Biological Activities of RUNX1 Mutants Predict Secondary Acute Leukemia Transformation from Chronic Myelomonocytic Leukemia and Myelodysplastic Syndromes

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Abstract

Purpose: Transcription factor RUNX1 is essential for normal hematopoiesis. High mutation frequencies of RUNX1 gene in chronic myelomonocytic leukemia (CMML) and myelodysplastic syndromes (MDS) have been described, whereas the biologic significances of the mutations were not investigated. Here, we aimed to correlate the biologic activities of the RUNX1 mutants with the clinical outcomes of patients.

Experimental Design: We examined the mutational status of RUNX1 in 143 MDS and 84 CMML patients. Then, we studied the DNA and CBP binding abilities of all the RUNX1 mutants identified by using electrophoretic mobility shift assay and co-immunoprecipitation assay, and also determined their activities on target C-FMS gene induction by Western blotting and luciferase reporter assay. Using luciferase reporter assay, the relative biologic activities of each RUNX1 mutant could be quantified and correlated with the patient outcomes by statistical analyses.

Results: We observed that most RUNX1 mutants had reduced abilities in DNA binding, CBP heterodimerization, and C-FMS gene induction. The relative biologic activities of RUNX1 mutants were grouped into high- and low-activity mutations. Correlation of the activities of RUNX1 mutants with the clinical outcomes revealed that patients harboring lower activities of RUNX1 mutants had a higher risk and shorter time to secondary acute myeloid leukemia transformation in MDS and CMML. In multivariate analysis, low RUNX1 activity remained an independent predictor for secondary acute myeloid leukemia–free survival in MDS patients.

Conclusions: The biologic activity rather than the mutational status of RUNX1 might be an indicator in predicting outcome of patients with MDS and CMML. Clin Cancer Res; 21(15): 3541–51. ©2015 AACR.

Introduction

Chronic myelomonocytic leukemia (CMML) and myelodysplastic syndromes (MDS) are clonal hematopoietic malignancies. Both are characterized by dysplasia of one or more myeloid lineages and with high possibilities of transformation to secondary acute myeloid leukemia (sAML). Cytogenetic and genetic alterations in patients with MDS and CMML have been a subject of investigation over the last decade. Previously, we and others have described a high mutation rate of RUNX1 in CMML (1–3). However, the clinical relevance of dysfunction of RUNX1 mutations has not been investigated. In the present study, we sought to study the biologic function of the RUNX1 mutants to further determine the prognostic impact of RUNX1 mutation.

RUNX1 is an essential transcription factor for normal fetal liver hematopoiesis (4). Knockout of RUNX1 caused severe hemorrhage within the brain and vertebral canal of the mouse embryo and lethality at E12.5 (4). In adult mice, RUNX1 was expressed in multiple hematopoietic lineage cells, mainly in myeloid, lymphoid, and megakaryocytic, and less in erythroid lineage cells (5, 6). RUNX1 was first identified in patients with translocation involving (8;21) AML. In addition to the translocation, intragenic mutations of RUNX1 were also frequently detected in de novo MDS (2–3, 7, 8), dominant familial platelet disorder (9), therapy-related MDS/AML (10), CMML (1), and de novo AML (11), especially AML M0 subtype (12, 13). Two distinct promoters generate 3 RUNX1 isoforms, including RUNX1a and RUNX1b transcribed from the P2 proximal promoter, and RUNX1c from the distal P1 promoter (14). RUNX1b and RUNX1c proteins are different at their first promoter-specific exons, but their remaining 448 amino acids are identical and exert similar functions. Structurally, RUNX1 protein is composed of an N-terminal Run homology domain (RHD) and a C-terminal transactivation domain (TAD) which mediates DNA binding and gene transactivation, respectively (15, 16). However, RUNX1a protein derived from alternative

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Translational Relevance

In the present study, we systematically analyzed the biologic activities of RUNX1 mutations identified from patients with chronic myelomonocytic leukemia or myelodysplastic syndromes by in vitro functional assays. Apart from the mutational status of RUNX1 gene, we demonstrated that the biologic activity of mutant RUNX1 was a more important predictor of disease progression. Patients with the lower activities of RUNX1 mutants had a higher risk and shorter time to secondary acute myelogenous leukemia transformation. Our study was the first one to directly correlate the biologic functions with clinical outcome and showed their prognostic relevance. Our results suggest that mutant RUNX1 activity would be a useful indicator in predicting the progression of the diseases, and potentially helpful in identifying patients for early therapeutic intervention, even in case of low-risk patients.

