# Epigenetic effects of decitabine on acute lymphoblastic and acute promyelocytic leukemia cells

Sina Dalvand MSc<sup>1</sup>, Fatemeh Pourrajab PhD<sup>2,3</sup>, Soudeh Moghadasi PhD<sup>3</sup>, Seyedhossein Hekmatimoghaddam PhD<sup>4,5,\*</sup>

- 1. International Campus, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
- 2. Nutrition and Food Security Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
- 3. Department of Biochemistry and Molecular Biology, School of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
- 4. Hematology & Oncology Research Center, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.
- 5. Department of Advanced Medical Sciences and Technologies, School of Paramedicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
- \*Corresponding author: Dr Seyedhossein Hekmatimoghaddam, Department of Advanced Medical Sciences and Technologies, School of Paramedicine, Mojtame Emam Reza, Daneshjoo Blvd, Yazd, Iran. Postal code: 8916188635; Mobile: +989133518314; Fax: +98 3536238561; E-mail: shhekmati2002@yahoo.com; hekmati@ssu.ac.ir. ORCID ID: 0000-0001-9859-3753

Received: 01 November 2019 Accepted: 28 March 2020

#### Abstract

**Background:** Decitabine (5-aza-2'-deoxycytidine, DAC) is a deoxycytidine analog currently used as an effective drug against myelodysplastic syndromes and acute myeloid leukemia. Although various studies have pointed out the epigenetic effects of this drug, its epigenetic mechanisms in different leukemic cell lines are not specified. In this lab trial study, possible epigenetic effects of decitabine on leukemia cell lines Hl-60 (acute promyelocytic leukemia) and Nalm-6 (acute pre-B cell lymphoblastic leukemia) vs. normal peripheral blood mononuclear cells (PBMCs) are compared.

Materias and Methods: At the logarithmic phase of growth, the cultured cells Hl-60 and Nalm-6 obtained from Tehran Pasteur Institute, Iran, were treated for 24 hr with 1  $\mu$ M of decitabine, a dose selected from literature and the MTT viability assay. Normal PBMCs were obtained from a pool of 3 healthy adult volunteer males, and cultured simultaneously in the same manner. The gene expressions of epigenetic enzymes DNA methyltransferases (DNMTs) were assessed with the real-time PCR technique before and after treatment. The GAPDH gene expression served as the calibrator, while normal PBMCs were used for comparison.

**Results:** The expressions of DNMT1 and DNMT3B in lymphoblasts were significantly (p=0.0017 and p=0.0489, respectively) decreased after treatment with decitabine, while the expression of DNMT3A was significantly (p=0.0022) increased. In leukemic promyelocytes the expressions of DNMT1 and DNMT3B in lymphoblasts were significantly (p=0.0222 and p=0.0452, respectively) decreased after treatment with decitabine, while the expression of DNMT3A was significantly (p=0.0013) increased.

**Conclusion:** One of the mechanisms by decitabine to inhibit the proliferation of both myeloid and lymphoid acute leukemia cells maybe by altering the gene expression of DNMTs.

Keywords: Decitabine; DNA methyltransferase 1; Epigenesis; Gene expression; Leukemia

#### Introduction

Acquired hematopoietic disorders are a group of blood diseases known to be induced by epigenetic modifications and can be characterized by changes in DNA methylation (1, 2). Acute myeloblastic leukemia (AML) is a malignancy of the hematopoietic myeloid cells, characterized by the rapid proliferation of genetically

abnormal leukocytes that build up in the bone marrow and interfere with the production of normal blood cells. AML is the most common acute leukemia affecting adults, and its incidence increases with age (3).

In addition to genetic variations, AML can also be characterized by epigenetic changes in the neoplastic cells. One of the most significant epigenetic alterations in these malignancies occurs in DNA methylation and histone modifications which affect expression the gene throughout the cell cycle (3, 4). The relationship between aberrant DNA methylation and various types of human cancers has been indicated over the past decade and has been a major research field aimed at finding effective drugs for cancer therapy (5, 6).

