

# Adrenomedullin in the growth modulation and differentiation of acute myeloid leukemia cells

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**Abstract.** Adrenomedullin (ADM) is a regulatory peptide endowed with multiple biological effects, including the regulation of blood pressure, cell growth and innate host defence. In the present study, we demonstrated that ADM signaling could be involved in the impaired cellular differentiation of myeloid leukemia cells to mature granulocytes or monocytes by modulating RAMPs/CRLR expression, PI3K/Akt cascade and the ERK/MAPK signaling pathway. When exogenously administered to *in vitro* cultures of HL60 promyelocytic leukemia cells, ADM was shown to exert a strong proliferative effect with minimal upregulation in the expression level of monocyte antigen CD14. Notably, the experimental inhibition of ADM signaling with inhibitor ADM<sub>22-52</sub> promoted a differentiative stimulation towards monocytic and granulocytic lineages. Moreover, based on the expression of CD31 relative to CD38, we hypothesized that an excess of ADM in bone marrow (BM) niche could increase the transendothelial migration of leukemia cells while any inhibitory event of ADM activity could raise cell retention in hyaluronate matrix by upregulating CD38. Taken into consideration the above evidence, we concluded that ADM and ADM<sub>22-52</sub> could differently affect the growth of leukemia cells by autocrine/paracrine mechanisms and may have clinical relevance as biological targets for the intervention of tumor progression.

## Introduction

Acute myeloid leukemias are a heterogeneous group of clonal neoplastic diseases due to genetic and epigenetic alterations of hematopoietic stem cells (HSCs) or committed progenitors, causing an aberrant growth of myeloid precursor cells.

Acute promyelocytic leukemia (APL), a subtype of AML, is characterized by an abnormal accumulation of promyelocytes following specific translocation t(15;17) (q21;12) and formation of promyelocytic leukemia (PML)/retinoic acid receptor  $\alpha$  (RAR $\alpha$ ) fusion gene. It has been demonstrated that the PML-RAR $\alpha$  fusion protein is involved in the pathogenesis of APL through the recruitment of a complex that, composed of nuclear co-repressor molecule (NCOR) and histone deacetylase (HDAC), inhibits the expression of myeloid differentiation genes (1). Under treatment with all-*trans*-retinoic acid (ATRA), the NCOR/HDAC complex is dissociated from RAR and the maturation of promyelocytes is restored. Standard protocols combining ATRA with anthracycline-based chemotherapy are demonstrated to guarantee ~70% cure rate (2).

Originally isolated from human pheochromocytoma, adrenomedullin is a 52 aa peptide belonging to the calcitonin gene-related peptide family (3). Its maturation involves the proteolytic cleavage of proadrenomedullin, a precursor of 185 amino acid residues that includes at amino terminal end the so-called proadrenomedullin N-terminal 20 peptide (PAMP), a peptide with known transient hypotensive activity (4,5).

The biological effects of ADM are mainly mediated by its interaction with two cell-surface receptors, multimeric complexes of calcitonin receptor-like receptor (CRLR) and receptor-activity-modifying proteins (RAMPs). It is known that the RAMP family includes three members (RAMP1, RAMP2 and RAMP3) and regulates both transport and ligand specificity of CRLR. When RAMP2 or RAMP3 is associated with CRLR, adrenomedullin receptors 1 (AMR1) and 2 (AMR2) are generated, respectively, while RAMP1 is included in calcitonin gene-related peptide (CGRP) receptors (6,7).

Although ADM was first described as a potent vasodilator and hypotensive factor, several studies reported that it exerts

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Table I. Antibodies used for flow cytometric analysis.

Antibodies	Manufacturing company
<b>Primary antibodies</b>	
FITC rat anti-human CD11b	BD Biosciences
FITC mouse anti-human CD11c	BD Biosciences
PE mouse anti-human CD14	Santa Cruz Biotechnology
PE mouse anti-human CD31	Dako
FITC mouse anti-human CD33	BD Biosciences
FITC mouse anti-human CD34	BD Biosciences
Mouse anti-human CD38	Santa Cruz Biotechnology
PE mouse anti-human CD45	Santa Cruz Biotechnology
PE mouse anti-human cKIT	Santa Cruz Biotechnology
PE mouse anti-human HLA DR	Santa Cruz Biotechnology
FITC mouse anti-human Lineage cocktail 1 (CD3, CD14, CD16, CD19, CD20, CD56)	BD Biosciences
Goat anti-human ADM	Santa Cruz Biotechnology
Rabbit anti-human RAMP1	Santa Cruz Biotechnology
Rabbit anti-human RAMP2	Santa Cruz Biotechnology
Rabbit anti-human RAMP3	Santa Cruz Biotechnology
Goat anti-human CRLR	Santa Cruz Biotechnology
Rabbit anti-human Akt	Santa Cruz Biotechnology
Rabbit anti-human p(Ser473)-Akt	Santa Cruz Biotechnology
Rabbit anti-human p44/42 MAPK	Cell Signaling Technology
Rabbit anti-human phosho (Thr202/Tyr204)-p44/42 MAPK	Cell Signaling Technology
<b>Secondary antibodies</b>	
PE goat anti-mouse	Santa Cruz Biotechnology
PE donkey anti-goat	Santa Cruz Biotechnology
Alexa Fluor 488 goat anti-rabbit	Invitrogen-Life Technologies
<b>Isotype controls</b>	
PE isotype control	Santa Cruz Biotechnology
FITC isotype control	BD Biosciences

various biological activities acting in an autocrine/paracrine manner (8). ADM is produced and secreted by several cell types, such as neurons, epithelial and endothelial cells supporting their survival and/or proliferation (9). Compelling evidence has shown that adrenomedullin can contribute to the pathogenesis of solid tumors in several ways (10). Firstly, the hypoxic conditions induce an upregulation of the peptide in the tumor cells leading to stimulation of cell growth and inhibition of apoptosis (11). Secondly, ADM exerts proangiogenic effects thus providing nutrients and oxygen to the tumor and allowing the spreading of tumor cells (12). Thirdly, it decreases the expression of proinflammatory cytokines, thus, inhibiting the immune system (13).

ADM is involved in the regulation of hematopoietic compartment as demonstrated by its expression in peripheral blood granulocytes, lymphocytes, monocytes and monocyte-derived macrophages under homeostatic and lipopolysaccharide-induced inflammation (14-16). Notably, ADM stimulates the proliferation of human cord blood hematopoietic stem cells through autocrine mechanism (17,18).

Based on the above evidence and considering that ADM plays a critical role in cancer cell proliferation, the aim of

the present study was to evaluate whether ADM signaling is involved in the maintenance of impaired differentiation of APL cells to mature granulocytes or monocytes. Thus, the proliferative and differentiative effects induced by ADM and its inhibitor, ADM<sub>22-52</sub>, were evaluated *in vitro* at different time-points in HL60 cells, a human promyelocytic leukaemia cell line widely used to study granulocyte differentiation (19).