Cell culture, DNA transfection, and lentivirus production

HEK293T cells were cultured in DMEM supplemented with penicillin/streptomycin, 1 mmol/L L-glutamine, and 10% FBS. Leukemia and lymphoma cell lines, including KG1a, HL60, NB4, U937, THP-1, MV4-11, RS4-11, Kasumi, K562, KU812, REH, BIA, Raji, and Jurkat cells, were all cultured in RPMI-1640 medium supplemented with penicillin/streptomycin, 1 mmol/L L-glutamine, and 10% FBS. All the cell cultures were kept in a 37° C humidified incubator supplemented with 5% CO2. Transfection of DNA into cells was performed using TransIT-LT1 Transfection Reagent (Minus) according to the manufacturer’s instructions. The methods for production and infection of lentiviruses were performed as our previous description (22). Briefly, 0.5 μg pBabe, 1 μg pMD2.G, and 1.5 μg pCMSCV vector or pCMSCV-FLAG-RUNX1b were cotransfected into 1.2 × 106 HEK293T cells. After 60 to 72 hours, the supernatants containing infectious lentiviruses were collected, filtered through a 0.45 μm filter, and incubated with target cells for transduction.

Electrophoretic mobility shift assay

HEK293T cells were seeded in 6-well plates at the density of 7.5 × 105 cells/well. After 24 hours, the cells were transfected with 0.5 μg pCR3-CBFβ combined with 0.5 μg expression plasmids of either wild-type (wt)-RUNX1b, its mutants, or control vector, pcDNA, respectively. The nuclear extracts of the cells were harvested as previously described (22) and applied for electrophoretic mobility shift assay (EMSA) by using the LightShift Chemiluminescent EMSA Kit (Thermo scientific) according to the manufacturer’s instructions. Briefly, both forward and reverse strands of the oligonucleotides were labeled with biotin at the 5’ ends and annealed together to form a double strand probe. The probe sequences consisting of C-FMS promoter are 5’-CAAACCTCTGGTGTCGATGGTGG-3’. The underlined nucleotides are recognized by RUNX1, and the mutant (mt) probe was substituted to TCGTAG. The binding reaction was carried out in a total volume of 20 μL containing 4 μg nuclear extracts, 1 ng biotin-labeled probe, 1 μg poly(dI-dC), 2.5% glycerol, and 0.05% Brij-35.
Co-immunoprecipitation assay

FLAG-wt-RUNX1b or FLAG-RUNX1b mutants were co-expressed with CBFβ in HEK293T cells. Cell lysates were extracted with RIPA buffer and incubated with anti-FLAG M2 affinity gel at 4°C for 2 hours. The gel was washed 4 times with RIPA buffer and subjected to SDS-PAGE and Western blot analysis.

 Luciferase reporter assay

K562 cells were seeded at a density of 1 × 10^5 cells per well in a 24-well plate and then transfected with 0.3 μg C-FMS promoter luciferase reporter plasmid, pMCSF-R(mB)-luc (Addgene; ref. 23), combined with 0.1 μg pcDNA or pcDNA-RUNX1b mutant plasmids, and 0.1 μg pEGFP-C1 (Promega) as internal control using TransIT-2020 transfection reagent (Mirus), and mixed with Bright-Glo Luciferase assay reagent (Promega) for detection of luciferase activities and GFP fluorescent intensity. The relative activity of each RUNX1b mutant was derived by normalization of each luciferase intensity with its GFP intensity and then divided by the value of wt-RUNX1b.

Statistical analysis

Fisher exact test, χ2 analysis, and the unpaired t test were used to make comparison between groups. The Cox proportional hazards regression model was used to estimate HRs of sAML-free survival according to the activities of the RUNX1 mutants on C-FMS promoter. The log-rank test was used to assess the probabilities of sAML transformation. All the statistical analyses were performed with an SPSS software version 8.0 for Windows (SPSS Inc.).

