PU.1 controls the expression of long noncoding RNA HOTAIRM1 during granulocytic differentiation

Shuyong Wei1, Ming Zhao1, Xiaoling Wang1, Yizhen Li1 and Kankan Wang1,2*

Abstract

Background: Long noncoding RNA HOX antisense intergenic RNA myeloid 1 (HOTAIRM1) has been characterized as a critical factor in all-trans retinoic acid (ATRA)-induced differentiation of acute promyelocytic leukemia (APL) cells. However, the essential transcription factor for gene expression of HOTAIRM1 is still unknown.

Findings: Chromatin immunoprecipitation (ChIP) assays revealed that PU.1 constitutively bound to the regulatory region of HOTAIRM1. Co-expression of PU.1 led to the transactivation of the regulatory region of HOTAIRM1 in a reporter assay. Detailed analysis showed that two PU.1 motifs, which were located around +1100 bp downstream of the transcriptional start site of the HOTAIRM1 promoter, were responsible for the PU.1-dependent transactivation. The induction of HOTAIRM1 by ATRA was dependent on PU.1, and ectopic expression of PU.1 significantly up-regulated HOTAIRM1. Furthermore, low HOTAIRM1 expression was observed in APL cells, which was attributed to the reduced PU.1 expression rather than the repression by PML-RARα via the direct binding.

Conclusion: PU.1 directly activates the expression of HOTAIRM1 through binding to the regulatory region of HOTAIRM1 during granulocytic differentiation. The reduced PU.1 expression, rather than PML-RARα itself, results in the low expression of HOTAIRM1 in APL cells. Our findings enrich the knowledge on the regulation of IncRNAs and the underlying mechanisms of the abnormal expression of lncRNAs involved in APL.

Keywords: HOTAIRM1, PU.1, APL, PML-RARα, Transcriptional regulation

Introduction

Recently, it has become increasing clear that long non-coding RNAs (lncRNAs) function as a class of versatile regulators through interaction with DNA, RNA, and proteins to modulate gene expression [1–3]. Extensive studies have focused on the functions of lncRNAs in cells and demonstrated that lncRNAs modulate transcriptional regulation, regulate protein activities, play structural or organizational roles, and serve as precursors to small RNAs [4–7]. Thus, aberrant expression of lncRNAs is associated with disease development. However, the molecular mechanisms underlying the regulation of lncRNAs are still largely unknown.

* Correspondence: kankanwang@shsmu.edu.cn
1 State Key Laboratory of Medical Genomics and Shanghai Institute of Hematology, Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, 197 Ruijin Er Rd, Shanghai 200025, China
2 Sino-French Research Center for Life Sciences and Genomics, Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai 200025, China

© 2016 Wei et al. Open Access This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.
Transcription factor PU.1 is a master regulator in the control of myeloid differentiation [11–13]. PU.1 transcriptionally regulates the genes necessary for myeloid differentiation of granulocytes and monocytes, including granulocyte/macrophage colony-stimulating factor receptor (GM-CSFR) [14–16], CD11b [17], CD18 [18], and myeloperoxidase [19]. A tightly regulated level of PU.1 is essential for normal hematopoiesis. Dysregulation of PU.1 can lead to the development of AML [20–22]. Our previous work [23, 24] showed that, in the development of APL, both the targets and the expression level of PU.1 are inhibited by the oncogenic PML-RARα fusion protein, which is generated by the chromosomal translocation, t(15;17). Afterwards, a series of PU.1-regulated genes, such as genes encoding HCK [25] and immunoproteosomes [26], have been reported to contribute to APL leukemogenesis due to the dysregulation of their expression. During the treatment of APL, ATRA restores the expression of both PU.1 and its downstream target genes by degrading PML-RARα, thus relieving the differentiation block [27–29]. Moreover, genome-wide binding profiling of these APL-associated transcription factors, e.g., PML-RARα and PU.1, has demonstrated that the molecular consequences of these transcription factors are undoubtedly complex, as they associate with and likely regulate a relatively large number of diverse genes accounting for as much as 10–15% of the genome [30]. Those target genes include not only protein-coding genes but also noncoding transcripts, especially IncRNAs.

