SIRT5 Is a Druggable Metabolic Vulnerability in Acute Myeloid Leukemia


RESEARCH ARTICLE

Association for Cancer Research.
INTRODUCTION

Acute myeloid leukemia (AML) is a genetically heterogeneous myeloid neoplasm with poor prognosis (1). With the exception of acute promyelocytic leukemia, standard therapy for AML remained unchanged for three decades, consisting of induction with anthracycline and cytarabine, followed by consolidation with high-dose cytarabine or bone marrow (BM) transplant (1–4). Despite high rates of complete response (CR) to initial chemotherapy, most patients relapse and eventually succumb to AML, suggesting that chemotherapy eliminates AML blasts, but not leukemia-initiating cells (LIC) that survive in the protective microenvironment of hematopoietic organs (5). Recently, therapy options have been enriched by inhibitors of FLT3 or mutant isocitrate dehydrogenase 1/2 (IDH1/2), validating the paradigm of genotype-directed therapy (6–9). Unfortunately, even with these new drugs, relapse is common and frequent due to selection of subclones with resistance mutations in the drug target (7, 10–12). Unlike FLT3 and IDH1/2 inhibitors, the BCL2 inhibitor venetoclax is active in multiple AML genotypes, indicating that targeting shared vulnerabilities in a genotype-agnostic manner can be effective (11, 13). However, many venetoclax-induced responses are not durable, as leukemia cells adapt by activating alternative antiapoptosis signaling or by reprogramming mitochondrial metabolism (14, 15). Thus, microenvironmental protection, intratumoral heterogeneity and metabolic flexibility limit the utility of current AML therapeutics.

Metabolic aberrancies are increasingly recognized as potential cancer therapy targets (16). One well-established example is elevated glycolytic flux despite adequate oxygen availability, which generates intermediates to sustain nucleic acid and protein biosynthesis in rapidly dividing cells, known as the Warburg effect (17, 18). Metabolic bottlenecks in AML include oxidative phosphorylation (OXPHOS), mitochondrial creatine kinase, branched-chain amino acid aminotransferase, glutaminase (GLS), the pentose phosphate pathway, and mitochondrial translation (19–26). While some dependencies are associated with specific genotypes such as GLS with FLT3 internal tandem duplications (ITD; refs. 24, 27), others are genotype agnostic or linked to cellular subsets such as quiescent LICs, suggesting that diverse genotypes can share metabolic vulnerabilities (28). The utility of targeting single metabolic pathways such as glycolysis (29) or GLS (30) is limited by the metabolic flexibility of cancer cells that allows for rapid adaptation and therapy escape (28, 31).

Sirtuins are NAD⁺-dependent lysine deacylases implicated in fundamental cellular processes such as senescence, DNA repair, and apoptosis (32). Posttranslational lysine acylation affects multiple protein classes, including metabolic enzymes (33). Among the seven mammalian sirtuins, sirtuin 5 (SIRT5) removes negatively charged acyl groups, specifically succiny1, malonyl, and glutaryl (34–36). Acylation is thought to occur nonenzymatically when relatively high pH and high concentration of acyl-CoA favor transfer of the acyl group to the deprotonated ε-amino group of lysines (34, 37). The
three SIRT5-dependent deacylations occur at overlapping as well as unique lysines within substrate proteins (38). SIRT5 regulates multiple metabolic pathways, including fatty acid β-oxidation, glycolysis, ketogenesis, OXPHOS, and urea cycle (34, 35, 37, 38). In several cases, deacylation of specific lysine residues was shown to modulate enzymatic activity, mechanistically linking SIRT5 and metabolic programming (39, 40). At steady state, Sirt5−/− mice exhibit only mild metabolic abnormalities, including reduced glycolysis and ketogenesis (37, 38, 41). More severe phenotypes are observed under stress, such as increased depaminergic neuronal damage upon challenge with 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) and cold intolerance upon caloric restriction (42–45). In several cases, phenotypes were attributable to SIRT5-dependent regulation of specific enzymes, such as uncoupling protein 1 in cold intolerance (43). These data indicate that SIRT5 orchestrates cellular responses to various stressors to reestablish tissue homeostasis.

We have discovered that knockdown (KD) or genetic absence of SIRT5 attenuates leukemia in multiple AML models and through several mechanisms, including oxidative stress. Inhibition of SIRT5 with NRD167, a cell-permeant SIRT5 inhibitor, impairs proliferation of AML, but not normal hematologic progenitors ex vivo, implicating SIRT5 as a therapy target in AML. Our data support the development of clinical SIRT5 inhibitors for the treatment of AML and other SIRT5-dependent cancers.