Results

Frequencies and patterns of RUNX1 mutations in patients with CMML and MDS

RUNX1 mutations were detected in 27 of 84 (32.1%) patients with CMML and 20 of 143 (14.0%) patients with MDS at initial diagnosis. The mutation patterns of RUNX1 of the patients with CMML and MDS are listed in Table 1. Of the patients carrying RUNX1 mutations at diagnosis, additional 19 genes related to myeloid neoplasms were also analyzed. The frequencies and distribution of co-operating mutated genes in RUNX1 mutation–positive patients are shown in Supplementary Fig. S1. The coexisting mutations included CEBPB, TET2, DNMT3A, IDH2, ASXL1, EZH2, FLT3, NRAS, PTPN11, CBL, and TP53, with epigenetic regulator genes being the most frequently involved in both CMML and MDS patients.

Abilities of RUNX1 mutants to bind DNA and heterodimerize with CBFβ

RUNX1 is a transcription factor. It directly binds to DNA but requires dimerization with CBFβ to stabilize its interaction with DNA. To assess biologic impacts of mutant RUNX1 proteins, we examined the abilities of DNA binding and heterodimerization with CBFβ of the RUNX1 mutants identified from our patients. Figure 1A is the result of EMSA, in which the top panel shows the RUNX1b mutants identified from CMML, and the bottom panel shows the RUNX1b mutants identified from MDS. All the RUNX1b expression constructs were in-frame fused with a FLAG tag at their N-termini. The wt-RUNX1b formed two clear complexes with the DNA probe comprised with the C-FMS promoter region. Anti-FLAG antibody (F) caused supershift of the RUNX1–DNA complexes, whereas equal amount of control mouse IgG (m) did not, indicating the presence of RUNX1b protein in the complexes. Cold probes are composed of the same DNA sequences (w) or mutant sequences (m) with the probe, but lacking biotin label at their 5’ termini, so they would not show any signal on the gel. Excess cold probes were served as competitors to compete the binding of RUNX1b protein with biotin-labeled probe. Two hundred–fold excess of wild-type (w) cold probes disrupted the 2 complexes on the gels, but mutant probes (m) did not, suggesting the binding of RUNX1b with the probe is sequence specific. The truncation mutants (Ile515Hisfs* 36 and Arg139*) with partially destructive RHD completely lost DNA binding abilities. However, all the truncation mutants retaining the intact RHD (Ser195Profs*15, Arg293*, Gln186Argfs*24, Thr219Hisfs*15, Gln245*, Met283* and Ser383*) exhibited comparable DNA binding ability with wt-RUNX1b, supporting the integrity of RHD is a determinant factor for DNA binding. The four missense mutants, Arg80Cys, Asn109Lys, Gly141Val, and Arg174Gln, completely abolished their DNA binding, confirming that they may affect the important residues for DNA recognition. The other mutations located within RHD showed various degrees of impaired DNA binding abilities, which is related to the polarity and charge of the mutant amino acids, and their distance to DNA binding amino acids. Cys772Trp, His787Gln, and Trp79Arg showed a decreasing affinity with DNA as they are closer to Arg80 (Fig. 1A, top left blot). Although Arg139Gly and Arg139Gln mutated at the same residue, the chemical properties of glycine and glutamine are very different, which might be attributed to their different DNA binding abilities (Fig. 1A, bottom right blot). All of the C-terminal frameshift mutants retained DNA binding ability, but their patterns of DNA complexes were different from wt-RUNX1b, suggesting different protein complexes were formed. The protein expression of RUNX1 mutants in the nuclear extracts subjected to EMSA was confirmed by Western blot analysis as shown in Fig. 1B.

Figure 2 showed the results of coimmunoprecipitation with CBFβ of the RUNX1 mutants. Six mutations, Arg139*, Ile150Hisfs*36, Asn109Lys, Ser114Leu, Glu111_Ser114 dup, and Ala160Thr, located within area I or area II, lost or diminished their interactions with CBFβ. Area 1 and area II are hydrophilic regions. Cys72Trp and Ser73Phe are both aromatic and hydrophobic residues. They may change the physical
Table 1. Mutation patterns of RUNX1 with their effects on C-FMS and risk of sAML transformation in patients with CMML and MDS