Aberrant DNA methylation can result in the silencing of tumor suppressor genes contributes which likely pathogenesis of AML. Aberrant DNA methylation can be reversed pharmacologically by inhibitors of DNA methyltransferases (DNMTs) (7, 8). Azanucleotide analogs such as decitabine (5aza-2'-deoxycytidine, DAC) have been introduced as DNA anti-methylation agents that act as DNMT inhibitors. Decitabine has been an effective drug and approved for the treatment of patients with myelodysplastic syndromes (MDS) as well as AML (8-15). Decitabine is transported into the cells where it is phosphorylated by deoxycytidine kinase (dCK) followed by conversion to active metabolite decitabinetriphosphate (decitabine-TP) which competes with endogenous dCTPs for incorporation into the DNA (16-18). It seems that a reduction in overall activity of DNMTs may be a strong demethylation activity by decitabine at zones that are normally hypermethylated, promoters of tumor suppressors or the genes necessary to control the cellular differentiation and multiplication (17, 19). However, the exact mechanisms of this DNMT inhibitor activity have not yet been clearly defined (9, 13).

Mammals have five DNMT enzymes (DNMT1, DNMT2, DNMT3A, DNMT3B and DNMT3L) but only DNMT1, DNMT3A and DNMT3B have a DNA methylation activity. In differentiating cells, the DNA methylation template is determined during primary development by de novo methyltransferases DNMT3A

and DNMT3B. However, in proliferating cells, the template of DNA methylation is propagated through excessive loyalty by the preservation of methyltransferase DNMT1 (20-24).

Though the level of DNMT expression and activity in normal cells is relatively stable, wide changes are expected to happen in cancer cells that lead to universal hypomethylation of the genome along with focal hypermethylation at promoter CG islands leading to silencing of the most critical tumor-suppressor genes including p21, RB1 and CDKN2A (25-27). Also, several studies report increases in the expression of de novo DNMTs in various cancers, which can contribute to the development of leukemia by inducing hypermethylation of tumor suppressor genes (28-30). As a result, abnormal expression of de novo DNMTs may serve as a marker for cancer cells and also as a potential target for future cancer therapy. Although various studies have pointed out the epigenetic effects of this drug, its epigenetic mechanisms in different cell lines are not specified. The aim of this lab trial study was to investigate possible impact of the effective chemotherapy drug decitabine on the expression profile of DNMTs in leukemic cell lines Hl-60 (acute promyelocytic leukemia) and Nalm-(acute pre-B cell lymphoblastic leukemia) compared to normal blood cells.

# Materials and Methods

#### Cell cultures

This study was approved by the ethics committee in Shahid Sadoughi University of Medical Sciences, Yazd, Iran (IR.SSU.MEDICINE.REC.1396.55). The human leukemia promyelocyte cell line Hl-60 and lymphoblastic cell line Nalm-6 were obtained from the Tehran Pasteur Institute, Iran. Normal peripheral blood mononuclear cells (PBMCs) were obtained from a pool of 3 healthy adult volunteer

males who had no disease sign or symptom and didn't have medication use. The cells were cultured in RPMI 1640 medium (GIBCO Invitrogen, US) containing 10% fetal bovine serum Invitrogen, (GIBCO US) and 1% penicillin/streptomycin (Sigma-Aldrich, US) in a humidified condition at 37 °C with 5% CO<sub>2</sub>.

# Cell treatment with decitabine

The cells were seeded at a density of 10<sup>5</sup> cells/mL in 6-well plates (Jet Biofiltration Co., China). When the cells arrived at logarithmic growth phase, the cultures were treated with 0.1, 1 and 5 µM of decitabine (Sigma-Aldrich, US) for 24, 48 and 72 h, with final selection of the optimal time regarding average proliferations. Finally, the selected dose was 1 µM according to literature and our data obtained from MTT viability assay which showed the highest possible (more than 90%) viability for normal cells. All the experiments were performed in independent triplicates (31, 32).

# MTT assay

The cytotoxicity of decitabine investigated by the MTT assay kit. After incubation of the cells in 96-well plate, they were treated with decitabine with concentrations of 0.5, 1 and 5 µL for 24, 48 and 72 hours. For testing, 10 μL of the MTT (Sigma-Aldrich, US) reagent at 5 mg/mL concentrations were added to each well and the plates were placed in the incubator for 4 hours. In the next step, the culture medium was removed and 100 µL of DMSO 100 added to each well and placed in the incubator to dissolve the formazan purple crystals. The absorbance of wells at 578 nm was read by the enzyme-linked immunosorbent (ELISA) reader (BioTek, US), and the growth percentage of the cells calculated. Finally, the obtained mean of three times (24, 48 and 72 h) was used for calculation of  $LC_{50}$  and the cells were treated with this dose.

