

## Endothelial Progenitor Cell Dysfunction in Myelodysplastic Syndromes: Possible Contribution of a Defective Vascular Niche to Myelodysplasia<sup>1,2</sup>

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### Abstract

We set a model to replicate the vascular bone marrow niche by using endothelial colony forming cells (ECFCs), and we used it to explore the vascular niche function in patients with low-risk myelodysplastic syndromes (MDS). Overall, we investigated 56 patients and we observed higher levels of ECFCs in MDS than in healthy controls; moreover, MDS ECFCs were found variably hypermethylated for *p15INK4b*, *DAPK1*, *CDH1*, or *SOCS1*. MDS ECFCs exhibited a marked adhesive capacity to normal mononuclear cells. When normal CD34+ cells were co-cultured with MDS ECFCs, they generated significant lower amounts of CD11b+ and CD41+ cells than in co-culture with normal ECFCs. At gene expression profile, several genes involved in cell adhesion were upregulated in MDS ECFCs, while several members of the Wingless and int (Wnt) pathways were underexpressed. Furthermore, at miRNA expression profile, MDS ECFCs hypo-expressed various miRNAs involved in Wnt pathway regulation. The addition of Wnt3A reduced the expression of intercellular cell adhesion molecule-1 on MDS ECFCs and restored the defective expression of markers of differentiation. Overall, our data demonstrate that in low-risk MDS, ECFCs exhibit various primary abnormalities, including putative MDS signatures, and suggest the possible contribution of the vascular niche dysfunction to myelodysplasia.

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### Introduction

Homeostasis of hematopoietic system requires that hematopoietic stem cells (HSCs) can either rest dormant or proliferate and differentiate in response to peripheral stimuli [1]. The bone marrow (BM) environment guarantees for these definite activities by keeping HSCs embedded within specialized niches [2]. The BM niches are composed by several kinds of cells, including osteoblasts and mesenchymal and endothelial cells [3–5]. The osteoblasts govern the quiescence and maintain the pool of HSCs through specific pathways including Jagged-Notch, Tie2/angiopoietin, and transforming growth factor  $\beta$ /SMAD signaling [2]. During the past decade, several evidences have been gathered, showing that endothelial cells also play a critical role in hematopoiesis government [5–7]. In this study, we investigated the crosstalk between endothelial microenvironment and HSCs in myelodysplastic syndromes (MDS). These clonal disorders are characterized by an increased BM cellularity, due to excessive apoptosis, coupled with aberrant differentiation [8]. Although MDS constitute a very heterogeneous group of diseases, all of them share variable degrees of ineffective hematopoiesis and susceptibility to leukemic transformation [8]. Importantly, aberrant morphology of

myelodysplastic cells mirrors specific functional defects, which significantly affects the disease course also in patients at low risk for leukemic evolution [9]. Indeed, patients with MDS are prone to serious infections

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chromosomal aberrations found in the neoplastic clone [16]. Because aberrant DNA methylation of CpG-rich promoters of a variety of genes is very frequent in MDS [17], we investigated in ECFCs an eventual deregulation of the epigenetic machinery. We examined in ECFC samples obtained from 20 patients the methylation status of four genes that frequently undergo hypermethylation in MDS hematopoietic cells: *p15INK4b* (*p15*), *DAPK1*, *CDH1*, and *SOCS1*. We found that all patients showed at least one hypermethylated gene, with 13 patients having multiple hypermethylated genes (Table 1 and Figure 2). All investigated genes are functional to various pathways of normal endothelial cells, thus excluding that hypermethylation might result from physiological gene silencing. In addition, none of 14 investigated healthy controls was found hypermethylated.

### ECFCs from MDS Patients Show Increased Adhesion to Normal Hematopoietic Cells

It has been recently reported that mesenchymal stromal cells (MSCs) from MDS patients have a defective expression of adhesive molecules and chemokines [18,19], and we evaluated the proficiency of ECFCs obtained from MDS patients to adhere to normal mononuclear cells in comparison with ECFCs isolated from healthy subjects. Normal mononuclear cells tracked with CFSE were incubated over ECFC layers obtained from healthy individuals and MDS patients: After 2 hours, non-adherent cells were discharged and adherent cells were recovered and counted by flow cytometry. Results obtained are shown in Figure 3. On the whole,  $40 \pm 4\%$  of tracked cells adhered to MDS ECFCs, in comparison with  $13 \pm 1\%$  remaining adherent to normal ECFCs ( $P = .005$ ). Altogether, these observations suggest that endothelial cells from MDS patients show an “adhesion-proficient” phenotype.

