination strategies may be convenient for patients at relapse after allogeneic stem cell transplantation [200].

Over-expressed or aberrantly expressed cellular proteins including Wilms Tumor-1 (WT1) have been evaluated in phase I/II clinical trials of active immunotherapy with promising results [201]. The WT1 gene located on chromosome 11p13 encodes a zinc finger transcription factor that is important in cell growth and differentiation [202]. The WT1 gene expression is a good marker for diagnosis of disease progression of MDS [203]. WT1 is one of the antigens that triggers

T cell-mediated myelosuppression in MDS [204]. Vaccination with WT1 peptide was found to be safe and well tolerated in MDS patients with only 8% of patients (7 out of 88 total patients with MDS) [204]. The isolated WT1 peptide vaccination may be insufficient to generate long-term protective immunity [204]. Coupling a vaccine approach with sequential blockade of checkpoint inhibition, such as cytotoxic T lymphocyte antigen 4 (CTLA-4) or PD1 blockade, may be required to increase therapeutic benefit [205,206].

Recent findings regarding innate immune and inflammatory signals in MDS have been exploited for the development of novel therapeutic strategies in MDS. Preclinical studies with the specific inhibition of the activity or expression of TLR2 and its downstream effectors in primary MDS bone marrow cells by shRNA significantly improved differentiation, induced apoptosis and impaired their clonal generation potential, particularly in cells from lower risk MDS patients [50]. Opsona Therapeutics Ltd (Dublin, Ireland), the innate immune drug development company focused on novel therapeutic approaches to treat autoimmune, inflammatory diseases and oncology, announced the issuances of US Patent 8,734,794 and European Patent, EP2,451,842, which cover the Opsona developed antibody OPN-305, which is directed against TLR-2 (<https://clinicaltrials.gov/ct2/show/NCT02363491>). OPN-305 is the first humanized IgG4 monoclonal antibody against TLR2 and is studied in phase II clinical trial to improve erythroid differentiation of MDS bone marrow CD34⁺ cells.

Preclinical studies using MyD88 inhibition by inhibitory peptide (Invivogen, San Diego, CA), IL-8 inhibition by neutralizing antibody (ABCAM, Cambridge, MA) and IRAK1 inhibition by RNAi or specific inhibitor molecule were described [60,149]. Using a physics-based computational approach, Nimbus and their co-founding partner, Schrödinger Inc., uncovered the first truly selective small molecule IRAK4 (interleukin-1 receptor associated kinase 4) inhibitors. The three Nimbus novel compounds, ND-346, ND-2110 and ND-2158 demonstrated high selectivity against a panel of 334 kinases, and potent in vitro inhibition of cytokine production in cells and whole blood. Roche's Genentech unit licensed IRAK4 inhibitors from Nimbus.

SCIO-469 is a small-molecule p38 mitogen-activated protein (MAP) kinase inhibitor developed by Scios Inc as a potential oral therapy for inflammatory diseases. Preclinical studies with SCIO-469 in MDS were described [137]. Phase II open-label study for patients with MDS has been completed (<https://clinicaltrials.gov/ct2/show/NCT00113893>). ARRY-614, a potent, small-molecule dual p38/Tie2 inhibitor, developed by Biopharma, is being studied in patients with IPSS low and intermediate-1 risk MDS (Phase 1 study, <https://clinicaltrials.gov/show/NCT01496495>). In an initial dose-escalation study, using a powder-in-capsule formulation of ARRY-614, multi-lineage activity was observed. The most promising effects were seen in patients with thrombocytopenia and neutropenia, with transfusion independence frequently observed in platelet transfusion-dependent patients. ARRY-614 decreased the presence of phosphorylated p38 MAPK in bone marrow and reduced bone marrow apoptosis in most MDS patients while efficiently decreasing the levels of some inflammatory factors and erythropoietin in patients' plasma [207].

Curis, Inc. in collaboration with Aurigene designed an orally bioavailable small molecule, which binds with high affinity to PD-L1 and disrupts the interaction between PD-L1 and PD1 receptors on T

cells. Preliminary results generated by Aurigene demonstrate that in vitro studies, such as small molecule PD-L1 antagonists can induce effective T cell proliferation and IFN- γ production by T cells that are specifically suppressed by PD-L1 in culture. In addition, such small molecules also appear to have effects similar to anti-PD1 antibodies in in vivo tumor models, including IFN- γ production and inhibition of tumor growth. The anti-tumor effect of the oral PD-L1 antagonist is similar to that seen with a known anti-PD1 antibody in this mouse model. In early trials in patients with hematological malignancies, antibodies targeting CTLA-4 or PD1 signaling pathway have displayed significant efficacy with minimal toxicity in patients [206]. A safety and pharmacology study of Atezolizumab (MPDL3280A, Anti-PD-L1 Antibody) administered alone or in combination with azacitidine in patients with myelodysplastic syndromes has been announced (<https://www.clinicaltrials.gov/ct2/show/NCT02508870>).

Sotatercept (formerly called ACE-011) is an investigational protein therapeutic that increases Red Blood Cell (RBC) levels by targeting molecules in the TGF- β superfamily. Acceleron is developing sotatercept in collaboration with Celgene Corporation for the treatment of anemia in rare blood diseases, including MDS. Sotatercept inhibits osteoclasts and promotes osteoblast survival in MDS bone marrow microenvironment. Phase 2 studies (<https://clinicaltrials.gov/ct2/show/NCT01736683>) of Sotatercept for the treatment of anemia in low-or intermediate-1 risk myelodysplastic syndromes (MDS) or non-proliferative CMML is ongoing.

An oral small molecule inhibitor of TGF- β receptor I kinase, LY-2157299, galunisertib, is also being tested in a phase II trial (<https://clinicaltrials.gov/ct2/show/NCT02008318>) in low and intermediate-1 risk MDS [208].

Inhibitor of IDO1 is an inhibitor of the enzyme Indoleamine 2,3-Dioxygenase (IDO). This inhibitor is proposed for the treatment of malignant diseases and has been used in phase II INCB024360 study for patients with MDS (<https://clinicaltrials.gov/ct2/show/NCT01822691>) [209].

Conclusion and Perspectives

Great progress has been made in recent years in understanding the role of innate immune deregulation in the MDS pathogenesis. Constitutively activated innate immune and inflammatory pathways affect directly hematopoiesis; lead to altered cytokine secretion and impact T-cell immunity. All these biological effects contribute to the development and progression of MDS. Innate immune deregulation could be induced by cellular stresses associated with senescent changes, genomic instability and other genetic and epigenetic abnormalities that occur in hematopoietic cells with aging, but could be also initiated by abnormal cellular interactions in the bone marrow environment (niche). However, it is necessary to identify the endogenous ligands responsible for Toll-like receptors activation and the conditions that contribute to their release. This information will help to develop new effective therapeutic approaches.

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