In this study, using chromatin immunoprecipitation (ChIP) and luciferase reporter assays, we found that PU.1 bound to the regulatory region of HOTAIRM1 in vivo and transactivated this region, which was mainly mediated through two PU.1 motifs around +1100 bp downstream to the transcription start site (TSS). Furthermore, PU.1 knockdown down-regulated HOTAIRM1 and PU.1 overexpression increased HOTAIRM1. Finally, we revealed that the reduced PU.1 expression was responsible for the low HOTAIRM1 expression in APL cells.

Results
The induction of HOTAIRM1 upon ATRA treatment requires intermediate protein synthesis
It has been shown that HOTAIRM1 is up-regulated in APL cells upon exposure to ATRA and plays a critical role in myeloid differentiation [8]. Since HOTAIRM1 has two variants, we designed variant-specific primers to examine the expression of each variant in APL-derived NB4 cells upon ATRA treatment. As shown in Fig. 1a, HOTAIRM1 variant 2 was the major isoform that was expressed both before and after ATRA treatment. By comparison, HOTAIRM1 variant 1 was far less abundant than variant 2. Both variants were up-regulated upon ATRA treatment. To investigate whether the induction of HOTAIRM1 was a direct effect of ATRA, NB4 cells were pretreated with a translation inhibitor cycloheximide (CHX) for 30 min prior to the addition of ATRA to interfere with the translation process of newly synthesized proteins. As shown in Fig. 1b, CHX significantly impaired the up-regulation of both HOTAIRM1 variants by ATRA, suggesting that the induction of HOTAIRM1 requires newly synthesized intermediate protein(s).

PU.1 directly binds to the regulatory region of HOTAIRM1
To search for the newly synthesized regulatory factors involved in the up-regulation of HOTAIRM1, we first identified the regulatory region responsible for the transcriptional regulation of HOTAIRM1, which can be defined using binding profiles of H3K4me3 and H3K27Ac. Due to the myeloid-specific expression of HOTAIRM1, we chose CD14+ monocytes (a myeloid lineage) for the analysis. We utilized the chromatin immunoprecipitation (ChIP)-seq data generated by the ENCODE Project Consortium [31]. The binding profiles were displayed using the UCSC Genome Browser (http://genome.ucsc.edu)
As shown in Fig. 2a, the enrichment of H3K4me3 and H3K27Ac binding was found to be located from about −100 bp upstream of the transcription start site (TSS) to approximately +1200 bp downstream of the TSS. The data indicated that this region mediated the transcription of HOTAIRM1 and this region was used in the following experiment and analysis. We then investigated the significantly enriched transcription factor binding sites within this regulatory region of HOTAIRM1 using MatInspector [33]. Interestingly, we found eight putative binding sites for PU.1 (Fig. 2b), which is a hematopoietic transcription factor involved in myeloid differentiation and up-regulated upon ATRA treatment. To analyze the binding of PU.1, we performed ChIP assays in ATRA-treated NB4 cells. We designed six primer pairs to search for the in vivo binding of PU.1 around these eight PU.1-motif-containing sites. The closely located motifs were investigated using the same set of the primers. The primer pair “+600” covered motifs at +586 and +629 and the primer pair “+1100” covered motifs at +1067 and +1123. The regions upstream (−400) and downstream (+1600) of the regulatory region and an irrelevant region (NC) were used as negative controls. As shown in Fig. 2c, the position around +1100 bp downstream to the TSS showed dramatically significant enrichment of PU.1 binding in NB4 cells, and this was far more noticeable than the other putative sites. Additionally, we also detected the PU.1 binding in another myeloid cell line, U937, which belongs to a different AML subtype but can also undergo myeloid differentiation upon ATRA treatment. The similar PU.1 binding pattern was observed in ATRA-treated U937 cells, ruling out cell line-specific phenomena. The data together indicated that PU.1 directly bound to the regulatory region of HOTAIRM1.