### The Contact with MDS Endothelial Cells Perturbs the Expansion and Differentiation of Normal CD34+ Cells

Preliminarily, we observed that underlying ECFCs supported the expansion and differentiation of cord blood CD34+ cells. In fact, when CD34+ cells were seeded over normal ECFCs in erythroid, granulo-monocytic, and megakaryocytic differentiation media, we observed at day 7 a mean increase of  $1.6 \pm 0.1$ ,  $1.4 \pm 0.1$ , and  $2.0 \pm 0.1$  in total nucleated cell (TNC) number, respectively, compared to cultures performed under the same conditions but without endothelial layers. This was the result of an increase in the number of both differentiated (i.e., CD71+, CD11b+, and CD41+) and undifferentiated (i.e., CD34+) cells (Figure 4A). Accordingly, at the molecular level, we observed the harmonized up-regulation of genes related to the early phase of differentiation, including *Friend of Gata* (*FOG*), *PU.1*, and *AML-1*, and subsequently, the up-regulation of genes related to terminal differentiation, as *Transferrin Receptor* (*TFR*), *Myeloperoxidase* (*MPO*), and *Glycoprotein Ib* (*GPIb*) (Figure 4B). Indeed, we investigated whether MDS ECFCs had the same supportive properties exerted by

normal ECFCs. We found that ECFCs isolated from MDS patients were scarcely able or even at all incapable to support the expansion and differentiation of hematopoietic cells (Figure 4A). Although this defect was apparently more evident in granulocyte and megakaryocytic cultures than in erythroid cultures, the pattern of expression of lineage-related genes was deeply perturbed, clearly suggesting an imbalance between proliferation and differentiation (Figure 4B). In particular, in granulo-monocytic and megakaryocytic cultures, lineage-related gene expression was abnormally low in both early (*PU.1* and *AML-1*, respectively) and late (*MPO* and *GPIb*, respectively) phases of differentiation. In contrast, in cells pushed toward the erythroid lineage, *FOG* and *TFR* reached abnormally high expression values (Figure 4B).

### Normal and MDS ECFCs Have Different Gene Expression Profiles

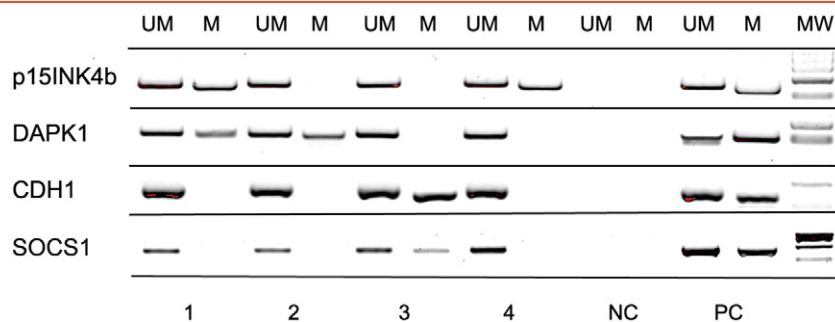
To discover the alterations underlying the impaired capability of MDS ECFCs to sustain hematopoiesis *in vitro*, we evaluated through microarray analysis their gene expression profiles in comparison with normal ECFCs. We initially focused on genes involved in a wide range of endothelial cell pathways, including adhesion, angiogenesis, cell activation, cell survival, and apoptosis (the gene set is available in the Supplementary Materials). Overall, among six significant upregulated genes, four codified for cell adhesion molecules [*ICAM-1*, *vascular cell adhesion molecule 1* (*VCAM-1*), *L-selectin* (*SELL*), and *von Willebrand factor* (*vWF*)]. Two additional genes found overexpressed were *nitric oxide synthase* and *tumor necrosis factor ligand superfamily, member 10* (Table 2, upper section). In contrast, *matrix metalloproteinase-1* (*MMP1*), *BCL2-like 1*, and *CASP2 and RIPK1 domain containing adaptor with death domain* were significantly downregulated in MDS ECFCs compared to normal controls (Table 2, upper section). Some of these genes are implicated in the regulation of blood cell production. For example, nitric oxide delivery not only induces megakaryocyte apoptosis and platelet formation but also controls HSC production in embryonic and adult lives [20–22]. Likewise, *MMP1* activates the hypoxia-inducible factor-1 pathway within niche cells, thereby inducing the transcription of hypoxia-inducible factor-responsive genes and terminal hematopoietic differentiation [23].

