

Brief report

MicroRNA29a regulates the expression of the nuclear oncogene Ski

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MicroRNAs (miRNAs) are small, noncoding RNA molecules that regulate growth and differentiation. miRNAs are frequently located at cancer-specific fragile sites in the human genome, such as chromosome 7q. The nuclear oncogene *SKI* is up-regulated in acute myeloid leukemia (AML) with $-7/\text{del}7\text{q}$. Here we asked whether loss of miRNAs on chromosome

7q may explain this up-regulation. miR-29a expression was found to be down-regulated in AML with $-7/\text{del}7\text{q}$. Forced expression of miR-29a down-regulated *Ski* and its target gene, *Nr-CAM*, whereas miR-29a inhibition induced *Ski* expression. Luciferase assays validated a functional binding site for miR-29a in the 3' untranslated region of

***SKI*. Finally, in samples of AML patients, we observed an inverse correlation of *Ski* and miR-29a expression, respectively. In conclusion, up-regulation of *Ski* in AML with $-7/\text{del}7\text{q}$ is caused by loss of miR-29a. miR-29a may therefore function as an important tumor suppressor in AML by restraining expression of the *SKI* oncogene. (*Blood*. 2011;118(7):1899-1902)**

Introduction

Patients with acute myeloid leukemia (AML) with monosomy 7 (-7) or deletion of 7q ($\text{del}7\text{q}$) have a poor prognosis. We recently reported that the nucleoprotein Ski, the cellular homologue of the avian leukosis retrovirus oncogene v-*SKI*, is up-regulated in AML, especially in AML with $-7/\text{del}7\text{q}$, which presumably represses retinoic acid-induced myeloid differentiation.¹ In keeping with this, AML patients with low levels of *SKI* may benefit from combination therapy with retinoic acid.² The molecular reason for up-regulation of *SKI* in AML with -7 is unclear. Therefore, we investigated whether a microRNA (miRNA) localized in the cancer fragile site of 7q could be a regulator of Ski. miRNAs are small RNA molecules that affect gene expression by posttranscriptional and translational mechanisms.³ Different miRNAs have been shown to regulate cell proliferation, differentiation, and apoptosis.⁴⁻⁶ Aberrant miRNA expression has been linked to leukemogenesis in chronic lymphocytic leukemia,⁷ acute lymphoblastic leukemia,⁸ and AML.⁹⁻¹¹ miRNAs contribute to malignant transformation by genomic loss, because many miRNAs are tumor-suppressive and localized in cancer fragile sites.¹² We describe here that expression of miR-29a localized on 7q32, is down-regulated in AML with $-7/\text{del}7\text{q}$ and that miR-29a regulates Ski. These data suggest that loss of miR-29a may contribute to leukemogenesis by derepressing the nuclear oncogene *SKI*.

Methods

Patient samples, cell lines, and transfections

For detailed descriptions of patient cohorts, cell lines, and transient transfections, see supplemental Methods (available on the *Blood* Web site; see the Supplemental Materials link at the top of the online article).

miRNA array

We used an oligonucleotide array (mirVANA miRNA probe set; Ambion) and tested the miRNA expression pattern of 17 AML samples. The AML study was approved by the local ethics committee, and patients and donors gave written informed consent. For details, see supplemental Methods.

Flow cytometry

For a description of flow cytometry, see Ritter et al.¹

Cell proliferation assay

For details about the cell proliferation (MTT) assay, see supplemental Methods.

Western blot

For Western blot, whole-cell proteins were extracted by use of a standard protocol for RIPA lysates. After SDS-PAGE, proteins were transferred to nitrocellulose membrane and incubated with antibody anti-Ski (sc-9140; Santa Cruz Biotechnology; 1:1000) or anti- β -actin (AC-74; Sigma-Aldrich; 1:5000).

Reverse transcription, Nr-CaM PCR, and quantitative real-time PCR for miR-29a

For conditions and primers, see supplemental Methods.