**PU.1 transactivates HOTAIRM1 through the +1100 region in the HOTAIRM1 promoter**

To further investigate whether PU.1 transactivates the regulatory region of HOTAIRM1 through the PU.1 binding sites identified above, we employed the luciferase reporter assay in HEK-293T cells, which lack endogenous PU.1. We cloned a 1370 bp fragment of the regulatory region of HOTAIRM1 spanning from −134 to +1237 into a luciferase reporter plasmid, which was designated as pGL3-HOTAIRM1 (Fig. 3a). We also included one mutant form of the complete regulatory region in which the core sequences of PU.1 sites at +1067 and +1123 were mutated from GGAA to CCAA, and one truncated construct spanning from −134 to +911 and lacking PU.1 sites on the +1100 region. As shown in Fig. 3b, co-expression of PU.1 resulted in significant activation of
the full-length regulatory region of HOTAIRM1. In contrast, the transactivation ability of PU.1 on the regulatory region of HOTAIRM1 was significantly reduced in both PU.1-mutated and PU.1-truncated constructs (Fig. 3b). The results indicated that PU.1 could transactivate the HOTAIRM1 promoter, and PU.1 motifs at +1067 and +1123 were essential for the transcriptional activation of HOTAIRM1.

The induction of HOTAIRM1 is dependent on PU.1 during granulocytic differentiation

Next, we investigated the dependency of HOTAIRM1 on PU.1 in a hematopoietic context. To examine the in vivo regulation by PU.1, we silenced PU.1 in NB4 cells, followed by ATRA treatment for 24 h. To rule out off-target effects, two siRNAs against PU.1 were used and their knockdown efficiencies were around 63 and 74 %, respectively (Fig. 4). As a positive control, ITGAM (encoding myeloid integrin CD11b), whose expression is known to rely on PU.1 [17], showed a significant reduction. We used HNRNPH1 as negative control, as its expression level was not affected by the PU.1 level. Both HOTAIRM1 variants were significantly reduced in PU.1 knockdown cells compared with negative control cells (Fig. 4), suggesting that PU.1 was essential for the expression of HOTAIRM1 during granulocytic differentiation.

Additionally, we also detected the effect of arsenic trioxide (ATO), another effective agent used in APL therapy, on HOTAIRM1 expression. We found that ATO had almost no effect on the expression levels of HOTAIRM1 and PU.1 (Additional file 1: Figure S1), further supporting the above observation that the induction of HOTAIRM1 depended on the up-regulation of PU.1.

Low HOTAIRM1 expression is observed in APL cells, which is attributed to the reduced PU.1 expression, rather than the direct binding and repression by PML-RARα

Since HOTAIRM1 expression is up-regulated during ATRA-induced granulocytic differentiation of APL cells, we were interested in HOTAIRM1 expression in APL cells. We first compared the expression of HOTAIRM1 between APL cells and non-APL cells using AML cell lines. In APL patient-derived NB4 cells, the expression abundance of both HOTAIRM1 and PU.1 was significantly lower than that in non-APL AML cells (U937 and HL60) (Fig. 5a). To validate this finding in a large cohort of patient samples, we utilized previously published transcriptome data [34] to compare their expression between APL patient samples and non-APL AML patient samples. As shown in Fig. 5b, compared to non-APL AML, HOTAIRM1 was noticeably lower in APL patients, which is consistent with a recent clinical study on AML.

![Figure 3](image1.png)

**Fig. 3** PU.1 transactivates HOTAIRM1 through the +1100 region in the HOTAIRM1 promoter. **a** Schematic representation of pGL3-HOTAIRM1 as well as its mutated and truncated forms. **b** PU.1-transactivated promoter activity of HOTAIRM1. Loss of major PU.1 binding sites significantly impaired PU.1 transactivation on the HOTAIRM1 promoter. The luciferase promoters were co-transfected with equal amount of the pcDNA3.1 or pcDNA3.1-PU.1 vector to HEK-293T cells. The data represent the mean of three replicates ± SD. *p < 0.05; **p < 0.01

![Figure 4](image2.png)

**Fig. 4** The induction of HOTAIRM1 is dependent on PU.1 during granulocytic differentiation. The expression of PU.1, HOTAIRM1, ITGAM, and HNRNPH1 after non-targeting or PU.1 siRNA transfection in NB4 cells, with ATRA treatment for 24 h. An average of two control genes (GAPDH and ACTB) was used for normalization. The data represent the mean of three replicates ± SD. *p < 0.05; **p < 0.01; ***p < 0.001
patients [10]. Similarly, PU.1 was also lower in APL, supporting the above cell line-based results.