## Materials and methods

**Cell culture.** Human promyelocytic leukaemia cell line HL60 (kindly provided by CRO, Aviano, Italy) was grown in Iscove's medium (Sigma-Aldrich, St. Louis, MO, USA) supplemented with 10% fetal bovine serum (FBS; Sigma-Aldrich) and 1% antibiotic antimycotic solution (Sigma-Aldrich) at 37°C in a humidified atmosphere containing 5% CO<sub>2</sub>.

**Flow cytometry (FCM).** The expression level of endogenous ADM (ADM<sub>endo</sub>), RAMP1, RAMP2, RAMP3 and CRLR was studied in HL60 cells cultured under resting or primed conditions with exogenous ADM (ADM<sub>exo</sub>) and ADM<sub>22-52</sub>. After washing with 0.5% BSA in PBS, the samples were

Table II. Primer sequences used for RT-PCR and qPCR analysis.

Target	Sequence (5'-3')	Accession	Length (bp)
Peptidylglycine $\alpha$ -amidating monooxygenase (PAM)	F-GCGCAAGCACTTTGATATGCCTCA R-TCTGCAATTCTGAGGAGGTGGGTT	NM_000919.3	220
Cullin 5 (Cul5)	F-GAACCAAAGACCCAGAGAGAAA R-GTCCTCCTAAGTTCAGCATCAG	NM_003478.3	81
Glyceraldehydes 3-phosphate dehydrogenase (GAPDH)	F-AGGTCCGAGTCAACGGATTTGGT R-ACAAAGTGGTCGTTGAGGGCAATG	NM_002046.3	910
Hypoxanthine-guanine phosphoribosyltransferase (HPRT)	F-ATGGACAGGACTGAACGTCTTGCT R-TGAGCACACAGAGGGCTACAATG	NM_000194.2	79

F, forward; R, reverse.

incubated with primary antibodies (Table I) for 15 min at room temperature (RT). For indirect staining, the detection of specific binding sites was carried out by staining for 15 min at RT with Alexa Fluor<sup>®</sup> 488- or PE-conjugated secondary antibodies. For intracellular staining, HL60 cells were prefixed with BD Cytotfix/Cytoperm solution (BD Biosciences, San Josè, CA, USA) for 20 min at 4°C. Data were analyzed by FACSCanto II flow cytometer (BD Biosciences) and expressed as percentage (%)  $\pm$  standard deviation (SD) of positive cells compared with II antibody (Ab)- or isotype-matched controls. Statistical significance was calculated by Student's t-test.

**Gene expression study of PAM.** Total mRNA of HL60 cells was isolated using TRIzol<sup>®</sup> reagent (Sigma-Aldrich), according to the manufacturer's protocol. From each sample, 1  $\mu$ g total RNA was reverse transcribed into cDNA by using M-MLV reverse transcriptase (Sigma-Aldrich), and oligo (dT)<sub>23</sub> primers (Invitrogen-Life Technologies, Paisley, UK). The amplification reaction was performed by PTC-100 thermal cycler (Bio-Rad Laboratories, Hercules, CA, USA) using ReadyMix<sup>™</sup> Taq PCR Reaction Mix with MgCl<sub>2</sub> (Sigma-Aldrich), primer pairs designed to detect peptidylglycine  $\alpha$ -amidating monooxygenase (PAM) and housekeeping gene GAPDH (Table II). PCR products were electrophoresed on 2% agarose gel (Sigma-Aldrich) pre-stained with GelRed<sup>™</sup>, and then visualized by UV transilluminator Gel Doc 2000 Gel Documentation system (Bio-Rad Laboratories).

**ADM secretion assay.** The constant release of endogenous ADM into culture medium was studied in HL60 cells using protein transport inhibition. Cells were seeded at density of 1x10<sup>5</sup> cells/ml and then cultured for 12, 36 and 60 h in proliferation medium before incubation for 12 h at 37°C with GolgiPlug<sup>™</sup> (BD Biosciences). At 24, 48 and 72 h after plating, the samples were collected and then submitted to permeabilization with BD Cytotfix/Cytoperm solution. The analysis was performed by intracellular ADM staining followed by flow cytometric analysis, as above reported. In the present study, cultures untreated with GolgiPlug<sup>™</sup> were used as positive control of ADM secretion. The acquired data were analyzed by the overton subtraction tool of Summit 4.3 software

(Beckman Coulter, Inc., Brea, CA, USA) and were reported as percentage (%)  $\pm$  SD of ADM positive cells compared with relative II Ab-matched control.

**Treatment of HL60 cells with exogenous ADM and ADM<sub>22-52</sub>.** Cells were seeded in 25-cm<sup>2</sup> flasks at a density of 1x10<sup>5</sup> cells/ml and then cultured for 72 h with different concentrations of ADM (ranging from 0.625x10<sup>-8</sup> M to 5x10<sup>-8</sup> M) (Sigma-Aldrich) or 5x10<sup>-7</sup> M ADM<sub>22-52</sub> (Sigma-Aldrich) (13,18,20). In parallel, untreated cultures were used as reference. At the end of the treatment, growth assay and FCM analysis of endogenous ADM system were carried out. In parallel, cytospin preparations for May-Grunwald Giemsa staining were made to detect morphological changes of the nuclei.

**Growth assay.** At 72 h, cell suspensions were collected and then centrifuged at 1,200 rpm for 5 min at 4°C. After resuspension of pellets in 1 ml of Iscove's medium, HL60 cells were counted by Nexcelom Bioscience-Auto T4 Cellometer (Invitrogen-Life Technologies). Data are expressed as mean of total cell number  $\pm$  SD of three independent experiments performed in triplicate. Statistical analysis was performed using the Student's t-test.

**Investigation of PI3K/Akt and MAPK/ERK signaling pathways.** At different time-points (5, 15 and 30 min) after stimulation, the activation of PI3K/Akt and MAPK/ERK signaling pathways was evaluated in HL60 cells treated with 5x10<sup>-8</sup> M ADM and 5x10<sup>-7</sup> M ADM<sub>22-52</sub>. The analysis was performed by FCM as previously described, using antibodies specific for phosphorylated and unphosphorylated forms of Akt and MAPK enzymes (Table I). In parallel, untreated samples were used as reference. For each marker and its corresponding II Ab-matched control, data were reported as geometric mean fluorescence intensity (MFI)  $\pm$  SD. Statistical significance was calculated using the Student's t-test comparing primed cells with resting samples.