RESULTS
SIRT5 Is Essential for Survival of Primary AML Blasts Cultured on BM Stroma

To identify essential AML genes, we performed a cancer-focused shRNA screen on primary AML blasts freshly isolated from patients with newly diagnosed AML (83%–95% CD34+; n = 12; Supplementary Table S1). As limited ex vivo growth and survival of primary AML cells hinder detection of relative shRNA abundance changes, most shRNA screens in AML have used cell lines. To enhance viability and growth, and mimic protective microenvironment effects, we cultured primary AML blasts on HS-5 human stromal cells (Supplementary Fig. S1A; ref. 46). We optimized the algorithm for identification of survival/growth-critical genes, prioritizing candidates based on at least two shRNAs targeting the same mRNA with a fold-reduction ranking in the top 2% of all scores, detected in at least two samples. Thirty-four genes met these criteria in at least two samples, and nine genes

AML Cells Are Selectively Dependent on SIRT5

Both tumor-promoting and tumor-suppressive roles have been attributed to SIRT5 in solid tumors, depending on the specific context, but its function in hematologic malignancies is unknown (39). We infected CD34+ cells from additional AML patients (n = 25; Supplementary Table S1) and cord blood (CB; n = 5) with doxycycline-shSIRT52311/2312. SIRT5 KD was comparable in AML (median 52.4%, range 24.7%–89.6%) and CB (median 65.9%, range 37.5%–80.1%; P = 0.26). SIRT5 KD selectively reduced AML colony formation, with no effect on CB (Fig. 1A). For genetic validation, we infected BM cells from Sirt5−/− and Sirt5−/− mice with retrovirus for expression of the myeloid leukemia alleles FLT3-ITD, MLL-AF9, RUNXI-RUNXT1/NRAS, BCR-ABL1, and MPL. Absence of Sirt5 reduced colony formation by approximately 50%, 60%, 25%, 50%, and 20% respectively, with comparison with Sirt5+/+ controls (Fig. 1B). Routine hematopoietic parameters and myeloid colony formation were comparable between Sirt5−/− mice and Sirt5−/− littermates (Fig. 1C; Supplementary Table S3). These data indicate that primary AML cells, but not normal CD34+ cells, are at least partially dependent on SIRT5.

We engineered 22 AML cell lines to express doxycycline-shSIRT52311/2312. In most cell lines, SIRT5 KD inhibited growth, reduced colony formation, and increased apoptosis, with the strongest effects on colony formation (Fig. 1D; Supplementary Fig. S2A–S2C). In seven lines (32%), colonies were reduced by >75%, in five lines (23%) by <25%, and by 25% to 75% in the remainder. The three lines most sensitive to SIRT5 KD (CMK, SKM-1, OCI-AML2; referred to as SIRT5-dependent) and three lines most resistant to SIRT5 KD (OCI-AML3, KG1a, Marimo; referred to as SIRT5-independent) were used in most subsequent studies (Fig. 1E and H). In view of the large range of sensitivity to SIRT5 KD, we assessed potential correlations between SIRT5 dependence and genotype. However, next-generation sequencing of 52 genes recurrently mutated in myeloid malignancies in patient samples (Fig. 1A;
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**Primary cells**

![Graph showing colony formation reduction](image)

**Cell lines**

![Graph showing colony formation reduction](image)

**Supplementary Figure S1**

![Image with labeled data](image)

**Supplementary Figure S2**

![Image with labeled data](image)
Supplementary Table S1) and cell lines (Supplementary Table S4) failed to identify obvious correlations. Similarly, SIRT5 dependence was not correlated with SIRT5 protein expression (Supplementary Fig. S2D–S2F).