Low expression of HOTAIRM1 in APL could be due to several possibilities. First, since PML-RARα generally acts as a repressor on its direct target genes by recruiting co-repressors, such as HDAC1, N-coR, and SMRT [27], HOTAIRM1 expression might be repressed by the direct PML-RARα binding. To test this possibility, we first examined whether PML-RARα could directly bind to the regulatory region of HOTAIRM1 using ChIP-qPCR assays. As shown in Fig. 5c, there was no enrichment of either PML or RARα binding around the regulatory region of HOTAIRM1 in NB4 cells, indicating that PML-RARα did not directly bind to the HOTAIRM1 promoter to repress its expression. The luciferase reporter assay also showed that PML-RARα had minimal impact on the promoter activity of HOTAIRM1 (Fig. 5d). Both tests excluded the possibility of the direct binding and repression by PML-RARα.

Second, since we showed that HOTAIRM1 was a PU.1 target gene and was activated by PU.1 (Figs. 2 and 3), and since PML-RARα is capable of repressing PU.1-regulated genes [23], another possibility might be that PML-RARα repressed PU.1-dependent transactivation of HOTAIRM1. This possibility was ruled out by the observation that PML-RARα led to a negligible change
in PU.1-mediated transactivation through the luciferase reporter assay (Fig. 5d).

Third, low HOTAIRM1 expression could be attributed to the reduced PU.1 expression in APL since PU.1 expression is repressed by PML-RARα due to disruption of PU.1 autoregulation [23, 35]. To test this possibility, we first examined the correlation between PU.1 and HOTAIRM1 in a large cohort of AML patient samples [34]. We found a significant positive correlation between PU.1 expression and HOTAIRM1 expression ($r = 0.493$, $p < 2.2e^{-16}$) (Fig. 5e). To support this finding, we rescued the PU.1 expression by over-expressing PU.1 in PML-RARα-positive NB4 cells. With PU.1 ectopic expression, HOTAIRM1 expression was increased more than fivefold in NB4 cells (Fig. 5f). This also provided an explanation for the up-regulation of HOTAIRM1 in NB4 cells upon ATRA treatment: ATRA restored the expression of PU.1 [29] and then the up-regulated PU.1 transactivated HOTAIRM1.

Taken together, the data suggested that low HOTAIRM1 expression in APL cells was attributed to the reduced PU.1 expression rather than repression by PML-RARα via the direct binding.

Discussion

Recently, extensive studies have been carried out to understand the functions of lncRNAs, but fewer studies have focused on the regulation of lncRNAs. In this study, we reveal that the transcription factor PU.1 controls the expression of the lncRNA HOTAIRM1, which acts as a critical noncoding regulator in ATRA-induced granulocytic differentiation of APL cells. On the one hand, we showed that HOTAIRM1 was not a direct ATRA-responsive gene, and the observed up-regulation of HOTAIRM1 induced by ATRA was a secondary event that was dependent on the expression of PU.1 activated by ATRA.

On the other hand, we observed low HOTAIRM1 expression in APL cells and revealed that low expression was attributed to the reduced PU.1 expression, rather than the direct binding and repression of PML-RARα. To support these observations, we provided the evidence that PU.1 constitutively bound to the regulatory region of HOTAIRM1 to transactivate the promoter activity of HOTAIRM1 and identified the two PU.1 motifs responsible for the PU.1-dependent transactivation. These findings enrich our knowledge on the regulation of lncRNAs and the underlying mechanisms of the abnormal expression of lncRNAs involved in APL.

Our first contribution is identifying HOTAIRM1 as a novel target of PU.1. This finding implicates that there still exist unidentified PU.1 targets that are essential for myeloid differentiation. To date, most of the known PU.1 direct target genes participating in myeloid differentiation belong to protein-coding genes [36]. To the best of our knowledge, few have reported the role of PU.1 in the modulation of lncRNAs during myeloid differentiation. Our work presents an example of lncRNAs as the PU.1 target. In addition to HOTAIRM1, there are perhaps hundreds of lncRNA candidates potentially under the transcriptional control of PU.1, among which some are likely correlated with or necessary for myeloid differentiation. Systematic approaches like ChIP-seq and RNA-seq would be a powerful tool to globally identify these PU.1 candidate targets. In addition, we also identified the direct binding site of PU.1 at the +1100 downstream of the TSS of the HOTAIRM1 promoter. It is worth mentioning that it was possible that the −122 region might also have a partial impact on the promoter activity of HOTAIRM1, although we focused on the +1067/+1123 locus in the luciferase reporter assay (Fig. 3b). The contribution from the −122 region was probably much less than the +1067/+1123 region, since the in vivo PU.1 binding signals at the +1067/+1123 locus were markedly higher than those at the −122 locus (Fig. 2c).