**Differentiative response of HL60 cells to ADM<sub>exo</sub> and ADM<sub>22-52</sub>**  
**Quantitative real-time polymerase chain reaction (qPCR).** The quantitative analysis of Cullin 5 (Cul5) gene expres-

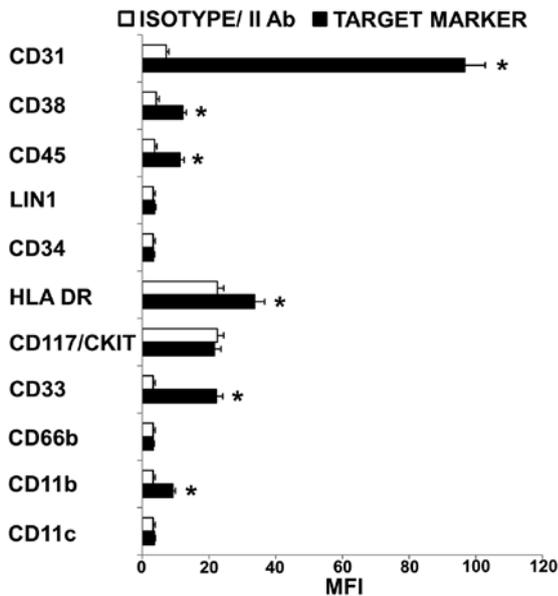


Figure 1. Characterization by flow cytometry of HL60 cells. Data were expressed as mean fluorescence intensity (MFI) ± SD. White bars, isotype- or secondary (II) Ab-matched control; black bars, target marker-matched samples.

sion was performed using Platinum® SYBR® Green qPCR SuperMix-UDG (Invitrogen-Life Technologies) and oligo primers (Invitrogen-Life Technologies) designed for the detection of Cul5 and hypoxanthine-guanine phosphoribosyltransferase (HPRT) housekeeping gene (Table II). The amplification reactions were performed using a DNA Engine

Opticon Real-Time Thermal Cycler (Bio-Rad Laboratories). The relative expression of Cul5 mRNA was determined using the  $\Delta\Delta C_T$  Livak method (21) and data were reported as fold increase calculated using the  $2^{-\Delta\Delta C_T} \pm SD$  equation.

**FCM.** At 72 h after stimulation with ADM<sub>exo</sub> and ADM<sub>22-52</sub>, the samples were collected and then analysed by flow cytometry to measure the expression of myeloid differentiation markers and adhesion molecules (CD45, CD34, CD66b, CD11b, CD11c, CD14, CD31 and CD38). The samples were prepared as described above using antibodies listed in Table I. For each marker, data were expressed as the ratio of geometric MFI (rMFI) ± SD derived from primed cells and relative resting samples. Statistical significance was calculated using the Student's t-test.

**Histochemistry.** Air-dried slides of cells were prepared using a Cytospin 4 (Thermo Fisher Scientific, Inc., Waltham, MA, USA) at 500 rpm for 5 min. The slides were fixed in methanol (Sigma-Aldrich) for 5 min and then stained for 5 min in 50% (v/v) May-Grunwald stain (Merck Millipore, Billerica, MA, USA) followed by 15 min in 10% Giemsa stain (Merck Millipore). Both stain solutions were freshly made using Sorenson's phosphate buffer (133 mM, pH 6.6). After staining, the slides were washed and destained for 5 min in the phosphate buffer.

**Results and Discussion**

**Immunophenotype of HL60 cells.** Before priming with ADM<sub>exo</sub> and ADM<sub>22-52</sub>, the immunophenotype of HL60 cells was explored by FCM evaluating the expression level

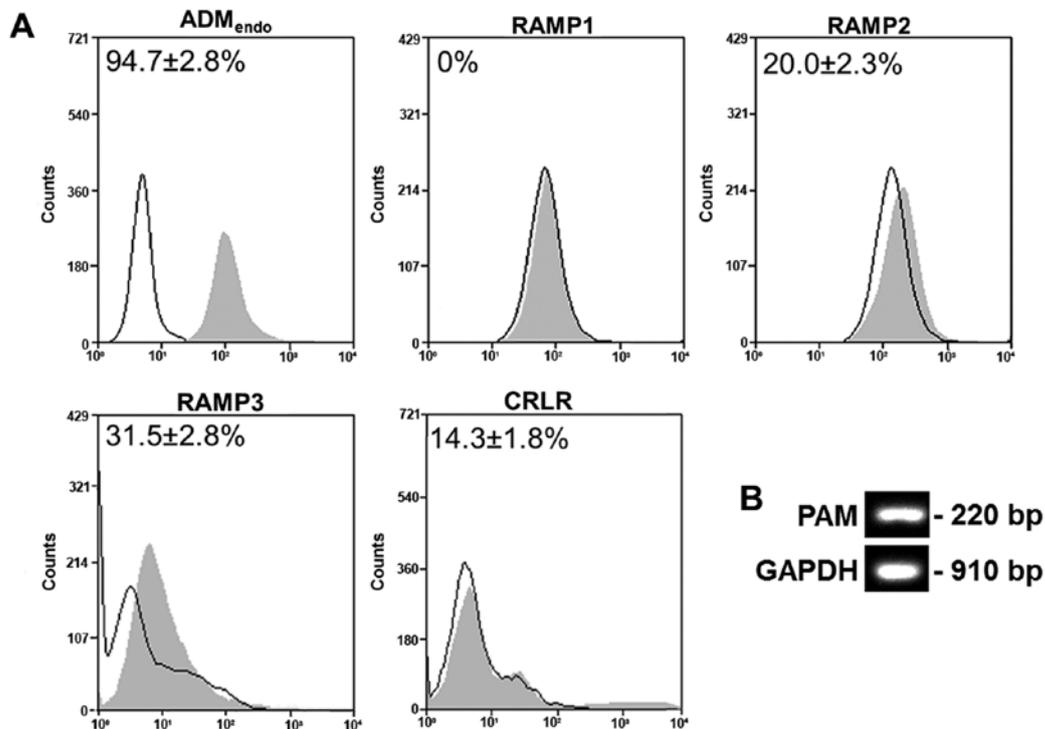


Figure 2. (A) The immunophenotypic analysis was performed by FCM to detect the expression of endogenous ADM (ADM<sub>endo</sub>), ADM receptors (RAMP1/2/3, CRLR) using specific primary antibodies and Alexa Fluor 488- and PE-conjugated secondary antibody. In parallel, secondary antibody-matched controls were used as reference. For each marker, the percentage (%) ± SD of positive cells (grey peak) was detected by the subtraction statistical tool of Summit 4.3 software using as reference II Ab-matched control (black peak). (B) Analysis by RT-PCR of PAM gene in HL60 cells cultured at basal conditions. In parallel, the expression of GAPDH housekeeping gene was considered. The amplification products were electrophoresed on 2% agarose gel and stained by GelRed™.