To explain our overall findings, we next examined additional pathways with putative effects on cell adhesion. Because the Wntless and int (Wnt) pathway is one of the main regulators of cell-to-cell interactions in hematopoietic tissues [24–26], we evaluated the expression profile of genes involved in the canonical and non-canonical Wnt pathways (gene sets, including ligands, receptors, and target of Wnt are available in the Supplementary Materials). We found that Wnt canonical signaling was significantly downregulated at multiple levels in MDS ECFCs (Table 2, middle section). Actually, MDS cells contained low RNA levels of several Wnt ligands (*Wnt3A*, *Wnt5A*, and *Wnt5B*), and several Wnt target genes were hence downregulated, including the transcriptional co-repressors *amino-terminal enhancer of split* and *C-terminal binding protein 1*, *cyclin D1*, and *inhibitor of differentiation 2* [27]. On the contrary, the *bone morphogenetic protein-4* (*BMP4*) and *follistatin* (*FST*), which are subjected to regulatory interactions with Wnt, were upregulated in MDS ECFCs in comparison with normal ECFCs (Table 2, middle section). Interestingly, both genes have specific activities in human hematopoiesis. In particular, *BMP4* is a powerful inducer of erythroid differentiation in stress erythropoiesis and acts in concert with SCF and hypoxia to promote the proliferation and differentiation of erythroid progenitors in response to acute anemia [28]. The increased

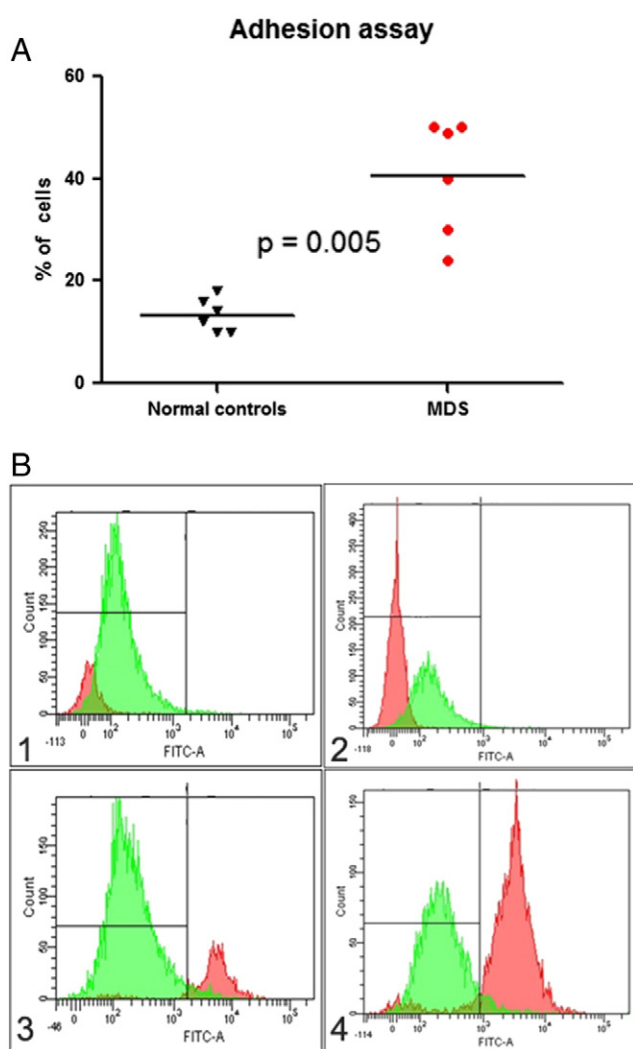
**Table 1.** Incidence of Aberrant DNA Methylation of CpG-Rich Promoters of *p15INK4b*, *CDH1*, *DAPK1*, and *SOCS1* genes in ECFCs Obtained from 20 Patients with MDS and 14 Controls

	Controls (n = 14)		MDS Patients (n = 20)		P
	Methylated	Unmethylated	Methylated	Unmethylated	
<i>p15INK4b</i>	0	14	8	12	.01
<i>CDH1</i>	0	14	7	13	.026
<i>DAPK1</i>	0	14	3	17	ns
<i>SOCS1</i>	0	14	4	16	ns
One of the above	0/14		20/20		<.0001





**Figure 2.** Methylation-specific PCR of *p15INK4b* (*p15*), *DAPK1*, *CDH1*, and *SOCS1* genes in ECFCs isolated from MDS patients: representative results of ECFCs isolated from four patients. UM indicates unmethylated gene; M indicates methylated gene; NC indicates negative control; PC indicates positive control for unmethylated and methylated DNA; MW indicates the molecular weight markers. Other abbreviations are detailed in the text.