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>Nucleotide*</th>
<th>Amino acid</th>
<th>DNA binding</th>
<th>CBFβ dimerization</th>
<th>C-FMS activation</th>
<th>sAML transformation</th>
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</thead>
<tbody>
<tr>
<td>CMML1</td>
<td>18G&gt;T</td>
<td>Glu61*</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>CMML2</td>
<td>184_185insC</td>
<td>Leu62Profs*</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>CMML10</td>
<td>1148C</td>
<td>Arg382</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>CMML14</td>
<td>216G&gt;C</td>
<td>Cys72Thr</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>CMML15</td>
<td>234C&gt;A</td>
<td>His78Gln</td>
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<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>CMML16</td>
<td>235T&gt;C</td>
<td>Trp79Arg</td>
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<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>CMML17</td>
<td>238C&gt;T     +</td>
<td>Ser73Phe</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>CMML18</td>
<td>327T&gt;A</td>
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<td>–</td>
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<td>+</td>
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<td>–</td>
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<tr>
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<td>Arg139Gly</td>
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<td>–</td>
<td>+</td>
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<td>–</td>
<td>+</td>
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<td>332_345dup</td>
<td>Glu112Ser14dup</td>
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<td>–</td>
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<tr>
<td>CMML24</td>
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<td>Ser268Glyfs*311</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>CMML25</td>
<td>969_988del</td>
<td>Gly242Aspfs*242</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>CMML26</td>
<td>1021_1028del</td>
<td>Met341Hisfs*229</td>
<td>+</td>
<td>+</td>
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<td>+</td>
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<tr>
<td>CMML27</td>
<td>1103_1104insC</td>
<td>Phe369Valfs*15</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>MDS1</td>
<td>51_52insA</td>
<td>Thr18Asnfs*</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>MDS2</td>
<td>270_271insGTGTTTATAG</td>
<td>Val92Phefs*6</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>MDS3</td>
<td>415C&gt;T</td>
<td>Arg139</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>MDS4</td>
<td>596del</td>
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<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<tr>
<td>MDS5</td>
<td>654_655insC</td>
<td>Thr219Hisfs*15</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>MDS6</td>
<td>733C&gt;T</td>
<td>Gin245</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<tr>
<td>MDS7</td>
<td>847del</td>
<td>Met283</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
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<tr>
<td>MDS8</td>
<td>877C&gt;T</td>
<td>Arg293</td>
<td>+</td>
<td>–</td>
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<td>+</td>
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<tr>
<td>MDS9</td>
<td>1148C&gt;A</td>
<td>Ser383</td>
<td>+</td>
<td>–</td>
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<td>+</td>
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<tr>
<td>MDS10</td>
<td>218C&gt;T</td>
<td>Ser73Phe</td>
<td>+</td>
<td>–</td>
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<td>+</td>
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<tr>
<td>MDS11-12</td>
<td>232C&gt;T+478G&gt;A</td>
<td>His78Tyr+Ala160Thr</td>
<td>–</td>
<td>–</td>
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<td>Arg135</td>
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<tr>
<td>MDS14</td>
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<td>Arg396</td>
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<tr>
<td>MDS15</td>
<td>416G&gt;A</td>
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<tr>
<td>MDS16</td>
<td>422G&gt;T</td>
<td>Gly141Val</td>
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<tr>
<td>MDS17</td>
<td>521G&gt;A</td>
<td>Arg139Gln</td>
<td>+</td>
<td>–</td>
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<td>+</td>
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<tr>
<td>MDS18</td>
<td>1247T&gt;G</td>
<td>Val425Gly</td>
<td>+</td>
<td>–</td>
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<td>+</td>
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<tr>
<td>MDS19</td>
<td>1315A&gt;T</td>
<td>Met439Leu</td>
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<td>–</td>
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<td>MDS20</td>
<td>314_315insC</td>
<td>Ser129Leufs*244</td>
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<td>MDS21</td>
<td>293_297insG</td>
<td>Asp424Glyfs*149</td>
<td>+</td>
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*Accession number: NM_0000001890.

†Single nucleotide variants also present in complete remission samples in AML (11).

Properties of area II by introducing hydrophobic amino acids near area II, therefore abrogated the interaction with CBFβ. Taken together, our results provided direct molecular evidences of structural lesions of the mutants correlated well with DNA and CBFβ binding changes.