Second, our work suggests the role of HOTAIRM1 in the PU.1-mediated regulation network during myeloid differentiation. PU.1 regulates differentiation as well as cell cycle and proliferation. For example, exogenous PU.1 expression up-regulates endogenous PU.1 levels in progenitor cells, which is achieved by the induction of cell cycle lengthening, suggesting a positive feedback circuit between PU.1 and the cell cycle in the modulation of myeloid differentiation [37]. PU.1 occupies the CDK6 gene promoter and directly stimulates CDK6 transcription, coordinating proliferation and differentiation [38]. Our work found that HOTAIRM1 was transcriptionally activated by PU.1 and their expression levels were significantly correlated in AML patients. Interestingly, HOTAIRM1 also regulates myeloid differentiation [8] and cell cycle arrest [9]. In addition, HOTAIRM1 modulates CD18 and ITGAM [8], which are known to be transcriptionally controlled by PU.1 [17, 18]. These findings suggest that HOTAIRM1 may participate in the downstream PU.1-dependent transcription regulation during myeloid differentiation. In another word, HOTAIRM1 may act as a downstream effector of PU.1 by regulating myeloid differentiation-associated genes and cell cycle-related genes.

Third, our research provides insights into the tissue specificity of HOTAIRM1. Tissue specificity is a characteristic of lncRNAs, which usually exhibit a more restricted expression pattern than protein-coding genes [39, 40]. Most recently, lncRNAs have been demonstrated to be dynamically expressed during erythropoiesis and these erythroid-specific transcripts are under the direct transcriptional control of core erythroid transcription factors GATA1, TAL1, or KLF1 [41]. In our work, we
dissected the regulation control of HOTAIRM1 by PU.1. Since PU.1 is prominent in myeloid cells, increases during myeloid differentiation, and achieves the highest level in mature granulocytes and monocytes [42], our results provide a reason to explain the high tissue specificity of HOTAIRM1 in myeloid cells. To fully explain the myeloid specificity of HOTAIRM1, more studies will be done to learn the whole picture of the combinational and coordinated regulation of HOTAIRM1 by other tissue-restricted transcription factors.

Finally, our work revealed the mechanism underlying the dysregulation of HOTAIRM1 in APL cells. PML-RARα is a critical factor required for the initiation and development of APL. At the transcriptional level, PML-RARα represses genes indispensable for normal granulocytic differentiation through multiple ways. First, PML-RARα interferes with the retinoid acid receptor α (RARα) signaling. As a potent transcriptional repressor, PML-RARα directly binds to the retinoic acid response elements (RAREs), recruiting co-repressor proteins such as DAXX, NcoR, and HDAC1 or methyla-"izing enzymes such as DNMT1 and DNMT3A, thereby leading to transcriptional repression [43]. Second, PML-RARα directly binds to PU.1-RAREh (RARE half) binding sites, physically interacts with PU.1, and thus inhibits PU.1-dependent transactivation of myeloid differentiation-associated genes, including SPI1 (PLL1), HCK, PSMB10, and IRF1 [23]. Our study provides an example of the third scenario, which receives less attention in the past compared to the former two scenarios. We did not observe the direct binding of PML-RARα in the regulatory region of HOTAIRM1. Instead, we found that the dysregulated expression level of HOTAIRM1 was due to the inhibition of PU.1, which suggested the PML-RARα-suppressive effect on HOTAIRM1 was indirect. Also, this explains the noticeably low level of HOTAIRM1 in APL and suggests that the indirect suppression by PML-RARα can also be potent. Considering the indispensable role of HOTAIRM1 in myeloid differentiation [8], our work shows that PML-RARα-indirect inhibition of HOTAIRM1 contributes to the differentiation block in APL, which provides an additional mechanism for leukemogenesis in APL.