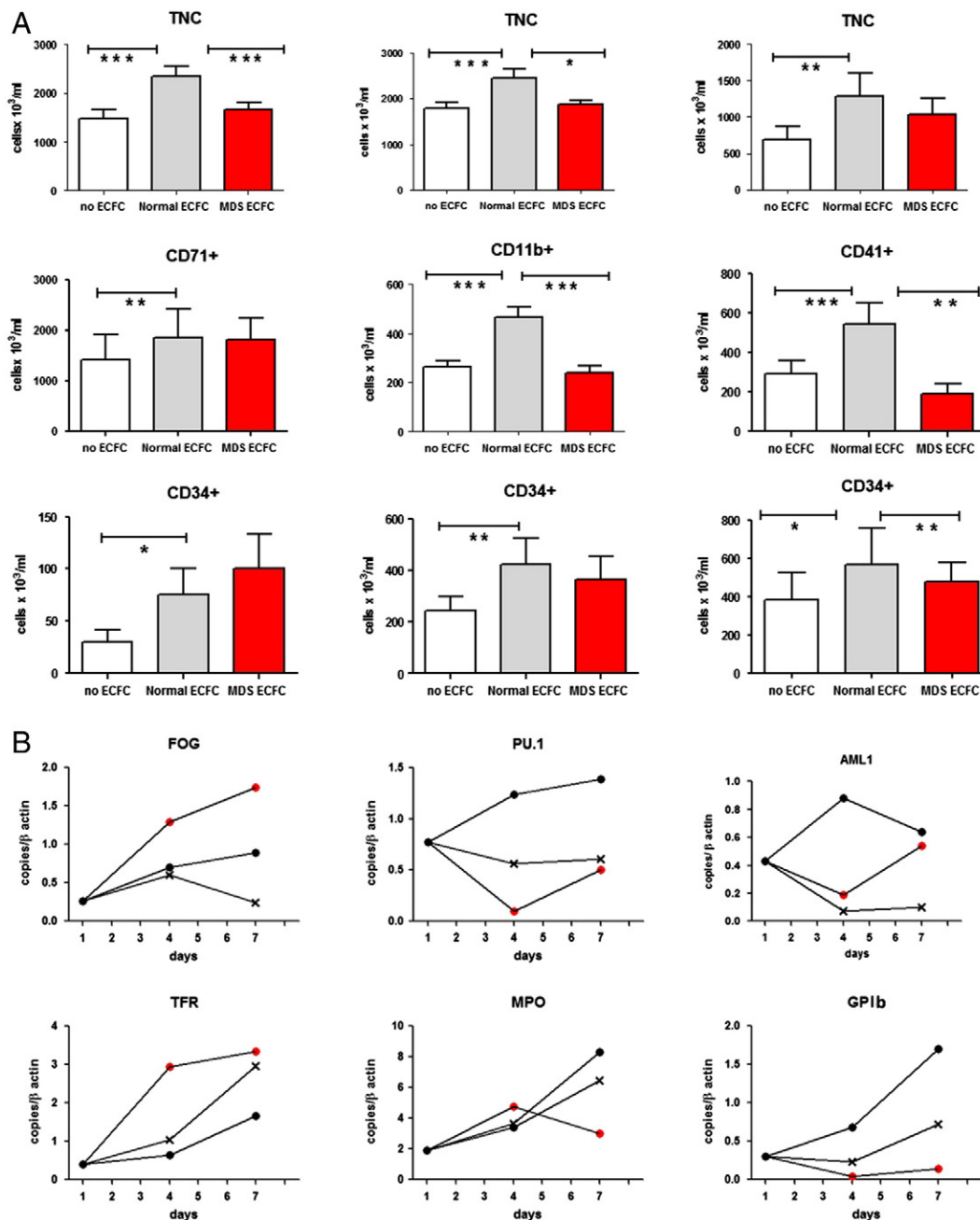


**Figure 3.** CFSE-labeled mononuclear cell adhesion to normal or MDS ECFCs. (A) Percentages of mononuclear cells adherent to ECFCs obtained from six healthy controls and from six MDS patients. (B) Representative experiment showing on the left the cytofluorimetric analysis of unstained peripheral blood mononuclear cells (negative control) and on the right the number of CFSE-labeled mononuclear cells bound by ECFC in a healthy control (upper panels) and in an MDS patient (lower panels). Abbreviations are detailed in the text.