SKI 3' UTR reporter constructs and luciferase gene assay

For luciferase constructs (Figure 2A) and luciferase assay, see supplemental Methods.

Statistical analysis

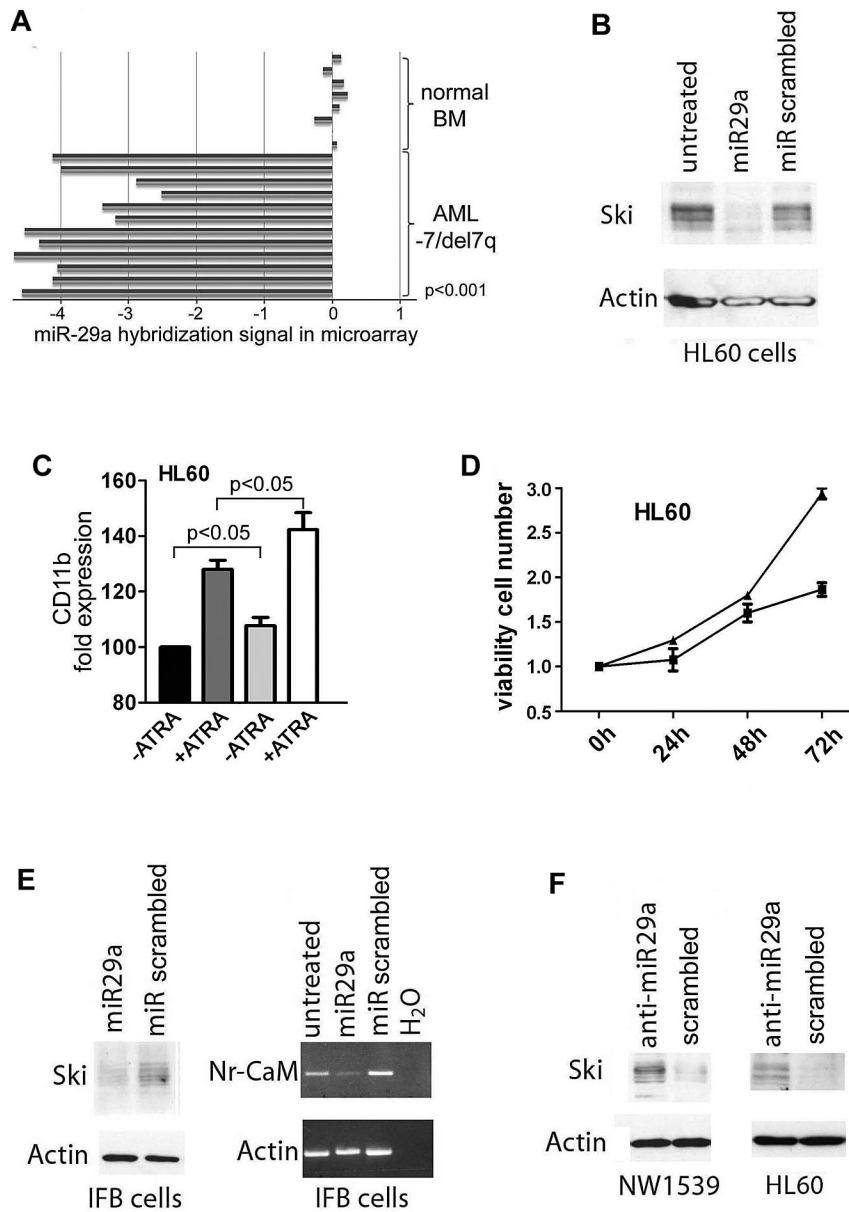
For scientific graphing and statistical analysis, we used GraphPad Prism 5 software (GraphPad Prism Software Inc).

Submitted September 10, 2010; accepted May 9, 2011. Prepublished online as *Blood* First Edition paper, June 17, 2011; DOI 10.1182/blood-2010-09-306258.