To rule out off-target shRNA effects, experiments were repeated with three doxycycline-inducible shRNAs and a non-inducible shRNA, each targeting different SIRT5 sequences, with consistent results (Fig. 1I; Supplementary Fig. S3A–S3C). Outgrowth after prolonged culture of SIRT5-dependent cells in doxycycline-containing media was associated with reexpression of SIRT5, suggesting cells are under selection pressure to reestablish SIRT5 expression (Supplementary Fig. S3D). Conditioned medium from HS-5 stromal cells can protect leukemia cells from cytotoxic and targeted therapies (47, 48), but did not protect AML cells from the effects of SIRT5 KD, consistent with the design of the initial screen (Fig. 1K; Supplementary Fig. S3E). Propidium iodide staining revealed increased sub-G1 cells upon SIRT5 KD in SIRT5-dependent cell lines, indicating increased apoptosis, but the proportion of cells in G0–1, S, and G2–M phases remained stable. SIRT5 KD induced neither markers nor morphologic signs of differentiation. We also confirmed that doxycycline-shSIRT52311/2312 had no significant effects on the expression of sirtuins other than SIRT5 (Supplementary Fig. S4A). Because doxycycline at high concentrations (~1 μg/mL) can inhibit mitochondrial protein synthesis (49, 50), we cultured parental cell lines in 100 ng/mL doxycycline, the concentration used in most experiments, but saw no effect (Supplementary Fig. S4B). Doxycycline at 6.25 ng/mL induced SIRT5 KD and growth inhibition in SIRT5-dependent cells as effectively as doxycycline at 100 ng/mL (Supplementary Fig. S4C and S4D). At yet lower concentrations, growth inhibition correlated with a decrease of SIRT5 protein, providing additional target validation (Supplementary Fig. S4E). Finally, we used CRISPR/Cas9 to generate single cell–derived SIRT5−/− cell lines. Compared with parental cells, SIRT5 deletion significantly reduced colony formation by CMK cells (SIRT5-dependent), but not OCI-AML3 cells (SIRT5-independent; Fig. 1I).

**SIRT5 Is Required for AML Establishment and Maintenance In Vivo**

To test whether SIRT5 is required for AML establishment and maintenance in vivo, we injected NOD-SCID IL2Rγ−/− (NSG) mice with CMK (SIRT5-dependent) or OCI-AML3 cells (SIRT5-independent) coexpressing doxycycline-shSIRT52311/2312 and luciferase, and randomized at 18 hours after injection to doxycycline-containing or regular water (control). Mice injected with CMK cells maintained on doxycycline showed no luminescence at week 3 (Fig. 2A, left), while controls were strongly positive (Fig. 2A, right). We next randomized mice to continue their regimen or switch to doxycycline-containing or regular water, respectively. In mice started on doxycycline-containing water, irrespective of randomization, we observed no luminescence until termination of the experiment (week 13; Fig. 2A, left). There was no leukemic involvement on autopsy, and BM and spleen were negative for hCD45* (Fig. 2B, left and left middle panels). In the group started on regular water, mice switched to doxycycline-containing water at week 3 showed reduction of luminescence at week 4, cleared all luminescence at week 8, and survived until termination of the experiment, without evidence for leukemia at autopsy (Fig. 2B, right middle panel, and C). In contrast, mice continued on regular water died between weeks 4 and 5 with extensive leukemic involvement (Fig. 2A and B, right). Recipients of OCI-AML3 cells rapidly developed systemic disease (Fig. 2D), and died on day 31 (doxycycline) and 29 (control), with extensive leukemic involvement (Fig. 2E and F). SIRT5 KD was maintained in hCD45* cells from doxycycline-treated mice, confirming that in vivo survival of OCI-AML3 cells was not due to reexpression of SIRT5 (Fig. 2G).

To assess the role of SIRT5 in a syngeneic context, we infected BM from Sirt5−/− and Sirt5+/+ mice with MLL-AF9 retrovirus and injected 3 × 10^5 cells/mouse into lethally irradiated Sirt5−/− mice. In this aggressive AML model, median survival in recipients of MLL-AF9–transduced Sirt5−/− cells was 60 days versus 49 days for controls (P = 0.428; Fig. 3A), with similar GFP expression (86.4% ± 1.9% vs. 85.7 ± 4.7%; P = 0.9). We transplanted 5 × 10^5 GFP−/−Lin−Kit−/− (LSK) cells/mouse from primary leukemic mice into secondary Sirt5−/− recipients. Recipients of MLL-AF9–transduced Sirt5+/+ BM developed leukocytosis, with mostly GFP+ cells, and showed massive splenomegaly at autopsy. White blood cells (WBC) in recipients of Sirt5−/− BM remained normal, with no or rare GFP+ cells, and no splenomegaly in the majority (Fig. 3B and C). Median survival in recipients of MLL-AF9/Sirt5+/+ cells was 23 days but had not been reached in recipients of MLL-AF9/Sirt5−/− cells at 8 weeks (P < 0.0001; Fig. 3C). Similarly, we infected BM cells from 5-fluorouracil (5-FU)–treated Sirt5−/− and Sirt5+/+ mice with BCR-ABL1p210-GFP retrovirus and injected 5,000 LSK cells/mouse into Sirt5−/− recipients. Median survival of mice receiving Sirt5−/− cells was 21 days, whereas 80% of mice receiving Sirt5−/− cells survived until day 47 (termination of experiment; P < 0.01; Fig. 3D). Finally, we probed the role of SIRT5 in a transgenic model of FLT3-ITD–positive myeloproliferative disease (MPD). The MPD in this model is mild, with modestly elevated WBCs and monocytosis at 4 to 6 months of age (51). FLT3-ITD transgenic mice were crossed with Sirt5−/− mice and bred to homozygosity, yielding...
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**A**

NSG mice injected with CMK<sup>shSIRT5</sup> or OCI-AML3<sup>shSIRT5</sup> were treated with Dox or No dox. 