Downregulation of target gene expression by RUNX1 mutants

After examining DNA binding ability of each RUNX1 mutant on C-FMS promoter, we further checked whether RUNX1 mutants affect C-FMS protein expression. RUNX1 gene encodes 3 isoforms RUNX1a, RUNX1b, and RUNX1c. In order to rule out the effects of endogenous RUNX1 protein, several leukemia and lymphoma cell lines were examined to select candidate cell lines for the following assays. Expression plasmids of C-FMS, PU.1, RUNX1a, RUNX1b, and RUNX1c were transfected into 293T cells, and these transfected cell lysates were taken as positive controls in Western blot. As shown in Fig. 3A, RUNX1b or RUNX1c protein was detected in KG1a, THP-1, MV4-11, Kasumi, K562, KU812, RS4-11, REH, and Jurkat cells, and none of the cells had detectable RUNX1a protein. We then transduced RUNX1b protein to RUNX1-negative HL60 and U937 cells to examine its effect on the induction of C-FMS. As shown in Fig. 3B and C, forced expression of wt-RUNX1b in HL60 and U937 cells could induce C-FMS protein and mRNA expression, respectively. Therefore, all the RUNX1 mutants were transduced to HL60 and U937 cells to compare their biologic activities with wt-RUNX1b. Figure 3D shows a representative result in U937 cells. Compared with wt-RUNX1b, C-FMS protein level was decreased in most RUNX1 mutant–expressing cells. Seven mutants, Cys72Trp, Ser114Leu, Pro398Leu, Val425Gly, Met439Leu, Asp424Glyfs*149, and Ala160Thr, showed relatively higher levels of C-FMS protein expression compared with other mutants. To more accurately estimate the activity of each RUNX1 mutant, luciferase reporter assay of C-FMS promoter

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was adapted and the results are shown in Fig. 3E. C-FMS is the most well-characterized promoter regulated by RUNX1 and is also the only commercially available one to estimate RUNX1 activity. The trend of C-FMS induction in Fig. 3D (C-FMS protein) and Fig. 3E (C-FMS promoter activity) is similar. To determine the activities of the RUNX1 mutants, the optimal cutoff point was estimated by ROC curve. A cutoff point at 0.520 of the relative activity on C-FMS promoter showed the best sensitivity (0.875) and specificity (1.0). The RUNX1 mutations with reporter activities higher than 0.520 were considered as high-activity mutations, and those with reporter activities lower than 0.520 belonged to low-activity mutations. The mutation types and mutant RUNX1 activities of the patients are summarized in Table 1. The seven mutants which induced comparable levels of C-FMS protein in Fig. 3D were set as high-activity mutations.

The correlation between mutant RUNX1 activities and clinicohematological characteristics

To further correlate the role of RUNX1 mutation in disease progression, clinicohematological characteristics and outcome were analyzed. The patients without RUNX1 mutation were counted as high activity. A comparison of clinicohematological features between the 2 groups of high and low activities in MDS and CMML is shown in Supplementary Table S1. No differences were observed with respect to gender, hemoglobin level, white blood cell (WBC) count, percentage of blasts in BM, WHO subtype, cytogenetic risk group, or revised International Prognostic Scoring System (IPSS-R) between mutation-positive and -negative patients in both MDS and CMML. Patients with low activity were significantly older in MDS (P = 0.0002) and younger in CMML (P = 0.027). Platelet counts were significantly lower in the low-activity group of CMML (P = 0.002). Fifteen of 24 (62.5%) patients with CMML in the low-activity group progressed to sAML compared with 19 of 60 (31.7%) patients with high RUNX1 activity (P = 0.014). CMML patients with low activities transformed to sAML more rapidly (23.3 ± 12.6 months vs. median not reached, P = 0.011; Fig. 4A). For patients with MDS, all of the patients in the low-activity group progressed to sAML compared with 69 of 124 (55.6%) in the high-activity group (P < 0.0001). Likewise, MDS patients with low activities had a shorter time to sAML (12.9 ± 3.1 months vs. 21.7 ± 4.7 months, P = 0.008; Fig. 4B). There were no significant differences in overall survival between the 2 groups in both CMML (median, 12.8 ± 2.5 months vs. 8.7 ± 1.9 months, P = 0.238; Fig. 4C) and MDS patients (median, 18.2 ± 2.1 months vs. 16.0 ± 1.4 months, P = 0.246; Fig. 4D).