The online version of this article contains a data supplement.

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Results and discussion

Microarray analysis shows miR-29a is down-regulated in AML samples with -7/del7q karyotype

We performed a miRNA oligonucleotide array and compared the miRNA profile of normal bone marrow samples ($n = 8$) with that of AML samples with isolated -7/del7q or complex karyotype including -7/del7q ($n = 17$, cohort 1; supplemental Tables 1 and 2; blast count $> 30\%$). A hierarchical cluster analysis demonstrated that AML samples had expression patterns different from normal bone marrow (supplemental Figure 1). Next, we looked for differential miRNA expression between normal bone marrow and AML with -7/del7q (supplemental Table 3). The only miRNA found to be down-regulated in AML samples and localized on 7q was miR-29a (Figure 1A). We then also analyzed 2 larger cohorts of patients for miR-29a expression using quantitative RT-PCR: cohort 2 (-7/del7q; $n = 61$; supplemental Table 4) and cohort 4 (normal karyotype; $n = 54$). Between these 2 cohorts, no signifi-

cant different expression of miR-29a was found, which could be attributed to technical reasons; however, both cohorts showed a down-regulation compared with normal CD34-positive cells (supplemental Figure 2; supplemental Table 5). miR-29a is down-regulated in chronic lymphocytic leukemia¹³ and solid cancers.^{14,15} Because our previous results indicated an overexpression of the nuclear oncogene *SKI* in AML with -7/del7q,¹ we examined whether miR-29a controls Ski expression.

miR-29a regulates Ski protein expression

We transfected HL60 cells with miRNA precursor 29a, 25, 183, or 335, localized on chromosome 7, and measured Ski using flow cytometry. Only miR-29a effectively lowered Ski in HL60 (supplemental Figure 3). Consistently, miR-29a reduced Ski compared with miR-scrambled in Western blot (Figure 1B). Flow cytometry revealed that overexpression of miR-29a (fold miR-29a expression compared with scrambled: 17) significantly increased expression of monocytic differentiation marker CD11b ($P = .023$). This could be enhanced by all-*trans* retinoic acid (ATRA; Figure 1C; $P = .043$).