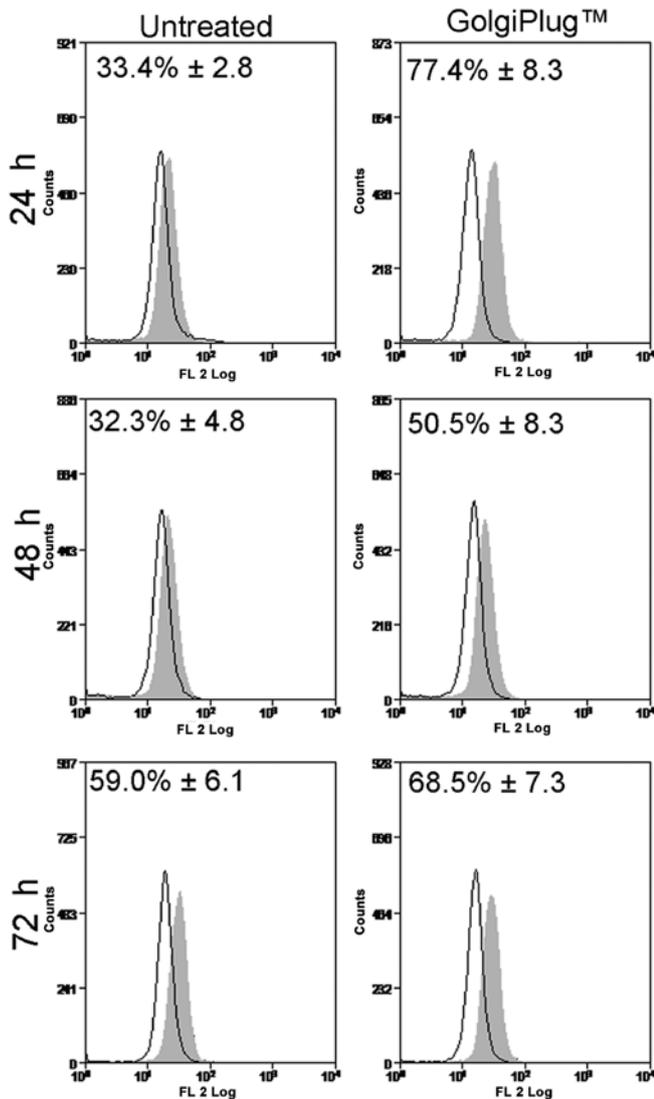


Figure 3. ADM secretion in HL60 cells was demonstrated using protein transport inhibition. Cells were cultured for 12, 36 and 60 h in proliferation medium before incubation for 12 h with Brefeldin A/GolgiPlug™. Thus, the samples were collected at 24, 48 and 72 h from plating and analyzed by intracellular ADM staining followed by flow cytometric analysis. In this analysis, cultures untreated with GolgiPlug™ were used as positive control of ADM secretion. The acquired data were expressed as a percentage (%) ± SD of ADM positive cells (grey filled peak) compared to II Ab-matched control (black profile).

of undifferentiated and differentiated state markers (Fig. 1). The myeloid phenotype was confirmed by the expression of CD33 while the presence of stem cell compartment was suggested by the absent expression of CD117/CKIT, Lin 1 and CD34 (22,23). Moreover, the undifferentiated state of cells was demonstrated by the negative or low fluorescence intensity of HLA-DR, CD45, CD11b, CD11c and CD66b (24-27). Among adhesion molecules expressed by acute myelogenous leukemia blasts, CD31 (28,29) and CD38 (30) are reported to play pivotal role in the interaction of tumor cells with microenvironmental elements, i.e. CD31 on the surface of marrow endothelial cells (CD31/CD31 and CD38/CD31 interactions) and hyaluronate (CD38/hyaluronate interactions). In the present study, an excess of CD31 relative to CD38 was detected (CD31/CD38 MFI ratio >1) suggesting that HL60 cells have a high potential

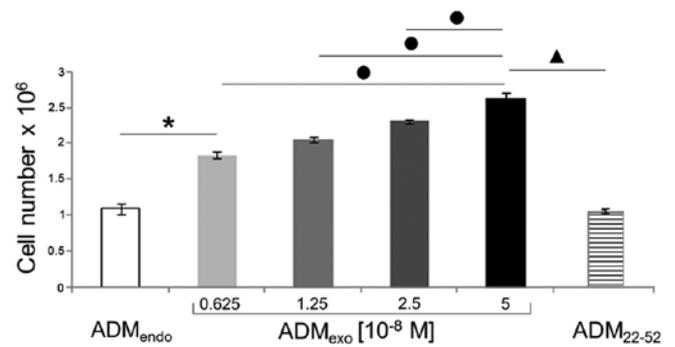


Figure 4. Proliferative effect of exogenous ADM solutions (from  $0.625 \times 10^{-8}$  M to  $5 \times 10^{-8}$  M) and  $5 \times 10^{-7}$  M ADM<sub>22-52</sub> on HL60 cells cultured for 72 h. Untreated cultures (ADM<sub>endo</sub>) were used as reference. Bars are means ± SD (n=10). \*P<0.05 using the Student's t-test. \*P<0.05 vs. ADM<sub>endo</sub> reference group; •P<0.05 and ▲P<0.05 vs.  $5 \times 10^{-8}$  M ADM<sub>exo</sub>.

of transendothelial migration (31-33). Similar expression level of CD31, CD33, CD38 in HL60 and APL cells was considered important to define a prospective correlation between *in vitro* and *in vivo* conditions.

**HL60 cells express ADM and its receptors.** As reported in Fig. 2A, HL60 cells were shown to express ADM<sub>endo</sub> ( $94.7 \pm 2.8\%$ ), RAMP2 ( $20.0 \pm 2.3\%$ ), RAMP3 ( $31.5 \pm 2.8\%$ ) and CRLR ( $14.3 \pm 1.8\%$ ). In contrast, RAMP1 was not detected. The gene expression of peptidylglycine  $\alpha$ -amidating mono-oxygenase (PAM), that is the enzyme producing  $\alpha$ -amidated bioactive peptide from the inactive precursor (34), confirmed the potential of cells to synthesize the active form of ADM (Fig. 2B). Produced by peripheral blood mononuclear and polymorphonuclear cells, ADM is known to regulate cell growth or differentiation through an autocrine mode of action (15). As shown in Fig. 3, the release of ADM endogenously synthesized by HL60 cells was evaluated using Brefeldin A/GolgiPlug™ kit, a protein transport inhibitor that is able to prevent the secretion process and to trap peptides into intracellular compartments. The increased immunoreactivity for ADM in GolgiPlug™-treated samples (24 h,  $77.4 \pm 8.3\%$ ; 48 h,  $50.5 \pm 8.3\%$ ; and 72 h,  $68.5 \pm 7.3\%$ ) compared to untreated cells (24 h,  $33.4 \pm 2.8\%$ ; 48 h,  $32.3 \pm 4.8\%$ ; and 72 h,  $59.0 \pm 6.1\%$ ) was interpreted as indicative of the cytoplasmic accumulation of ADM<sub>endo</sub> while the decreased fluorescent signal suggested that HL60 constitutively secrete ADM into culture medium after synthesis, as previously reported (15).