We also analyzed the correlation of cytogenetics and mutational status of the coexisting mutated genes with the risk of sAML transformation (Supplementary Table S2). Cytogenetics did not predict sAML transformation in both MDS and CMML patients. Mutational status of RUNX1 and its mutant activity were the most significant predictors of sAML transformation. Of the additional coexisting mutations in both MDS and CMML, only IDH2 mutation was associated with the risk of sAML transformation in CMML. Among the coexisting mutations, NPM1 and TP53 mutations predicted inferior sAML-free survival in MDS patients, and CEBPa mutation was associated with rapid sAML progression in CMML patients. Multivariate analyses showed that mutant RUNX1 activity remained an independent predictor for sAML-free survival (P = 0.010) in MDS, but not for CMML (P = 0.26).

Although NPM1 mutation (n = 6) in MDS and CEBPa mutation (n = 5) in CMML had a higher HR for sAML-free survival, the numbers of patients carrying these mutations were very small. Taken together, RUNX1 mutation status with its mutant activity had the most important impact on sAML transformation.

Discussion

We systematically analyzed all RUNX1 mutants by in vitro functional assays to unveil the possible underlying mechanisms of sAML transformation. Our study provided clear molecular evidences to verify DNA binding and heterodimerization activities of mutant RUNX1. We found that DNA binding ability of RUNX1 was more important than heterodimerization with CBFβ on its target gene regulation. Here, we chose C-FMS as an indicator for measuring the remaining biologic activities of mutant RUNX1, because the regulatory region of RUNX1 on C-FMS promoter is much well-defined compared with other RUNX1 target genes (21, 23). We adapted the luciferase reporter assay to determine mutant RUNX1 activities quantitatively, and also provided clear evidences to prove that transcriptional activities of mutant RUNX1 well reflecting their biologic activities on target protein induction in myeloid cells. RUNX1 could also regulate the promoters of IL3 and GM-CSF, and we predicted that the regulation trend of mutant RUNX1 on IL3 or GM-CSF activation might be similar, but the relative cutoff activity on IL3 or GM-CSF might be different from that (0.52) of C-FMS activity. Because we correlated the reporter assay data of C-FMS promoter with the clinical outcomes and determined all the cutoff value (0.52), the bias of only using C-FMS promoter activity to represent RUNX activity as the experimental readout might be limited.

Based on our data, DNA and CBFβ binding abilities of RUNX1 mutants could be easily predicted according to their locations and patterns. However, the ambiguous mutations, such as single point mutation within RHD or TAD, still need functional assays to determine their binding activities. Moreover, the DNA and CBFβ binding assays could not necessarily reflect the biologic activities of RUNX1 mutants on the induction of C-FMS. The Ser114Leu mutant could not bind well to C-FMS promoter and CBFβ in vitro, but could induce C-FMS expression with comparable level as wt-RUNX1 in U937 cells. The C-terminal frameshift mutants all displayed strong interaction with DNA and CBFβ, but only weak activities on C-FMS induction, except the Asp424Glyfs*149 mutant which does not affect the TAD. The dominant-negative effects of these C-terminal frameshift mutants were demonstrated by Harada and colleagues previously (2, 10), and our data were consistent with their observation. Recently, Bresciani and colleagues reported that RUNX1 can drive the emergence of nascent hematopoietic stem cells without its heterodimeric partner CBFβ (24), suggesting parts of RUNX1’s biologic functions are independent of CBFβ. In addition, lots of cellular proteins, Myb, Ets, ALY, TLE/Groucho, p300, CBP, YAP, Sin3A, MOZ, PML, PRMT1, TAL1, MLL, Shp2, SWI/SNF, etc., have been described to interact with RUNX1 (25). Of note, RUNX1 interacted with several transcriptional factors through a dynamic combinatorial mechanism to orchestrate hematopoietic differentiation (26, 27). The interacting partners that determine turn-on or turn-off of the RUNX1-targeting genes and downstream signal cascades with respect to the cell fate might be more important than mutant RUNX1 per se. Therefore, to more accurately evaluate the biologic activity of
RUNX1 mutants, in vivo cellular functional tests would be much more representative, which would take all the complicated partnerships of mutant RUNX1 into account. RUNX1a protein, which retains the RHD but lacks the TAD, is considered as an antagonist for RUNX1b and may inhibit RUNX1b function (17). In Fig. 3A, none of the cell lines had detectable RUNX1a protein. We had also performed RT-Q-PCR to examine the RUNX1a mRNA level in these cell lines. Consistent with the Western blot results, none of the cells were detectable of RUNX1a mRNA (data not shown). It has been reported that RUNX1a is preferentially expressed in immature hematopoietic cell compartments in cord blood and plays a role in stem/progenitor cells (28, 29). All the cell lines we