# Quantitative polymerase chain reaction (qPCR)

Total cellular RNA was extracted using a TRIzol® kit (Invitrogen, Thermo Fisher Scientific, US). The cDNA was obtained from the cDNA Synthesis Kit (Thermo Fisher Scientific, US). For qPCR, cDNA (1 μL) was mixed with EvaGreen® qPCR Mix Plus (Solis BioDyne, Estonia), and the following primers were used: DNMT1 forward: 5'-CCT CAG GGA CCA CAT CTG TA- 3' and reverse: 5'-TCT TCC TGT CAT GGT GGG TA-3'; DNMT3A forward: 5'- GCC CAA GGT CAA GGA GAT TA- 3' and reverse: 5'- CAG ATG TCC TCA ATG TTC CG-3'; DNMT3B forward: 5'- CCT TCT TCA CCA GTG ACA CG-3' and reverse: 5'- CCA TGA CAG GAC TCG AAT GG- 3'; which were designed and synthesized by Pishgam Biotech Co, Iran. Temperature protocol for qPCR was: 95 °C for 10 min, 95 °C for 15 sec, 60 °C for 20 sec, 72 °C for 25 sec, 72 °C for 10 min. Real-time PCR reactions were performed in triplicate. The statistical tests performed were t-test and analysis of variance. The relative gene expression was calculated according to the  $2^{-\Delta\Delta Ct}$  formula.

### Results

# Cell treatments, MTT assay

In the first step, to assess the real effect of decitabine on the gene expression of DNMTs, we tried to carefully create a reversible and low-toxicity situation for cells to investigate changes occurred in DNMTs' gene expression after treatment with the drug. The Hl-60 and Nalm-6 cells were treated with the selected dose (1  $\mu$ M)

of decitabine for 24, 48 and 72 h based on MTT test results. This low concentration of the drug allows the intracellular cycles to be active. A substantial cellular toxicity would be associated with higher concentrations (33,34) and was undesirable because of secondary effects related to apoptosis that would interfere with the primary gene expression changes induced by the drug. Furthermore, highdose protocols of DNMT inhibitors are no longer recommended clinically. The low dose of decitabine assessed in this experiment is comparable to the potential concentration of decitabine in the plasma previous treatment regimen therapies and may induce hypomethylation of DNA (35).

# Confirming the specificity and selectivity of the qRT-PCR method for gene expression

After the decitabine treatment and confirming the cell viability of more than 90%, the expression profile of the epigenetic genes DNMT1, 3A, 3B was investigated. Also, to confirm the real-time

PCR assay specificity and selectivity, the qRT-PCR products were loaded onto the gel. Figure 1 shows the bands, confirming the real-time PCR specificity and selectivity.

# The expression profiles of *DNMT1*, 3A, 3B in Hl-60 and Nalm-6 cells compared to the normal cells

After normalization with GAPDH and in comparison to the expression profile of these genes in normal PBMCs, the fold changes in expression of DNMT1, 3A and 3B in Hl-60 cells and also in Nalm-6 cells were obtained, which reveal significant (p<0.05) alteration toward their level in after normal cells treatment decitabine (Table I and Figures 2, 3, 4, 5, 6, 7). Since the relative fold changes vary, the figures are not merged. In all cases, the difference in gene expression of DNMTs between normal PBMCs and leukemic cells before treatment were significant (P values not shown).

Table I: Fold changes in expression of DNMT1, 3A, 3B in decitabine-treated Hl-60 and Nalm-6 cell lines vs. the healthy control group (as a calibrator), after normalization to GAPDH (P values compare before treatment vs. after treatment).

Gene	Control group	Cell line	Cell line before treatment	Cell line after treatment	P-value
DNMT1, mean ± SD	$1.005 \pm 0.147$	Hl-60	$5.238 \pm 1.345$	$1.379 \pm 0.222$	0.0222
DNMT1, mean <u>+</u> SD	$1.002 \pm 0.093$	Nalm-6	$8.063 \pm 0.513$	$1.837 \pm 0.776$	0.0017
DNMT3A, mean ± SD	1.02 ± 0.286	Hl-60	$0.179 \pm 0.059$	$3.438 \pm 0.235$	0.0013
DNMT3A, mean ± SD	$1.020 \pm 0.286$	Nalm-6	$0.400 \pm 0.289$	$4.25 \pm 0.062$	0.0022
DNMT3B, mean ± SD	$0.966 \pm 0.061$	Hl-60	$5.790 \pm 1.569$	$0.715 \pm 0.021$	0.0452
DNMT3B, mean <u>+</u> SD	$1.003 \pm 0.122$	Nalm-6	$5.790 \pm 1.569$	$2.65 \pm 0.49$	0.0489