**ADM<sub>exo</sub> enhances the proliferation of HL60 cells.** It is known that ADM is produced not only by cancer cells but also by endothelial, macrophages, and mast cells of tumor microenvironment (35), where it contributes to cancer pathogenesis both directly stimulating cancer cell growth or indirectly inducing angiogenesis and reducing the effectiveness of the immune system.

Our data (Fig. 4) show that exogenous ADM exerted a strong proliferative effect on HL60 cells, as already observed in several cell types (36-39). Indeed, after a 72 h incubation period, significant increases in cell number were detected in cultures treated with ADM<sub>exo</sub> compared to resting cells. In particular,  $5 \times 10^{-8}$  M ADM was shown to be the most effective

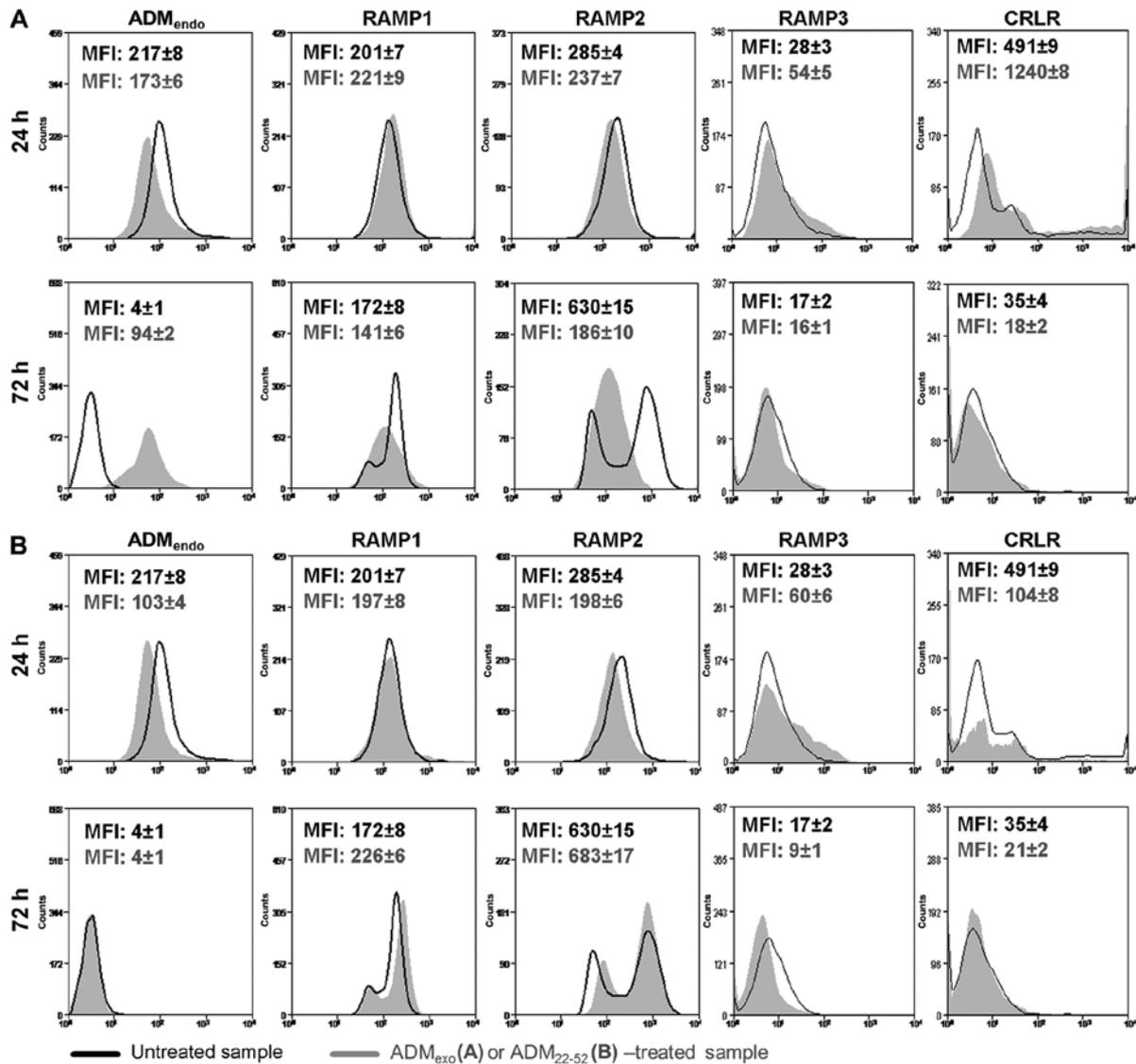


Figure 5. Expression of ADM<sub>endo</sub>, RAMP1, RAMP2, RAMP3 and CRLR in HL60 cells cultured for 24 and 72 h with  $5 \times 10^{-8}$  M ADM<sub>exo</sub> (A) or  $5 \times 10^{-7}$  M ADM<sub>22-52</sub> (B) solubilized in growth medium. The positive expression of each marker was expressed as mean fluorescence intensity (MFI)  $\pm$  SD. Grey peak, samples treated with ADM<sub>exo</sub> or ADM<sub>22-52</sub>; black profile, untreated samples. The profiles are representative of three independent experiments.

concentration. In contrast, ADM<sub>22-52</sub> demonstrated not to affect the proliferation of HL60 cells, since total cell number in primed cultures was comparable to that of untreated samples.