Figure 2. Heterodimerization ability of RUNX1 mutants with CBFβ. CBFβ combined with either wt-RUNX1b, its mutants, or control vector, pcDNA, was co-expressed in HEK293T cells. After 72 hours, the cell lysates were collected with RIPA buffer, immunoprecipitated with anti-FLAG M2 affinity gel, and analyzed by immunoblotting (IB) using anti-CBFβ Ab and anti-FLAG Ab. Protein lysates (20 µg) of each transfectant were taken as input control and analyzed by Western blotting using anti-CBFβ and β-ACTIN antibodies to confirm the expression of CBFβ and the equal loading of protein lysates.

Figure 1. DNA binding ability of the RUNX1 mutants on C-FMS promoter. The RUNX1 mutations identified from CMML and MDS were separately assayed in independent experiments. All the RUNX1b expression constructs were in-frame fused with a FLAG tag at their N-termini. CBFβ combined with either wild-type (wt)-RUNX1b, its mutants, or control vector, pcDNA, was co-expressed in HEK293T cells. Nuclear extracts and protein lysates of the cells were harvested at 72 hours after transfection, and applied for EMSA experiment (A) and Western blotting (B). A, top, the RUNX1b mutants identified from CMML; bottom, the RUNX1b mutants identified from MDS. Wt-RUNX1b protein formed 2 complexes with the biotin-labeled probe, and the complexes were supershifted by adding of anti-FLAG antibody (F), but not control mouse IgG (m). Two hundred-fold excess unlabeled wild-type (w) or mutant (m) probes were added in the reaction as cold competitors of the RUNX1-DNA complex. Each RUNX1 mutant protein formed a unique binding pattern with the probe. B, protein lysates (15 µg) of each transfectant were analyzed by Western blotting to confirm the expression of mutant RUNX1 proteins (anti-FLAG Ab); β-ACTIN served as a loading control.
Figure 3.
Aberrant regulation of C-FMS by RUNX1 mutants. A, cell lysates (20 μg) of various leukemia and lymphoma cell lines were detected for endogenous RUNX1 and C-FMS protein expression by Western blotting. HEK293T cells transfected with pMSCV-C-FMS, pCR5-Pu.1, or pcDNA-RUNX1a, b, or c, respectively, served as positive control. B–C, HL60 and U937 cells were infected with lentiviruses carrying RUNX1b expression plasmid or its control vector, pCMSCV, at MOI = 2. Four days after infection, the cells were selected with 2 μg/mL puromycin for 2 weeks and then harvested with RIPA buffer and Trizol reagent. Protein lysates (20 μg) were applied for Western blot analysis and probed with anti-C-FMS, RUNX1, and β-ACTIN antibodies (B). RNA (2 μg) of each cell was reverse transcribed and detected for C-FMS mRNA level by Q-PCR (C). D, U937 cells were infected with pCMSCV or various pCMSCV-RUNX1 mutant lentiviruses (MOI = 2). Four days after infection, the cells were selected with 2 μg/mL puromycin for 2 weeks and then harvested with RIPA buffer. The protein lysates (20 μg) were applied for Western blot analysis and probed with anti-C-FMS, FLAG, and GAPDH antibodies. E, K562 cells were cotransfected with luciferase reporter plasmid of C-FMS promoter with each RUNX1 mutant plasmid. Seventy-two hours later, luciferase intensity of each transfectant was measured and normalized with the intensity of wt-RUNX1b.
tested are lineage committed and differentiated cells, hence RUNX1a expression might be shut down in these cell lines. Val 425Gly and Met439Leu variants of RUNX1 were described in de novo AML patients previously but were also detected in complete remission samples (11), indicating both mutations are not related to AML pathogenesis. In our functional assays, the 2 mutants always displayed equivalent biologic activities as those for wt-RUNX1, supporting they are single nucleotide variants without functional changes. As these 2 variants were not leukemia-associated, we thus did not count them as mutations in the outcome analyses. Figure 5 provides a brief summary of all the results of our functional assays.