expression of *BMP4* can partly explain why MDS ECFCs forced the expression of FOG and TFR during erythroid differentiation of normal progenitors. In contrast, *FST* regulates the hematopoietic cell adhesiveness to fibronectin, favoring the expansion of immature progenitors [29]. We hypothesized that the extensive hypo-expression of several Wnt genes could depend on the aberrant hypermethylation of their promoters. Nevertheless, our search for methylation of the *Wnt5A* gene promoter region was unsuccessful (data not shown). We then investigated the expression profile of a set of 84 miRNAs with predictable effects on the Wnt pathway. Actually, we demonstrated that, in comparison with normal ECFCs, MDS ECFCs contained significantly lower amounts of miR-142-3p, miR-424-5p, and miR-196b-5p (Table 2, lower section). Whereas all these miRNAs are variously involved in hematopoiesis [30,31] or angiogenesis [32], the low levels of miR-142-3p were particularly interesting, because it has been demonstrated to modulate the Wnt pathway to balance proliferation and differentiation of mesenchymal cells [33]. Interestingly, miR-142-3p was predicted to inhibit the expression of *BMP4* at both “Ingenuity” and “microRNA.org-Target and Expression” software.

#### *The Addition of Soluble Wnt3A Modifies the Adhesive Profile of MDS ECFCs*

Overall, the analysis of gene expression profiles suggested that MDS endothelial progenitor cells show a defective expression of several Wnt pathway constituents. Previous studies demonstrated that canonical Wnt pathway signaling regulates hematopoietic homeostasis by shaping the niches supportive of hematopoietic stem/progenitor cells [25]. In particular, Wnt signaling modulates VCAM-1 expression by marrow stromal cells and controls the production of extracellular matrix components [34]. Therefore, our model suggests that the increased adhesiveness of MDS ECFCs may result from the ineffective Wnt signaling and that the aberrant attachment of hematopoietic cells to the endothelial environment could interfere with their normal differentiation programs. To test this hypothesis, we investigated whether the addition of 100 ng/ml of soluble Wnt3A and/or Wnt5A to ECFC cultures could influence the abnormally high RNA expression of *ICAM-1*, *VCAM-1*, *vWF*, and *SELL*. We observed that *ICAM-1* RNA expression was the most significantly affected: either Wnt3A or Wnt5A was able to reduce *ICAM-1* expression, but Wnt3A induced a more sustained and deep decrease (Figure 5A). These findings were further confirmed by flow cytometry. In particular, we found a significant reduction of *ICAM-1* expression in MDS ECFC but not in normal ECFC after Wnt3A addition (Figure 5, B and C). In addition, we investigated



**Figure 4.** Co-cultures of normal cord blood CD34<sup>+</sup> cells in the absence of endothelial layers or over ECFC obtained from healthy controls and from MDS patients. Results represent the mean of six experiments. (A) Day 7 concentrations of total nucleated cells, CD71<sup>+</sup> or CD11b<sup>+</sup> or CD41<sup>+</sup> cells, and CD34<sup>+</sup> cells in cultures supporting erythroid, granulo-monocytic, and megakaryocytic differentiation, respectively. (B) Real-time PCR expression of early (*FOG*, *PU.1*, and *AML1*) and late differentiation markers (*TFR*, *MPO*, and *GPIb*) in cells recovered at days 4 and 7 from the experiments illustrated in A. \**P* < .05; \*\**P* < .005; \*\*\**P* < .001. —•— refers to cultures without ECFCs; —●— refers to cultures with normal ECFCs; —●— refers to cultures with MDS ECFCs.

the effect of Wnt3A addition on the capacity of MDS ECFCs to support hematopoietic differentiation. We found that the expression pattern of differentiation markers was positively affected by the Wnt3A addition, with a significant decrease in abnormally high *TRF* RNA values and a significant increase in both *MPO* and *GPIb* RNA expression (Figure 5D).