**ADM<sub>exo</sub> and ADM<sub>22-52</sub> affect the ADM system.** In the present study, we explored by FCM the modulation of adrenomedullin system (ADM<sub>endo</sub> and its receptors) in HL60 cells treated with exogenous  $5 \times 10^{-8}$  M ADM or  $5 \times 10^{-7}$  M ADM<sub>22-52</sub>. When HL60 cells were *in vitro* cultured with ADM<sub>exo</sub> (Fig. 5A) and ADM<sub>22-52</sub> (Fig. 5B), a different expression profile of ADM<sub>endo</sub> was detected in comparison to resting samples. In particular, at 24 h, a decreased immunoreactivity for ADM was observed in primed samples suggesting that, probably due to an increased level of intracellular Ca<sup>2+</sup> (40), a major release of endogenous ADM was promoted. At 72 h, the secretion rate of ADM was negatively controlled by ADM<sub>exo</sub> (Fig. 5A) but not under treatment with ADM<sub>22-52</sub> (Fig. 5B). It is known that the expression of RAMP isoforms may change between physiological and pathological conditions (41), determining the degree of cell

response to ADM. The cell sensitivity to ADM stimulation is defined both by a balanced expression of RAMPs and CRLR at cell membrane and their rapid rate of recycling. It is reported that RAMPs play pivotal roles in the transport of CRLR to plasma membrane (42). At physiological conditions, the most abundant isoform is RAMP2. Under pathological conditions, significant changes in RAMP expression levels are active under a concomitant increase in plasma ADM level (43). In the present study, the expression of AMR1 (CRLR/RAMP2), AMR2 (CRLR/RAMP3) and CGRP (CRLR/RAMP1) components was demonstrated to be altered following the treatment with exogenous ADM and ADM<sub>22-52</sub>. Indeed, at 24 h, ADM<sub>exo</sub> upregulated RAMP1, RAMP3 and CRLR (Fig. 5A) while ADM<sub>22-52</sub> was effective in increasing the expression of RAMP3, but drastically reduced CRLR (Fig. 5B). In both primed groups, probably due to a receptor degradation after internalization (43), RAMP2 significantly decreased (Fig. 5), suggesting that ADM<sub>exo</sub> and ADM<sub>22-52</sub> mediated their activity at early phase by AMR1. These data were in accordance with

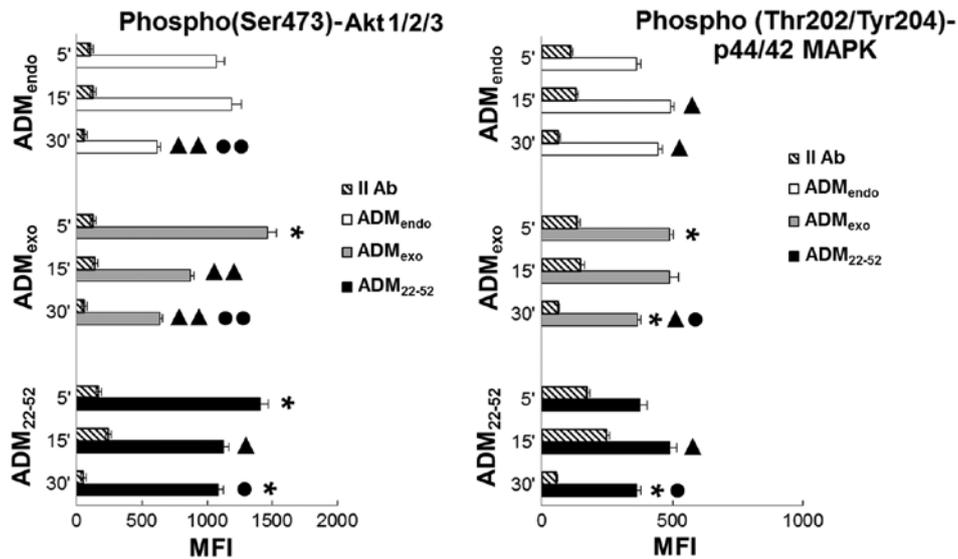


Figure 6. Changes in the activation state of Akt and MAPK upon treatment with  $5 \times 10^{-8}$  M  $ADM_{exo}$  and  $5 \times 10^{-7}$  M  $ADM_{22-52}$ . The samples were collected at 5, 15 and 30 min from stimulation and analyzed by intracellular detection of phospho(Ser473)-Akt1/2/3 and phospho(Thr202/Tyr204)-p44/42 MAPK followed by flow cytometric analysis. In parallel, untreated cultures ( $ADM_{endo}$ ) were used as reference. Hatched bars, II Ab-matched control; white bars, untreated samples ( $ADM_{endo}$ ); grey bars,  $ADM_{exo}$ -treated samples; black bars,  $ADM_{22-52}$ -samples. Bars are means  $\pm$  SD (n=3). \*P<0.05 vs. relative value of  $ADM_{endo}$  reference group;  $\blacktriangle$ P<0.05 and  $\blacktriangle\blacktriangle$ P<0.01 vs. relative value detected at 5 min in each experimental group;  $\bullet$ P<0.05 and  $\bullet\bullet$ P<0.01 vs. relative value detected at 15 min in each experimental group.

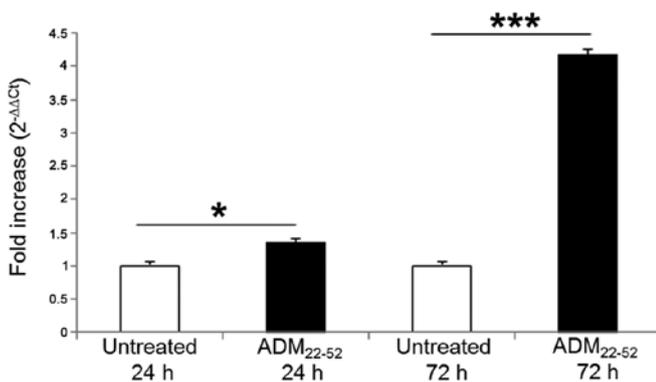


Figure 7. Quantitative RT-PCR analysis of Cul5 expression in HL60 cells treated with  $5 \times 10^{-7}$  M  $ADM_{22-52}$  or untreated ( $ADM_{endo}$ ) for 24 and 72 h. In parallel, the expression of HPRT housekeeping gene was evaluated. The relative expression of Cul5 mRNA was determined using the  $\Delta\Delta CT$  method. Data are reported as the fold difference calculated from the equation  $2^{-\Delta\Delta CT} \pm$  SD. \*P<0.05 and \*\*\*P<0.01 vs.  $ADM_{endo}$  reference group.

the hypothesis that an excess of ADM in bone marrow matrix could increase the responsiveness of leukemia cells to ADM upregulating CRLR, RAMP1 and RAMP3 (44), while the inhibition of ADM signaling could raise the cell insensitivity to stimulation by a significant reduction of ADM receptor system. At 72 h, a correlation between the increased expression level of RAMP1/2 and the release of ADM was observed in resting samples suggesting that HL60 cells could combine the release of ADM with the exposure of ADM receptors at cell membrane to control their growth. Notably, the treatment of HL60 cells with exogenous ADM reduced the release of  $ADM_{endo}$  and the expression of RAMP1 and RAMP2 while no change was induced by  $ADM_{22-52}$  compared to resting cells. The expression of RAMP3 and CRLR was drastically reduced at 72 h in all experimental groups. Unlike previously reported

by Poyner *et al* (42),  $ADM_{22-52}$  exerted inhibitory activity of ADM signaling in leukemia cells through a negative regulation of CRLR expression, either by an increased receptor internalization followed by degradation or a block of receptor transport to plasma membrane.