In conclusion, we identify the IncRNA HOTAIRM1 as a novel PU.1-targeted gene and PU.1 mediates the myeloid-specific expression of HOTAIRM1. PU.1-dependent transactivation of HOTAIRM1 relies on the two PU.1 motifs at the +1100 region of the HOTAIRM1 promoter. The inhibition of PU.1 by PML-RARα contributes to the low HOTAIRM1 level in APL cells, which allows us to understand further how the oncofusion protein PML-RARα blocks myeloid cells at the promyelocytic stage during the development of APL.

**Materials and methods**

**Cell culture and reagents**

HEK-293T cells were cultured in DMEM (Gibco, Carlsbad, CA, USA) containing 10% fetal bovine serum (Moregate Biotech, Bulimba, QLD, Australia), and NB4, HL60, and U937 cells were cultured in RPMI 1640 (Gibco) supplemented with 10% fetal bovine serum. Cells were maintained at 37 °C in a 5% CO2 incubator. All-trans retinoic acid (Sigma-Aldrich, St Louis, MO, USA) was added to NB4 or U937 cells at a final concentration of 1 μM.

**RNA extraction and qRT-PCR**

Total RNA was extracted using an RNeasy Mini Kit (QIAGEN, Hilden, Germany) according to the manufacturer’s directions. Reverse transcription was performed using the SuperScript III Reverse Transcriptase (Invitrogen, Carlsbad, CA, USA). Real-time PCR was performed using the SYBR Green real-time PCR Master Mix (Toyobo, Osaka, Japan) in the Vii7 Real-Time PCR System (Applied Biosystems Inc., Foster City, CA, USA). All primers for quantitative reverse transcription-PCR (qRT-PCR) are listed in Additional file 1: Table S1.

**Plasmid construction**

The regulatory region of HOTAIRM1 was amplified using NB4 genomic DNA and then cloned to a pGL3-basic luciferase reporter vector (Promega, Madison, WI, USA). The PU.1-coding sequence was amplified using NB4 cDNA and then cloned to the MigR1 vector (Addgene).

**Chromatin immunoprecipitation assay**

Chromatin immunoprecipitation (ChIP) was performed according to the Affymetrix protocol as previously described [44]. The following antibodies were used: anti-PU.1 (#2258; Cell Signaling Technology, Danvers, MA, USA), anti-RARα (C-20 X; Santa Cruz Biotechnology, Santa Cruz, CA, USA), and anti-PML (H238 X; Santa Cruz). All primers for ChIP-qPCR are listed in Additional file 1: Table S2.

**Luciferase reporter assay**

Luciferase assays were conducted in HEK-293T cells as previously described [25]. Dual-luciferase reporter assays (Promega) were performed 24 h after transfection by Lipofectamine 2000 (Invitrogen). Renilla luciferase plasmids were used as an internal control for transfection efficiency correction.

**siRNA transfection**

The siRNA oligos were transiently transfected to NB4 cells using Nucleofector Kit V (Amaxa Biosystems, Gaithersburg, MD, USA) according to the manufacturer’s instructions. PU.1-targeting siRNA oligos matching the sequences: CACUCAAGGCUCUUUGCUU (siPU.1
Arsenic trioxide had minimal effect on the regions containing PU.1 consensus and RARE half sites in acute

and PU.1 in

contributions

concerned with the leukemia cell proliferation in acute

promyelocytic leukemia. J Hematol Oncol 2015;8:126.

Dhir A, Dhir S, Proudfoot NJ, Jollling CL. Microprocessor mediates

transcriptional termination in genes encoding long noncoding microRNAs.

Nat Struct Mol Biol. 2014;21:1–11.

Zhang X, Tian Z, Padden C, Gerstein MB, Rozowsky J, Snyder M, et al. A

myelopoesis-associated regulatory intergenic noncoding RNA transcript

within the human HOXA cluster. Blood. 2009;113:2526–34.

Zhang X, Weisman SM, Newburger PE. Long intergenic non-coding RNA

HOTAIRM1 regulates cell cycle progression during myeloid maturation in

NB4 human promyelocytic leukemia cells. RNA Biol. 2014;11:777–87.

Diaz-Beyá M, Brunet S, Nomdedéu J, Pratcorona M, Cordeiro A, Gallardo D, et al. The lncRNA HOTAIRM1, located in the HOXA genomic region, is expressed in acute myeloid leukemia, impacts prognosis in patients in the intermediate-risk cytogenetic category, and is associated with a distinctive microRNA signature. Oncotarget. 2015;6:31613–27.