Figure 4.
Activities of the RUNX1 mutants on C-FMS induction predict sAML transformation. Kaplan-Meier estimates of sAML transformation in patients with CMML (A) and MDS (B), and overall survival for CMML (C) and MDS (D) according to RUNX1 activities on the induction of C-FMS.

Figure 5.
A cartoon of RUNX1b mutants in regulating C-FMS activation. Mutation in RUNX1 may affect its dimerization with CBFβ, DNA binding activity, or downstream C-FMS activation. Effects of individual mutants were listed according to the results from current study. Dimerization, DNA binding activity, and C-FMS induction activity were detected by co-IP assay, EMSA analysis, and luciferase reporter assay, respectively.

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RUNX1 Activity Predicts sAML from MDS/CMML
According to the results of luciferase reporter assay and Western blot, we can postulate general rules to predict the biologic activities of RUNX1 mutants: (i) the mutations with nucleotide insertion or deletion that resulted in frameshift or destructing the integrity of RHD or TAD are all low-activity mutations; (ii) missense mutations that directly affect DNA interaction (Arg60, Arg174, and Arg177) or DNA recognition (Lys83, Arg142, and Asp171) are low-activity mutations; (iii) missense mutations located outside RHD or TAD are possibly high-activity mutations; (iv) point mutations that are located within RHD or TAD and nonsense mutations terminated behind TAD could be determined for their activities by luciferase reporter assay. We have previously reported a high frequency of RUNX1 mutations in CMML and the C-terminal mutations had a significant higher risk of sAML transformation (1). However, the underlying mechanisms of sAML transformation related to RUNX1 mutation were poorly understood. Herein, we provided molecular evidences to link mutant RUNX1 activities with the expression level of its target gene, C-FMS. Moreover, we showed that the activities of RUNX1 mutants had prognostic impact on sAML transformation. Apart from the mutational status of RUNX1 gene (1), we demonstrated that the biologic activity of mutant RUNX1 was a more important predictor of disease progression. Patients with lower activities of RUNX1 mutants had a higher risk and shorter time to sAML transformation. Not only in CMML, the similar impact of RUNX1 mutations was also observed in MDS. Although RUNX1 mutations and their functional studies have been reported in several studies of MDS, CMML, and AML (2, 11), the present study was the first one to directly link the biologic functions with clinical outcome and showed their prognostic relevance. Most importantly, the remaining activities of mutant RUNX1 could be a predictor of disease progression. The luciferase reporter construct of C-FMS promoter and reagents are commercially available. If wt- and mutant RUNX1 expression plasmids are available, the results are directly correlate the biologic functions with clinical outcome.

Familial platelet disorder (FPD) is an autosomal dominant disorder caused by germline heterozygous–inherited mutation of RUNX1 gene (30). Patients with FPD have propensity to develop myeloid malignancies with a rate ranging between 20% and 65%. RUNX1 mutations identified in FPD/AML patients were mainly located at N-terminus (9, 30–32). Those mutants would express low-activity RUNX1 according to our above postulation, which further supports our findings that RUNX1 mutant activity is a predictor of sAML transformation. As additional gene mutations and chromosomal abnormalities might affect outcomes and thereby the correlation with functional attributes of RUNX1 might be affected. We thus also examined the impacts of additional 19 coexisting mutations related to myeloid neoplasms. We found that the two mutated genes with higher HR, i.e., NPM1 and CEBPU, were present in very few patients. Our detailed analysis in results demonstrated that the activities on C-FMS of RUNX1 mutants had the most important impact on sAML transformation among all the coexisting mutations analyzed in the present study.

In summary, we demonstrated the prognostic relevance of the biologic activities of RUNX1 mutants in patients with CMML and MDS. Patients with lower activities of RUNX1 mutants exhibit a higher risk and shorter time to sAML transformation. In these patients, our results showed that mutant RUNX1 activity was a useful indicator to predict the outcome of the diseases, which in turn had clinical implications of identifying patients for early therapeutic intervention with a more effective agent even in patients who did not have high risk IPSS-R.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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Biological Activities of RUNX1 Mutants Predict Secondary Acute Leukemia Transformation from Chronic Myelomonocytic Leukemia and Myelodysplastic Syndromes

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