*AKT and MAPK signaling pathways were differently modulated by  $ADM_{exo}$  and  $ADM_{22-52}$ .* Pleiotropic effects of ADM are reported to be mediated through several intracellular signal transduction pathways (43). Using HL60 leukemia cells, we explored by FCM the modulation exerted by  $5 \times 10^{-8}$  M ADM and  $5 \times 10^{-7}$  M  $ADM_{22-52}$  on PI3K/Akt and ERK/MAPK signaling pathways, that are involved in several haematopoiesis malignancies, including AML (45-49). As shown in Fig. 6, the simultaneous detection of p(Ser473)-Akt1/2/3 and phospho(Thr202/Tyr204)-p44/42 MAPK in resting cells ( $ADM_{endo}$ ) suggested a constitutive activity of both pathways in HL60 cells. Hayashi and colleagues (50) reported that PI3K/Akt positively regulates the MAPK cascade, facilitating maximal ERK responses to physiological stimuli, whereas activated ERK, in turn, negatively controls the PI3K/Akt pathway. In the present study (Fig. 6), the phosphorylation level of Akt in  $ADM_{endo}$  reached the maximum value at 5 to 15 min and decreased at 30 min. In parallel, the upregulation in MAPK activity from 15 to 30 min could be indicative of a reciprocal regulation loop between Akt and MAPK. Notably, the stimulation of HL60 with  $ADM_{exo}$  and  $ADM_{22-52}$  differently affected the activity of both pathways. Under stimulation with  $ADM_{exo}$ , an increase in the expression level of p(Ser473)-Akt and phospho(Thr202/Tyr204)-p44/42 MAPK was observed at 5 min indicating that HL60 cells were responsive to exogenous ADM via the PI3K/Akt and ERK/MAPK cascade. In samples treated with  $ADM_{exo}$  compared to  $ADM_{endo}$  group, the activation level of MAPK unchanged from 5 to 15 min

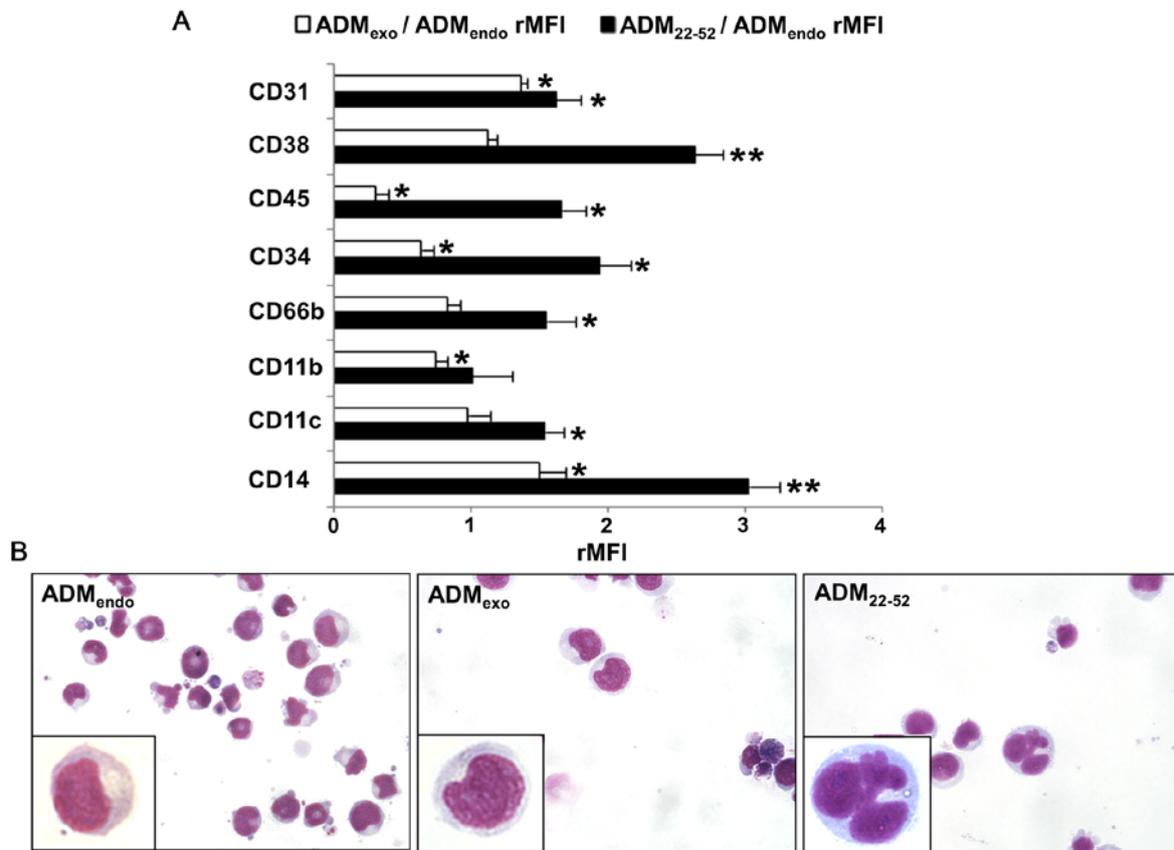


Figure 8. (A) Expression of differentiation markers in HL60 cells stimulated with  $5 \times 10^{-8}$  M ADM<sub>exo</sub> or  $5 \times 10^{-7}$  M ADM<sub>22-52</sub> for 72 h. The analysis was performed by flow cytometry and data are reported as the ratio of geometric mean fluorescence intensity (rMFI) obtained for samples treated with ADM<sub>exo</sub> or ADM<sub>22-52</sub> and untreated (ADM<sub>endo</sub>) cultures. White bars, ADM<sub>exo</sub>/ADM<sub>endo</sub> rMFI; black bars, ADM<sub>22-52</sub>/ADM<sub>endo</sub> rMFI. \* $P < 0.05$  and \*\* $P < 0.01$  vs. rMFI value  $\neq 1$ . (B) Morphological analysis by May Grunwald-Giemsa staining of untreated (ADM<sub>endo</sub>) and treated cells with ADM<sub>exo</sub> or ADM<sub>22-52</sub>. Low magnification,  $\times 400$ ; high magnification,  $\times 1,000$ .

while a significant decrease in phosphorylated Akt expression was observed. In contrast, the stimulation with ADM<sub>22-52</sub> promoted the maximum activation of Akt at 5 to 30 min and a downregulation of MAPK activity at 30 min. Based on this evidence, we hypothesized that the activity of ADM<sub>exo</sub> was mainly mediated by the ERK/MAPK pathway while that of ADM<sub>22-52</sub> was especially involved in PI3K/Akt signaling.