Tenen DG, Hoynes R, Licht JD, Zhang DE. Transcription factors, normal myeloid development, and leukemia. Blood. 1997;90:489–519.

Voso MT, Burn TC, Wulf G, Lim B, Leone G, Tenen DG. Inhibition of hematopoiesis by competitive binding of transcription factor PU.1. Proc Natl Acad Sci U S A. 1994;91:2932–6.

Mossadegh-Keller N, Sarrazin S, Kandalla PK, Espinosa L, Stanley ER, Nutt SL, et al. Mi-CSR instructs myeloid lineage fate in single haematopoietic stem cells. Nature. 2013;497:239–43.

Hohaus S, Petrovick MS, Voso MT, Sun Z, Zhang DE, Tenen DG, PU.1 (Spi-1) and C/EBP alpha regulate expression of the granulocyte-macrophage colony-stimulating factor receptor alpha gene. Mol Cell Biol. 1995;15:5830–40.

Zhang DE, Hethington CJ, Chen HM, Tenen DG. The macrophage transcription factor PU.1 directs tissue-specific expression of the macrophage colony-stimulating factor receptor. Mol Cell Biol. 1994;14:737–81.

Smith LT, Hohaus S, Gonzalez DA, Dziennies SE, Tenen DG. PU.1 (Spi-1) and C/EBP alpha regulate the granulocyte colony-stimulating factor receptor promoter in myeloid cells. Blood. 1996;88:1234–47.

Pahl HL, Scheibe RJ, Zhang DE, Chen HM, Galson DL, Maki RA, et al. The proto-oncogene PU.1 regulates expression of the myeloid-specific CD11b promoter. J Biol Chem. 1993;268:5014–20.

Rosmarin AG, Caprio D, Levy R, Simkевич C. CD18 (beta 2 leukocyte integrin) promoter requires PU.1 transcription factor for myeloid activity. Proc Natl Acad Sci U S A. 1995;92:801–5.

Ford AM, Bennett CA, Healy LE, Tovatdai M, Greaves MF, Enver T. Regulation of the myeloperoxidase enhancer binding proteins Pu1, C/EBP alpha, beta, and -delta during granulocyte-lineage specification. Proc Natl Acad Sci U S A. 1996;93:10838–43.

Vangala RK, Heiss-Neumann MS, Rangatia JS, Singh SM, Schoch C, Tenen DG, et al. The myeloid master regulator transcription factor PU.1 is inactivated by AML1-ETO in (8;21) myeloid leukemia. Blood. 2003;101:270–7.

Huang G, Zhang P, Hira H, Elf S, Yan X, Chen Z, et al. PU.1 is a downstream target of RUNX1 in adult mouse hematopoiesis. Nat Genet. 2008;40:51–60.

Rosenbauer F, Wagner K, Kukol J, Iwaski H, Le Beau MM, Okuno Y, et al. Acute myeloid leukemia induced by graded reduction of a lineage-specific transcription factor, PU.1. Nat Genet. 2004;36:624–30.

Wang X, Wang P, Shi J, Zhu X, He M, Jia X, et al. PML/RARα targets promoter regions containing PU.1 consensus and RARE sites on chromosome 16 in acute promyelocytic leukemia. Blood. 2000;96:5198–20.

Wang X, Zhang H, Qian M, Xiao X, Wang W, et al. The significance of low PU.1 expression in patients with acute promyelocytic leukemia. J Hematol Oncol. 2012;5:22.

Zou D, Yang X, Tan Y, Wang P, Zhu X, Yang W, et al. Regulation of the hematopoietic cell kinase (HCK) by PML/RARα and PU.1 in acute promyelocytic leukemia. Leuk Lymphoma. 2013;54:2541–9.