## Discussion

This study demonstrates that endothelial progenitor cells isolated from patients with low-risk MDS have an increased adhesion

capacity and fail to adequately sustain hematopoiesis, particularly in myeloid and megakaryocyte differentiation. Although the increased level of ECFCs in these patients has been previously reported [16], our findings suggest that the molecular defects underlying MDS endothelial progenitor dysfunctions are likely primary in their nature, since these cells differ from their normal counterparts in both genetic and epigenetic profiles. Since the transplant of allogeneic endothelial progenitor cells in myelosuppressed mice shortens the duration of aplasia and fosters blood cell recovery, it is conceivable that circulating ECFCs normally contribute to the BM

**Table 2.** Genes Differentially Expressed in ECFCs Isolated from MDS Patients and Healthy Controls. The Upper Section Includes Genes Functional to Adhesion, Angiogenesis, Activation, Survival, and Apoptosis of Endothelial Cells; the Middle Section Includes Genes Belonging to the Wnt Pathway, and the Lower Section Includes miRNAs

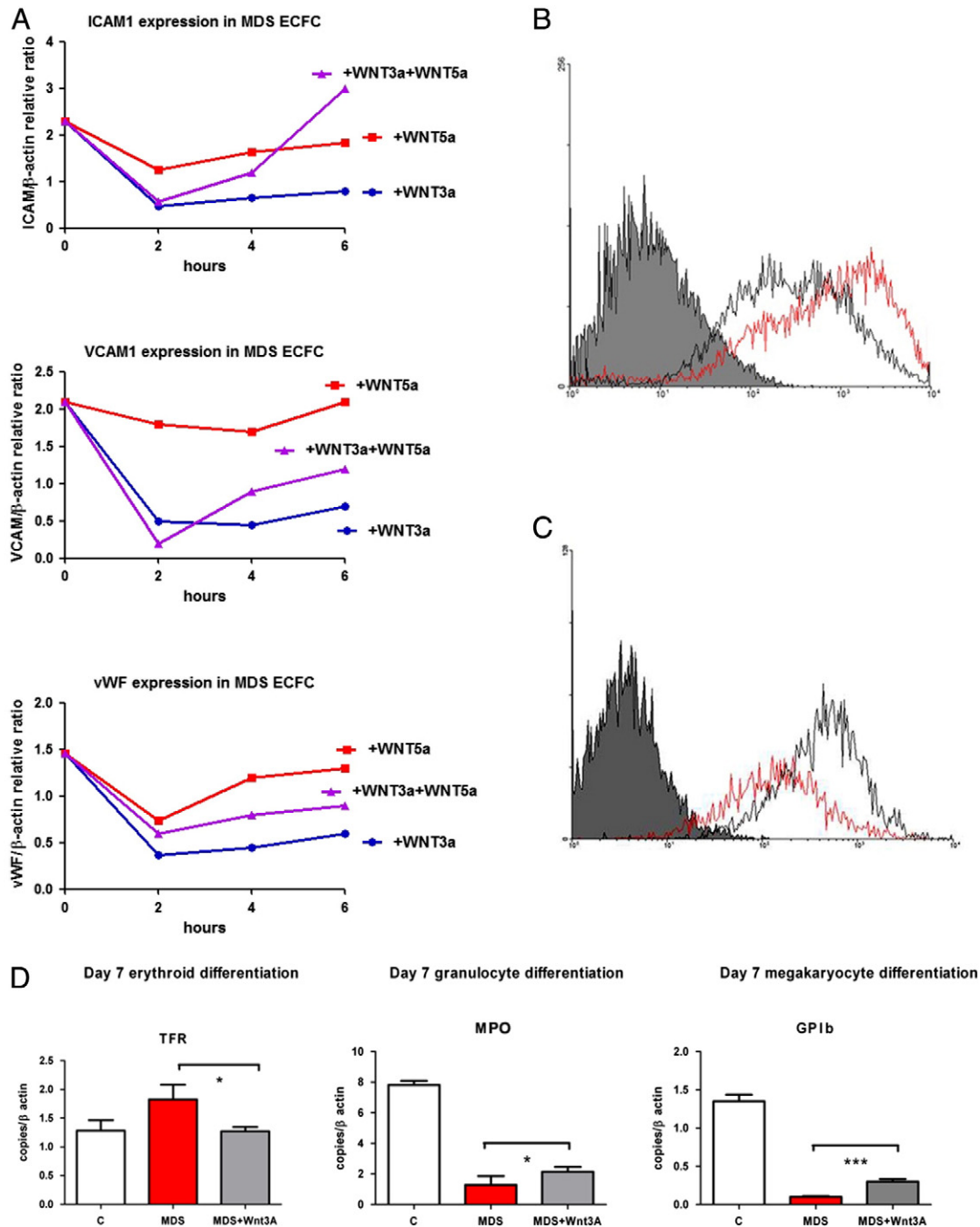
Gene	Fold Regulation	P
<i>ICAM-1</i>	14.06	.012
<i>Constitutive nitric oxide synthase 3</i>	13.17	.015
<i>SELL</i>	7.26	.041
<i>Tumor necrosis factor ligand superfamily, member 10</i>	11.08	.019
<i>VCAM-1</i>	5.46	.008
<i>vWF</i>	6.86	.001
<i>BCL2-like 1</i>	-8.51	.006
<i>CASP2 and RIPK1 domain containing adaptor with death domain</i>	-4.92	.032
<i>MMP1</i>	-4.78	.002
<i>FST</i>	5.38	.043
<i>BMP4</i>	4.85	.001
<i>Amino-terminal enhancer of split</i>	-4.48	.001
<i>Cyclin D1</i>	-5.59	.004
<i>C-terminal binding protein 1</i>	-4.32	.003
<i>Inhibitor of differentiation 2</i>	-4.96	.024
<i>Wnt3A</i>	-4.54	.010
<i>Wnt5A</i>	-4.51	.021
<i>Wnt5B</i>	-83.51	.031
<i>miR-142-3p</i>	-6.99	.003
<i>miR-424-5p</i>	-4.33	.001
<i>miR-196b-5p</i>	-9.89	.033