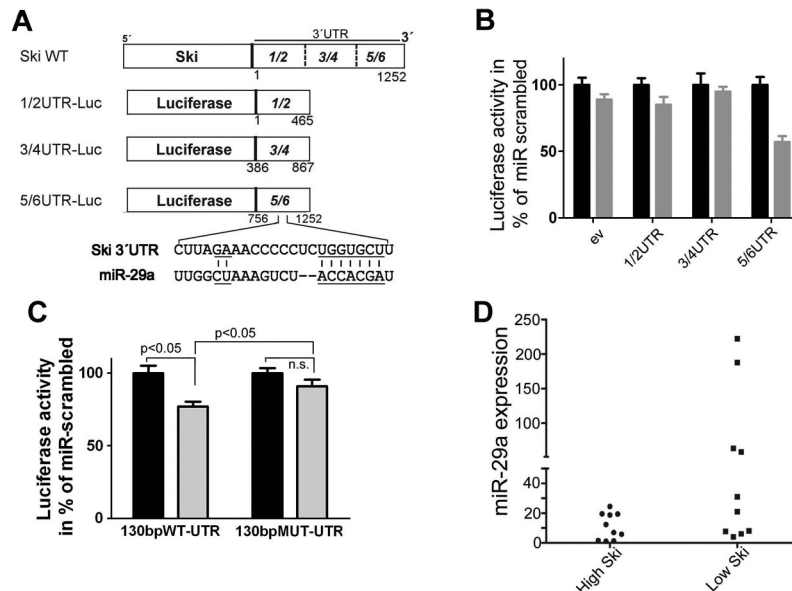


Figure 2. miR-29a binds to 3'UTR of *SKI* and is associated with low *Ski* expression in primary AML cells. (A) Scheme of the luciferase constructs. The 3'UTR of *Ski* was subdivided into 3 approximately 450-bp overlapping fragments (1/2 bp 1-465, 3/4 bp 386-867, 5/6 bp 756-1252) and cloned in the 3' direction of the luciferase gene in the pGL3 control vector. A putative binding site for miR-29a in fragment 5/6 of *SKI* 3'UTR at bp 1066-1088 is shown. Underlined are complementary parts of miR-29a and *SKI* 3'UTR. (B) miR-29a targets the 3'UTR of *Ski* in vitro. The empty luciferase reporter plasmid (ev) or luciferase reporter plasmids carrying the 1/2, 3/4, or 5/6 fragment of the 3'UTR of *Ski* (1/2-UTR, 3/4-UTR, 5/6-UTR) were cotransfected with scrambled precursor miRNA or miR-29a precursor and with pRL-TK-Luc in HeLa cells. Twenty-four hours after transfection, *Firefly* luciferase activity was measured. Black bars indicate miR-scrambled; gray bars, miR-29a. Results are representative of 3 individual experiments with 5 replicates. Normalized *Renilla* luciferase expression in cells transduced with the different *SKI*-3'UTR plasmids and miRNA-scrambled was set at 100%. Values are mean \pm SEM. (C) miR-29a targets its predicted binding site in *SKI*-3'UTR. The luciferase reporter plasmids 130bpWT-UTR or 130bpMUT-UTR contained a 130-bp fragment of 5/6-UTR that flanked the putative binding site in 5/6 at position 1066-1088. The original putative binding sequence CUUAGAAACCCCCUCUGGUGCUU was mutated to CUUAGCAACCTCCUCUCGUACCU. The changed bases are underlined in Figure 2A. HeLa cells were cotransfected with scrambled precursor miRNA (black bars) or miR-29a precursor (gray bars) and with pRL-TK-Luc. Twenty-four hours after transfection, *Firefly* luciferase activity was measured. Results are representative of 3 individual experiments with 5 replicates. Normalized *Renilla* luciferase expression in cells transduced with the different 3'UTR-plasmids and miRNA-scrambled was set at 100%. Values are mean \pm SEM. (D) miR-29a and *Ski* expression are inversely associated in human AML samples. Statistical analysis of *Ski* Western blot data and miR-29a quantitative RT-PCR data showed a significant correlation ($P = .020$) of high miR-29a expression and low *Ski* expression in AML patient samples ($n = 21$).

In keeping with this, overexpression of miR-29a decreased proliferation of HL60 cells (Figure 1D).

Ski may be a transcriptional corepressor¹⁶ or coactivator.¹⁷ In IFB melanoma cells, *Ski* acts as a coactivator of the neuronal cell adhesion molecule gene, *Nr-CAM*.¹⁸ We transfected IFB cells with miRNA precursor 29a (fold expression compared with scrambled: 25) and determined expression of *Ski* using Western blot and of *Nr-CAM* using PCR. Expression of miR-29a inhibited *Ski* protein and *Nr-CAM* gene expression, in keeping with our hypothesis (Figure 1E).

We next investigated whether inhibition of miR-29a would lead to increased *Ski* expression. NW1539 melanoma and HL60 cells express miR-29a (supplemental Figure 4). These cells were incubated with an inhibitor oligonucleotide against miR-29a or scrambled. Addition of anti-miR-29a induced *Ski* expression in NW1539 (Figure 1F) and HL60 (Figure 1F; fold down-regulation of miR-29a compared with scrambled: 10).