Yang X-W, Wang P, Liu J-Q, Zhang H, Xi W-D, Jia X-H, et al. Coordinated regulation of the immunoproteasome subunits by PML/RARα and PU.1 in acute promyelocytic leukemia. Oncogene. 2014;33:2700–8.

de Thé H, Chen Z. Acute promyelocytic leukaemia: novel insights into the mechanisms of cure. Nat Rev Cancer. 2010;10:775–83.
28. Wang ZY, Chen Z. Acute promyelocytic leukemia: from highly fatal to highly curable. Blood. 2008;111:2505–15.
29. Mueller BU, Pabst T, Fos J, Petkovic V, Fey MF, Asou N, et al. ATRA resolves the differentiation block in t(15;17) acute myeloid leukemia by restoring PU.1 expression. Blood. 2006;107:3330–8.
30. Qian M, Jin W, Zhu X, Xia X, Yang X, Du Y, et al. Structurally differentiated cis-elements that interact with PU.1 are functionally distinguishable in acute promyelocytic leukemia. J Hematol Oncol. 2013;6:25.
31. Consortium EP, Bernstein BE, Birney E, Dunham I, Green ED, Gunter C, et al. An integrated encyclopedia of DNA elements in the human genome. Nature. 2012;489:57–74.
32. Rosenbloom KR, Armstrong J, Barber GP, Casper J, Clawson H, Diekhans M, et al. The UCSC genome browser database: 2015 update. Nucleic Acids Res. 2015;43(Database issue):D670–81.
33. Cartharius K, Frech K, Grote K, Klocke B, Haltmeier M, Klingenhoff A, et al. MatInspector and beyond: promoter analysis based on transcription factor binding sites. Bioinformatics. 2005;21:2933–42.
34. Tomasson MH, Xiang Z, Walgren R, Zhao Y, Kasai Y, Miner T, et al. Somatic mutations and germline sequence variants in the expressed tyrosine kinase genes of patients with de novo acute myeloid leukemia. Blood. 2008;111:4797–808.
35. Chen H, Ray-Gallet D, Zhang P, Hetherington CJ, Gonzalez DA, Zhang DE, Moreau-Gachelin F, Tenen DG. PU.1 (Spi-1) autoregulates its expression in myeloid cells. Oncogene. 1995;11:1549–60.
36. Friedman AD. Transcriptional control of granulocyte and monocyte development. Oncogene. 2007;26:6816–28.
37. Kueh HY, Champhekar A, Champhekhar A, Nutt SL, Bowitz MB, Rothenberg EV. Positive feedback between PU.1 and the cell cycle controls myeloid differentiation. Science. 2013;341:670–3.
38. Choe KS, Ufjelly O, Wontakal SN, Skoultchi AI. PU.1 directly regulates cdk6 gene expression, linking the cell proliferation and differentiation programs in erythroid cells. J Biol Chem. 2010;285:3044–52.
39. Kutter C, Watt S, Stefflova K, Wilson MD, Goncalves A, Ponting CP, et al. Rapid turnover of long noncoding RNAs and the evolution of gene expression. PLoS Genet. 2012;8:e1002841.
40. Derrien T, Johnson R, Bussotti G, Tanzer A, Djebali S, Tilgner H, et al. The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. Genome Res. 2012;22:1775–89.
41. Alvarez-Dominguez JR, Hu W, Yuan B, Shi J, Park SS, Gromatzky AA, et al. Global discovery of erythroid long noncoding RNAs reveals novel regulators of red cell maturation. Blood. 2014;123:570–81.
42. Chen HM, Zhang P, Voso MT, Hofhaus S, Gonzalez DA, Glass CK, et al. Neutrophils and monocytes express high levels of PU.1 (Spi-1) but not Spi-B. Blood. 1995;85:2019–28.
43. Lin RJ, Sterngold T, Tini M, Evans RM. Transcriptional regulation in acute promyelocytic leukemia. Oncogene. 2001;20:7204–15.
44. Carroll JS, Liu XS, Brodsky AS, Li W, Meyer CA, Szary AJ, et al. Chromosome-wide mapping of estrogen receptor binding reveals long-range regulation requiring the forkhead protein FoxA1. Cell. 2005;122:33–43.
45. Wang Y, Jin W, Jia X, Luo R, Tan Y, Zhu X, et al. Transcriptional repression of CDKN2D by PML/RARα contributes to the altered proliferation and differentiation block of acute promyelocytic leukemia cells. Cell Death Dis. 2014;5:e1431.
46. Irizarry RA, Hobbs B, Collin F, Beazer-Barclay YD, Antonellis KJ, Scherf U, et al. Exploration, normalization, and summaries of high density oligonucleotide array probe level data. Biostatistics. 2003;4:249–64.