microvasculature homeostasis [35]. Even though our observations have been gathered in an *in vitro* model where ECFCs represent the surrogate of the BM vascular niche, they suggest a possible “diseased vascular niche” in low-risk MDS patients.

The relevant role of endothelial cells in hematopoiesis was clearly demonstrated several decades ago by Knospe et al. [36]. At that time, the authors showed that in mice subjected to local BM curettage followed by radiation and HSC transplantation the earliest foci of hematopoiesis occurred just into the areas of sinusoidal vascular regeneration [36]. Subsequent studies highlighted that the engraftment and reconstitution of hematopoiesis are mediated by vascular endothelial growth factor receptor 2 through the regeneration of sinusoidal endothelial cells [37]. While these effects have been partly attributed to the secretion of soluble growth factors, additional evidences indicate that the direct contact between HSCs and endothelial cells is relevant to hematopoiesis regulation. For instance, the contact with HSCs triggers in endothelial cells the activation of Akt and the release of paracrine factors that balance HSC self-renewal and differentiation [38]. Similarly, in normal BM, the areas of SCF/c-kit-mediated hematopoiesis are in tight spatial co-localization with endothelial and perivascular cells [39]. In addition, E-selectin expressed by endothelial cells has been recently recognized as a new regulator of HSC proliferation and differentiation [40]. We show here that, in contrast to normal ECFCs, circulating endothelial cells obtained from low-risk MDS patients are scarcely efficient in supporting hematopoietic differentiation: This defect is associated to the increased adhesion to hematopoietic cells that is likely induced by the low expression of various members of the Wnt pathway. In particular, stromal Wnt3A has been indicated as a powerful negative regulator of several adhesion molecules, including ICAM-1 and VCAM-1 [34], and in our experiments, the addition of exogenous Wnt3A both reduced ICAM-1 expression and partially restored cell differentiation.