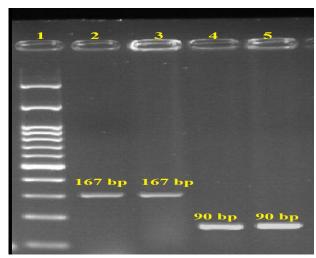


Figure 1. Gel patterns of real-time PCR (qRT-PCR) products of *DNMT1*, *3A*, *3B* obtained under non-saturating conditions on a 3% agarose gel stained with ethidium bromide. 1 (ladder 50 bp), 2 (*DNMT1* gene in Hl-60 cell line), 3 (*DNMT1* gene in Nalm-6), 4 (*DNMT3A* gene in Hl-60 cell line), 5 (*DNMT3A* gene in Nalm-6), 6 (*DNMT3B* gene in Hl-60 cell line), 7 (ladder 50 bp), 8 (*DNMT3B* gene in Nalm-6).

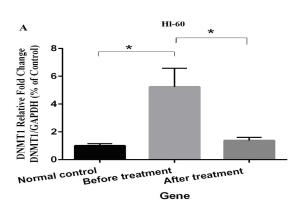


Figure 2. The relative fold change in expression of *DNMTI* in the decitabine-treated HI-60 cell line compared to the normal PBMCs, after normalization to GAPDH which is expressed constantly in every cell type. Data were considered significantly different with p<0.05.

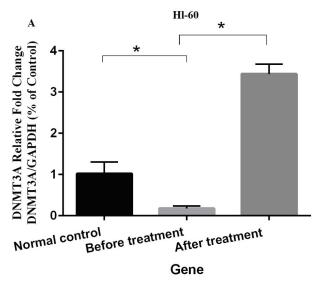


Figure 3. The relative fold change in expression of *DNMT3A* in the decitabine-treated Hl-60 cell line compared to the normal PBMCs, after normalization to GAPDH which is expressed constantly in every cell type. Data were considered significantly different with p<0.05.

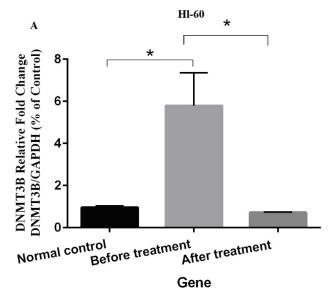


Figure 4. The relative fold change in expression of *DNMT3B* in the decitabine-treated HI-60 cell line compared to the normal PBMCs, after normalization to GAPDH which is expressed constantly in every cell type. Data were considered significantly different with p<0.05.

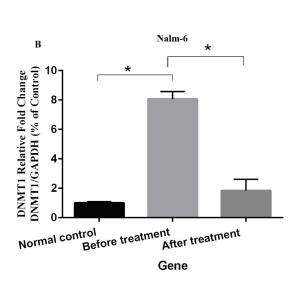


Figure 5. The relative fold change in expression of *DNMT1* in the decitabine-treated Nalm-6 cell line compared to the normal PBMCs, after normalization to GAPDH which is expressed constantly in every cell type. Data were considered significantly different with p<0.05.

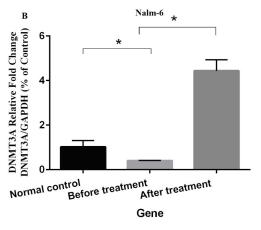


Figure 6. The relative fold change in expression of *DNMT3A* in the decitabine-treated Nalm-6 cell line compared to the normal PBMCs, after normalization to GAPDH which is expressed constantly in every cell type. Data were considered significantly different with p<0.05.

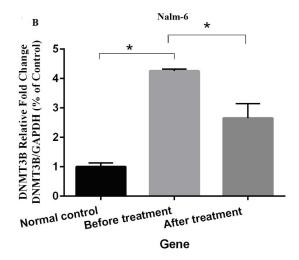


Figure 7. The relative fold change in expression of *DNMT3B* in the decitabine-treated Nalm-6 cell line compared to the normal PBMCs, after normalization to GAPDH which is expressed constantly in every cell type. Data were considered significantly different with p<0.05.