#### ADM<sub>22-52</sub> induces a strong differentiative induction on HL60 cells

*qPCR*. To verify the differentiative induction after the inhibition of ADM system, the expression of Cul5 was assessed by quantitative RT-PCR (Fig. 7). Cul5 belongs to the *Cullins* gene family, including 7 isoforms identified in mammals. Cul5, Asb-2 (ankyrin repeat SOCS box 2), a RING finger protein (ROC/Rbx), and an adapter protein complex (elongin B/C) form an E3 ubiquitin ligase complex that, due to an E2 ubiquitin-conjugating enzyme, leading to the degradation of target proteins by 26S proteasome (51). As component of this complex, Cul5 brings the enzyme the substrate recognition components (52). Furthermore, it seems to act as tumor suppressor in breast cancer (53) and its expression decreases in B-cell chronic lymphocytic leukemia (54). At 24 and 72 h after stimulation with ADM<sub>22-52</sub>, Cul5 mRNA increased 1.35- and 4.18-fold, respectively, in primed cells vs. resting cultures. Our data were in agreement with the increase of Cul5 mRNA and

protein detected by Baxter *et al* (19) during ATRA-mediated differentiation of HL60 cells.

*FCM*. Several reports highlighted that PI3K/Akt and ERK/MAPK signaling pathways control the self-renewal and differentiation of leukemia cells. Akt was demonstrated to exert its activity (55) activating nuclear factor-kappa B (NF- $\kappa$ B) (56), phosphorylating GSK-3 (57) and inhibiting transcription factors of FOXO family (58). Marcinkowska *et al* (59) demonstrated that ERK/MAPK pathway stimulates the monocytic differentiation of HL60 cells through the phosphorylation of transcription factor C/EBP $\beta$ . As shown in Fig. 8A, the treatment with  $5 \times 10^{-8}$  M ADM<sub>exo</sub> was accompanied by an upregulation in the expression level of CD14 and CD31, which are associated with monocytic differentiation of HL60 cells (59,60). Interestingly, a decreased (rMFI<1) or unchanged (rMFI=1) expression level of other markers was observed in comparison to resting samples (ADM<sub>endo</sub>), suggesting that ADM<sub>exo</sub> could exert a negative control on the granulocytic differentiation process. In samples treated for 72 h with ADM<sub>22-52</sub>, FCM analysis evidenced a significant increase in the expression level of CD11b, a subunit of  $\alpha$ M $\beta$ 2 integrin, CD11c, an integrin  $\alpha$ X, and CD66b, a granulocyte-specific activation antigen expressed on secondary granule membranes, that are all associated with granulocytic differentiation of HL60 cells (21,61,62). Moreover, we observed the upregulation of CD45

and CD38, that are reported to increase during myeloid maturation (63,64) and ATRA-induced granulocytic/monocytic differentiation (24,64). The increased MFI value of CD14 in ADM<sub>22-52</sub> compared to that of ADM<sub>endo</sub>-samples further confirmed the granulocytic/monocytic maturation of HL60 cells (65). It is known that the expression of CD31 and CD38 on leukemic cells could exert a balanced control between extramedullary dissemination and marrow retention of leukemic cells. As previously demonstrated in ATRA-induced HL60 differentiation (66), an excess of CD38 relative to CD31 (CD31/CD38 MFI ratio <1) was detected in ADM<sub>22-52</sub>-treated cells, suggesting a higher retention of cells in bone marrow through the interaction with hyaluronate. In contrast, the excess of CD31 relative to CD38 (CD31/CD38 MFI ratio >1) in samples treated with ADM<sub>exo</sub> evidenced an increased ability of transendothelial migration.

**Histochemistry.** To investigate HL60 cell differentiation, nuclear morphology of cells stained with May-Grunwald-Giemsa was performed (Fig. 8B). In ADM<sub>exo</sub>-treated cells, only ovoid and intended nuclei were detected, whereas ADM<sub>22-52</sub> determined the appearance of differentiated cells characterized by several multilobulated segmented nuclei.

## Conclusions

Understanding the aberrant expression of self-renewal pathways in myeloid malignancies is an emerging area of investigation for the development of novel treatment strategies. Extrinsic factors driven by bone marrow microenvironment are reported to regulate the growth of hematopoietic stem cells (67) within supportive osteoblastic and vascular niches (68). Among the soluble factors secreted in BM niches by stem cells (69) and stromal compartment (10), ADM synergizes with stem cell factor and Flt-3 (FMS-like tyrosine kinase-3) ligand to induce the proliferation of primitive human CD34<sup>+</sup>CD38<sup>lin</sup> cells and to promote the expansion of CD34<sup>+</sup> progenitors in culture (70). The development of hematopoietic malignancies causes a remodeling of BM microenvironment followed by the alteration of HSC function, leukemia survival, protection of cancer cells from apoptotic stimuli and development of drug-resistant phenotype (67,71). Hypoxic conditions in leukemia niche are demonstrated to support the progression of cancer and to upregulate ADM (72), thus, suggesting a correlation between the survival of leukemia cells and the increased release of ADM in tumor microenvironment (10). Consistent with the above evidence, and studies in several human tumor cell lines, including HL60 and chronic monocytic leukemia (U937) (73), our results suggest for ADM a regulatory role in the proliferation of APL by paracrine effects, as already demonstrated for ADM in modulating the activity of the hypothalamo-pituitary-adrenal axis (74), the growth of cardiac and vascular smooth muscle cells (75), the hemodynamics of brain, lungs, and kidneys (76), physiological and pathological angiogenesis (12). Using the *in vitro* model of HL60 cells, we demonstrated that exogenously administered ADM preserves promyelocytic leukemia cells from differentiation as shown under ADM signaling inhibition with ADM<sub>22-52</sub> by the detection of typical differentiation features such as multilobulated segmented nuclei, Cul5 expression and increased expression level of

granulocytic and monocytic antigens. As the treatment with exogenous ADM significantly stimulated the growth of HL60 cells, we speculated that paracrine ADM acts in APL niche supporting the survival of leukemia cells and promoting their transendothelial migration upregulating the cellular expression of CD31 (64). Based on the consideration that ADM<sub>22-52</sub> stimulates both the maturation and the retention in the bone marrow of leukemia cells through an increased expression of CD38, as previously demonstrated in HL60 and human primary APL cells treated with ATRA (64), our data provide strong evidence for the therapeutical potential that the inhibition of ADM signaling could have in the treatment of APL. A potentially important therapeutic effect of the blockade of ADM<sub>22-52</sub>-sensitive receptors has been already demonstrated for endotoxic shock (77) and expansion of keratinocytes, fibroblasts (78) and adrenal cortical cells (79).

Further studies will be necessary to verify ADM expression in bone marrow microenvironment and its involvement in the induction and progression of hematopoietic malignancy.

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