miR-29a targets the 3'UTR region of *Ski*

To analyze the function of miR-29a, we transfected HeLa cells with 3 different luciferase constructs of *SKI* wild-type 3'UTR (Figure 2A) and miRNA precursor 29a. miR-29a significantly reduced activity of the 5/6-UTR construct compared with other constructs (Figure 2B). Endogenous miR-29a also reduced activity of the 5/6-UTR construct (supplemental Figure 5), which indicates a binding site for miR-29a in this region (756-1252 bp). In silico analysis (www.targetscan.org) identified a putative binding site for miR-29a in the *SKI* 3'UTR at 1066-1088 bp (Figure 2A), which is conserved in *Homo sapiens*, mouse, rat, and dog. To confirm, we

transfected HeLa cells with miRNA precursor 29a and luciferase constructs carrying wild-type or mutated predicted miR-29a binding site flanked by 130 bp of 5/6-UTR. The introduction of mutations of the putative binding region abolished the effect on luciferase activity, which supports the notion that miR-29a binds to this region (Figure 2C).

Expression of miR-29a and *Ski* is inversely correlated in human AML samples

To address whether miR-29a is negatively associated with *Ski* expression in vivo, we analyzed 21 AML samples with different karyotypes (cohort 3; supplemental Table 6 and supplemental Figure 6). Samples with very high miR-29a expression revealed low *Ski* protein expression ($P = .020$; Figure 2D). Consistent with robust repression of *Ski* by miR-29a, no single patient sample showed high-level expression of *Ski* in the presence of miR-29a.

In conclusion, we show here that miR-29a regulates *Ski* expression in AML, thus suggesting a tumor-suppressive role of miR-29a, as has been described by others.¹⁹ In contrast, Han et al²⁰ observed that miR-29a is overexpressed and induces aberrant self-renewal in AML. We also observed a broad range of miR-29a expression in primary AML samples (Figure 2D). Because miRNAs do not regulate just one target, it is conceivable that in different AMLs, specific miRNAs may play different roles. Therefore, it is likely that the loss of miR-29a expression contributes to the up-regulation of the oncogene *SKI* in this subgroup of patients. This provides a mechanistic explanation for our original observation of high *Ski* expression in AML with $-7/\text{del}7q$. Because high-level expression of *Ski* is experimentally and clinically linked

to retinoic acid resistance, this directly links drug resistance to a defined genetic aberration. Of note, it has been shown recently that miR-29a also regulates DNA methyltransferases.²¹ Together with our finding of miR-29a as a regulator of Ski, which is known to function in association with histone deacetylase in nuclear corepressor complexes,²² this suggests that the tumor-suppressive role of miR-29a is based at least in part on deregulated epigenetic control of leukemogenic gene expression.

Acknowledgments

The authors thank the members of the AML-2003 study group for contributing patient samples and the participating patients for letting them study their tumor samples. They thank Professor Elke Jäger, Nord West Krankenhaus Frankfurt, Germany, for providing the cell line NW 1539. They thank Lukas Rycak and Lisa-Marie Weiss for technical support.

This work was supported in part by grants from the Bundesministerium für Bildung und Forschung (NGFN2: FKZ 01GS0449, NGFNplus: FKZ 01GS0880), the Deutsche Forschungsgemeinschaft (Transregio 17, project C3; KFO 210, project 3), the

Deutsche José Carreras Leukämie Stiftung, and a nonrestricted grant from Dr Reinfried Pohl.

Authorship

Contribution: S.T. designed and performed research, collected data, analyzed and interpreted data, and wrote the manuscript; T.I. performed research, collected, analyzed, and interpreted data, performed statistical analysis, and wrote parts of the manuscript; J.R. performed research experiments and analyzed data from experiments; D.O. designed research and contributed analytical tools; T.S. designed research, interpreted data, and wrote parts of the manuscript; and A.N. designed research, interpreted and analyzed data, performed statistical analysis, and wrote the manuscript.

Conflict-of-interest disclosure: The authors declare no competing financial interests.

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2011 118: 1899-1902
doi:10.1182/blood-2010-09-306258 originally published
online June 17, 2011

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