# Discussion

Epigenetic changes in leukemia. contrary genetic to lesions. are pharmacologically reversible and therefore a good target for novel therapeutic approaches. According to previous studies, DNMT3A and 3B seem to be essential for neoplastic transformation and tumor progression (28). DNMT3A is known as one of the most frequently mutated genes in hematological cancers. Additionally, it been observed that eliminating DNMT3B limits tumor growth in vivo. In hematological malignancies, excessive expression of DNMT1 has been shown in 12 leukemia samples including AML, ALL and MDS. It is noteworthy that among the 3 DNMT genes (DNMT1, 3A, 3B), DNMT3B shows the greatest role in AML. As a result, abnormal expression of de novo DNMTs may serve as a marker for cancer cells, as well as a potential aim for future cancer therapy (30).

In the present study, the expression profile of DNMTs in both types of leukemic cells was completely different from those in normal cells, which was consistent with the previous findings (30, 32). Consistent

with the results of this study, other experiments have also reported that the expression of DNMT1 and DNMT3B are increased in solid tumors such as ovarian tumors (31, 32). In the current study, under the effect of chemotherapy drug decitabine on the cell lines, the expression levels of DNMT1 and DNMT3B were significantly reduced and approached the normal one, a phenomenon which has also been observed with azacitidine (30). Previous studies have also shown that the activity of DNMT3B should be decreased for the inhibition of proliferation of some human cancer cells (36, 37). In the present study, the expression of DNMT3A in leukemic cell lines was lower than the normal cells, which increased after treatment with decitabine, as in some past works (38, 39). The effect of decitabine on a lymphoid cell (Nalm-6) suggests that further research on its potential applications in lymphoid malignancies would be justified. One mechanism attributed to decitabine is that it can covalently bind to DNMT, leading to a decrease in the DNA methylation of specific genes involved in the cell cycle (30, 39). Thus, it can be assumed that decitabine causes not only direct DNA demethylation, but also indirect changes in the expression of DNMTs. Although several experiments have been done regarding the effect of drug on gene expression, including in breast and colon cancer, the impact of decitabine on DNMTs in these two leukemia cell types was cleared by the current study.

Side effects of decitabine are many, including pyrexia, anemia, thrombocytopenia, febrile neutropenia, nausea, and diarrhea (40). It is not yet obvious which of them could be attributed to direct or indirect DNA demethylation in specific genes. Attempts have been made in recent years toward development of new delivery systems for enhanced efficacy and ease of use of decitabine (41).

## Conclusion

According to qRT-PCR analysis, the expression profiles of DNMT1, 3A, and 3B in leukemic cell lines Hl-60 (i.e., myeloid) and Nalm-6 (i.e., lymphoid) were completely different from those in normal PBMCs. The decitabine treatment changed the cancerous profile of DNMTs in Hl-60 and Nalm-6 cells toward the normal one in PBMCs.

# **Acknowledgments**

We appreciate the funding for this study provided by the International Campus, Shahid Sadoughi University of Medical Sciences, Yazd, Iran.

# **Conflicting of Interest**

There is no conflict of interest between the authors

## References

- 1. Duy C, Beguelin W, Melnick A. Epigenetic mechanisms in leukemias and lymphomas. Cold Spring Harb Perspect Med 2020; a034959-a0349562.
- 2. Swerdlow SH, Campo E, Harris NL, Jaffe ES, Pileri SA, Stein H, Thiele J. WHO classification of tumours of haematopoietic and lymphoid tissues. Revised 4th ED. Lyon: Internationa Agency for Research on Cancer; 2017.
- 3. Siegel RL, Miller KD, Jemal A. Cancer statistics, 2019. CA Cancer J Clin 2019; 69: 7-34.
- 4. Jirtle RL, Skinner MK. Environmental epigenomics and disease susceptibility. Nat Rev Genet 2007; 8: 253-262.
- 5. Vicente-Duenas C, Hauer J, Cobaleda C, Borkhardt A, Sanchez-Garcia I. Epigenetic priming in cancer initiation. Trends Cancer 2018; 4(6): 408-417.
- 6. Fong CY, Morison J, Dawson MA. Epigenetics in the hematologic malignancies. Haematologica 2014; 99 (12): 1772-1783.
- 7. Herman JG, Baylin SB. Gene silencing in cancer in association with promoter