The microenvironment participation in determining clinical and biologic features of MDS has been extensively investigated. Tennant et al. first showed that the adherent layers obtained from BM of MDS patients were significantly defective in supporting hematopoiesis in long-term Dexter-type cultures [41]. Tauro et al. observed heterogeneous abnormalities of MDS stromal cells including altered matrix molecule expression and changes in superoxide production, possibly contributing to the abnormal survival and development of hematopoietic cells [42]. Moreover, BM stromal cells of MDS patients exhibit abnormal production of several cytokines contributing to the impaired immune function observed in these patients [43]. More recently, Ferrer et al. showed that primary MSCs obtained from MDS patients express low levels of adhesion and cell surface molecules and, when co-cultured with CD34+ cells from healthy donors, produce lower numbers of cobblestone area-forming cells and fewer colony-forming units [18]. Similarly, Geyh et al. found that MSCs from patients with all MDS subtypes exhibit impaired growth and osteogenic differentiation, associated with specific methylation patterns and altered expression of several molecules involved in the interaction with HSCs, including osteopontin, Jagged1, Kit-ligand, and angiopoietin as well as several chemokines [19]. Finally, Pavlaki et al. observed that MSCs obtained from low- to intermediate-risk patients displayed downregulated canonical Wnt pathway due to up-regulation of inhibitors [44]. When pharmacologically activated, Wnt signaling led to an increased cell proliferation and restored their osteogenic differentiation ability [44]. The findings obtained in our model suggest for the first time that specific primitive perturbations could occur also at the level of the MDS vascular niche. Primitive abnormalities of endothelial cells or endothelial cell progenitors have been previously demonstrated in chronic myeloproliferative neoplasms. In these conditions, the “diseased vascular niche” facilitates clonal stem cell proliferation, favors extramedullary hematopoiesis through mobilization and homing of neoplastic HSCs in new niches in the spleen, and contributes to vascular complications [15,45,46]. In contrast, in MDS patients, endothelial niche dysfunctions could sustain BM hypercellularity embedded in dense microvasculature scaffolds. In addition, the pathologic involvement of the circulating endothelial compartment might be implicated in the association between MDS with systemic vasculitis [47] or in thrombotic proficiency of MDS patients subjected to specific therapies despite concomitant thrombocytopenia [48].

The canonical and non-canonical Wnt pathways consist of a complex network of interrelated and reciprocally connected signals [24–26]. Previous studies carried out in MDS hematopoietic cells reported hypermethylation of several Wnt antagonists, contributing to the activation of the Wnt pathway and the expression of  $\beta$ -catenin [49,50]. In these patients, a correlation between risk of leukemic transformation and nuclear  $\beta$ -catenin expression or Wnt antagonist hypermethylation was noticed, confirming the linkage between Wnt pathway activation and leukemogenesis [49,50]. Our observations, in contrast, suggest that the defective function of the Wnt pathway in vascular niches could mainly affect the physiological differentiation processes of hematopoietic cells, resulting in the myelodysplasia observed also in patients at low risk for leukemic transformation. Accordingly, harvest of immature progenitors (i.e., CD34+ cells) in cultures supported by MDS endothelial cells was not so different from that obtained in the presence of normal endothelial cells. Furthermore, we found that supplementation of exogenous Wnt3A to cultures



**Figure 5.** (A) Real-time PCR expression of *VCAM-1*, *vWF*, and *ICAM-1* RNA in MDS ECFCs incubated with Wnt3A, Wnt5A, and Wnt3A plus Wnt5A (each at 100 ng/ml concentration). The data represent the mean values of three experiments (SDs are <10% and have been omitted). (B and C) The flow cytometry expression of ICAM-1 in normal (gray line) and MDS (red line) ECFCs without Wnt3A (B) and after incubation with Wnt3A (C). We observed a significant reduction of ICAM-1 in MDS ECFCs. Data refer to a representative experiment; mean fluorescence intensity is reported in the x axis and number of events in the y axis. (D) Co-cultures of normal cord blood CD34+ cells with normal ECFCs (white columns), MDS ECFCs (red columns), or MDS ECFCs plus 100 ng/ml Wnt3A (gray columns). Real-time PCR expression of *TRF*, *MPO*, and *GPIb* RNA after day 7 of culture in erythroid, granulo-monocytic, and megakaryocytic differentiating media. Results represent the mean of five experiments. \* $P < .05$ ; \*\*\* $P < .001$ .

partly reverted the impaired hematopoietic differentiation of hematopoietic cells.

**Conclusion**

Overall, our observations add a new tile to the complex mosaic of the MDS pathogenesis and offer an innovative perspective on these

diseases, pointing to the primary dysfunctions of the vascular niche as important drivers for myelodysplasia.

**Appendix A. Supplementary Materials**

Supplementary data to this article can be found online at <http://dx.doi.org/10.1016/j.neo.2015.04.001>.



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