- hypermethylation. N Engl J Med 2003; 349: 2042-2054.
- 8. Kantarjian H, Issa JP, Rosenfeld CS, Bennett JM, Albitar M, DiPersio J, et al. Decitabine improves patient outcomes in myelodysplastic syndromes: results of a phase III randomized study. Cancer 2006; 106: 1794-1803.
- 9. Flotho C, Claus R, Batz C, Schneider M, Sandrock I, Ihde S, et al. The DNA methyltransferase inhibitors azacitidine, decitabine and zebularine exert differential effects on cancer gene expression in acute myeloid leukemia cells. Leukemia 2009; 23: 1019-1028.
- 10. Hollenbach PW, Nguyen AN, Brady H, Williams M, Ning Y, Richard N, et al. A comparison of azacitidine and decitabine activities in acute myeloid leukemia cell lines. PLoS One 2010; 5(2): e9001-e9005.
- 11. Qin T, Jelinek J, Si J, Shu J, Issa JP. Mechanisms of resistance to 5-aza-2'-deoxycytidine in human cancer cell lines. Blood 2009; 113: 659-667.
- 12. Qin T, Castoro R, El Ahdab S, Jelinek J, Wang X, Si J, et al. Mechanisms of resistance to decitabine in the myelodysplastic syndrome. PLoS One 2011; 6(8): e23372-e23377.
- 13. Kimura S, Kuramoto K, Homan J, Naruoka H, Ego T, Nogawa M.Antiproliferative and antitumor effects of azacitidine against the human myelodysplastic syndrome cell line SKM-1. Anticancer Res 2012; 32: 795-798.
- 14. Lubbert M, Suciu S, Baila L, Ruter BH, Platzbecker U, Giagounidis A, et al. Low-dose decitabine versus supportive care in elderly patients with intermediate- or high-risk myelodysplastic syndrome (MDS) ineligible for intensive chemotherapy: final results of the randomized phase III study of the European Organisation for Research and Treatment of Cancer Leukemia Group and the German MDS Study Group. J Clin Oncol 2011; 29(15): 1987-1996.
- 15. Lubbert M, Ruter BH, Claus R, Schmoor C, Schmid M, Germing U, et al.

- A multicenter phase II trial of decitabine as first-line treatment for older patients with acute myeloid leukemia judged unfit for induction chemotherapy. Haematologica 2012; 97(3): 393-401.
- 16. Momparler RL. A perspective on the comparative antileukemic activity of 5-aza-2'-deoxycytidine (decitabine) and 5-azacytidine (Vidaza). Pharmaceuticals 2012; 5(8): 875-881.
- 17. Palii SS, Van Emburgh BO, Sankpal UT, Brown KD, Robertson KD. DNA methylation inhibitor 5-aza-2'-deoxycytidine induces reversible genomewide DNA damage that is distinctly influenced by DNA methyltransferases 1 and 3B. Mol Cell Biol 2008; 28(2): 752-771.
- 18. Quintas-Cardama A, Santos FP, Garcia-Manero G. Therapy with azanucleosides for myelodysplastic syndromes. Nat Rev Clin Oncol 2010; 7(8): 433-444.
- 19. Tsai HC, Li H, Van Neste L, Cai Y, Robert C, Rassool FV, et al. Transient low doses of DNA demethylating agents exert durable antitumor effects on hematological and epithelial tumor cells. Cancer Cell 2012; 21(3): 430-446.
- 20. Jaenisch R, Bird A. Epigenetic regulation of gene expression: how the genome integrates intrinsic and environmental signals. Nat Genet 2003; 33: 245-54.
- 21. Scarano MI, Strazzullo M, Matarazzo MR, D'Esposito M. DNA methylation 40 years later: its role in human health and disease. J Cell Physiol 2005; 204: 21-35.
- 22. Gonzalo S, Jaco I, Fraga MF, Chen T, Li E, Esteller M, et al. DNA methyltransferases control telomere length and telomere recombination in mammalian cells. Nat Cell Biol 2006; 8: 416-424.
- 23. Portela A, Esteller M. Epigenetic modifications and human disease. Nat Biotechnol 2010; 28: 1057-1068.
- 24. Jin C, Qin T, Barton MC, Jelinek J, Issa J-PJ. Minimal role of base excision

- repair in TET-induced global DNA demethylation in HEK293T cells. Epigenetics 2015; 10(11): 1006-1013.
- 25. Parry L, Clarke AR. The roles of the methyl-CpG binding proteins in cancer. Genes & cancer 2011; 2(6): 618-630.
- 26. Taby R, Issa JPJ. Cancer epigenetics. CA Cancer J Clin 2010; 60(6): 376-392.
- 27. Baylin SB, Jones PA. A decade of exploring the cancer epigenome biological and translational implications. Nature Rev Canc 2011; 11(10): 726.
- 28. Rhee I, Bachman KE, Park BH, Jair KW, Yen RW, Schuebel kE et al. DNMT1 and DNMT3b cooperate to silence genes in human cancer cells. Nature 2002; 416: 552-556.
- 29. Yang L, Rau R, Goodell MA. DNMT3A in haematological malignancies. Nat Rev Cancer 2015; 15(3): 152.
- 30. Wong Y-F, Jakt LM, Nishikawa S-I. Prolonged treatment with DNMT inhibitors induces distinct effects in promoters and gene-bodies. PloS One 2013; 8(8): e71099-e71810.
- 31. Rahman MM, Qian ZR, Wang EL, Yoshimoto K, Nakasono M, Sultana R, et al. DNA methyltransferases 1, 3a, and 3b overexpression and clinical significance in gastroenteropancreatic neuroendocrine tumors. Human pathology 2010; 41(8): 1069-1078.
- 32. Ahluwalia A, Hurteau J, Bigsby R, Nephew K. DNA methylation in ovarian cancer: II. Expression of DNA methyltransferases in ovarian cancer cell lines and normal ovarian epithelial cells. Gynecol oncol 2001; 82(2): 299-304.
- 33. Steensma DP, Baer MR, Slack JL, Buckstein R, Godley LA, Garcia-Manero G, et al. Multicenter study of decitabine administered daily for 5 days every 4 weeks to adults with myelodysplastic syndromes: the alternative dosing for outpatient treatment (ADOPT) trial. J Clin Oncol 2009; 27: 3842-3848.
- 34. Stresemann C, Brueckner B, Musch T, Stopper H, Lyko F. Functional diversity of DNA methyltransferase inhibitors in

- human cancer cell lines. Cancer Res 2006; 66(5): 2794-2800.
- 35. Berg T, Guo Y, Abdelkarim M, Fliegauf M, Lu"bbert M. Differential p15/INK4B reactivation and growth inhibition induced by 5-aza-20-deoxycytidine in AML1/ETO-positive and negative myeloid cells. Leuk Res 2007; 31: 497-506.
- 36. Beaulieu N, Morin S, Chute IC, Robert M-F, Nguyen H, MacLeod AR. An essential role for DNA methyltransferase DNMT3B in cancer cell survival. J Biol Chem 2002; 277(31): 28176-28181.
- 37. Soejima K, Fang W, Rollins BJ. DNA methyltransferase 3b contributes to oncogenic transformation induced by SV40T antigen and activated Ras. Oncogene 2003; 22(30): 4723-4727.
- 38. Sharma S, De Carvalho DD, Jeong S, Jones PA, Liang G. Nucleosomes containing methylated DNA stabilize DNA methyltransferases 3A/3B and ensure faithful epigenetic inheritance. Plos Genet 2011; 7(2): e1001286-e1001290.
- 39. Chowdhury B, McGovern A, Cui Y, Choudhury SR, Cho I-H, Cooper B, et al. The hypomethylating agent decitabine causes a paradoxical increase in 5-hydroxymethylcytosine in human leukemia cells. Sci Rep 2015; 5: 9281-9291.
- 40. Nieto M, Demolis P, Béhanzin E, Moreau A, Hudson I, Flores B, et al. The European medicines agency review of decitabine (Dacogen) for the treatment of adult patients with acute myeloid leukemia: summary of the scientific assessment of the committee for medicinal products for human use. Oncologist 2016; 21(6): 692-700.
- 41. Briot T, Roger E, Lautram N, Verger A, Clavreul A, Lagarce F. Development and in vitro evaluations of new decitabine nanocarriers for the treatment of acute myeloid leukemia. Int J Nanomedicine 2017; 12: 8427-8442.