**B**

Human CD45 ratios in mouse CD45 were measured at Weeks 3, 4, and 8.

**C, D, E**

Survival curves for CMK<sup>shSIRT5</sup>, OCI-AML3<sup>shSIRT5</sup>, and OCI-AML3<sup>shSIRT5</sup> mice treated with Dox or No dox.

**F**

Human CD45 ratios in mouse CD45 were measured at Week 3.

**G**

Western blot analysis of SIRT5 and α/β-tubulin levels in spleen and BM of CMK<sup>shSIRT5</sup> mice treated with Dox or No dox.
SIRT5 Is Required for Oxidative Phosphorylation in SIRT5-Dependent AML Cells

SIRT5 desuccinylates multiple mitochondrial proteins, including electron chain components (34, 37, 38). To identify the mechanism by which SIRT5 KD kills SIRT5-dependent but not SIRT5-independent cells, we assessed mitochondrial protein succinylation in CMK cells (SIRT5-dependent) and KG1a cells (SIRT5-independent). Succinylation, malonylation, and acetylation increased in both upon SIRT5 KD, while glutarylation was low and unchanged, altogether suggesting that SIRT5 is active in SIRT5-dependent and SIRT5-independent cells (Fig. 4A; Supplementary Fig. S4F). AML cells depend on mitochondrial protein translation and OXPHOS, and exhibit reduced spare respiratory capacity (19, 25, 28). We measured the effect of SIRT5 KD on OXPHOS and glycolysis in AML cell lines upon SIRT5 KD. OXPHOS was consistently reduced in SIRT5-dependent cell lines, starting ∼24 hours after doxycycline addition, but not in SIRT5-independent cell lines.

FLT3ITD/ITD/Sirt5+/+ and FLT3ITD/ITD/Sirt5−/− genotypes. At 5 months, WBCs, granulocytes, and monocytes were reduced in FLT3ITD/ITD/Sirt5−/− compared with FLT3ITD/ITD/Sirt5+/+ mice (Fig. 3E). Altogether these data show that SIRT5 is required for leukemogenesis by several myeloid oncogenes.

Figure 3. Absence of SIRT5 attenuates myeloid leukemia in syngeneic mouse models. A, BM from Sirt5−/− versus Sirt5+/+ C57Bl6 mice was transduced with MLL-AF9 retrovirus and injected into irradiated Sirt5−/− recipients. Kaplan–Meier survival analysis of primary recipients (n = 6/group). KO, knockout; WT, wild-type. B, GFP+Lin−Kit+ BM cells were sorted from leukemic primary recipients and injected into secondary Sirt5−/− recipients. WBC counts and percent of GFP+ blood cells were quantified at week 3, and spleen weights were measured at the time of sacrifice (unpaired t test). C, Left, Kaplan–Meier survival analysis of secondary recipients of MLL-AF9-expressing cells. Right, representative blood smears at week 3. D, Kaplan–Meier survival analysis of primary recipients of BCR-ABL1×2×2 transduced Sirt5−/− versus Sirt5+/− Lin−Sca−Kit+ cells (n = 10/group). E, Left, WBC parameters in 5-month-old FLT3ITD/Sirt5−/− (left; n = 2) compared with FLT3ITD/Sirt5+/− mice (n = 6; right; unpaired t test). Right, representative blood smears at 5 months. The log-rank (Mantel–Cox) test was used for comparisons of survival (*, P < 0.05; **, P < 0.01; ***P < 0.001). Scale bars in C and E are 50 micrometers.
Figure 4. SIRT5 KD reduces OXPHOS in SIRT5-dependent, but not SIRT5-independent, cell lines. A, CMK (SIRT5-dependent) and KG1a (SIRT5-independent) cells expressing doxycycline (dox)-shSIRT5231/2321 were cultured ± 100 ng/mL doxycycline for 48 hours. Mitochondria were isolated and proteins resolved by SDS-PAGE, followed by immunoblotting with anti-succinyl-lysine and anti-SIRT5 antibodies, with Ponceau S staining as loading control. B–F, CMK (SIRT5-dependent) and OCI-AML3 (SIRT5-independent) cells expressing doxycycline-shSIRT5231/2321 were cultured ± 100 ng/mL doxycycline for up to 72 hours and subjected to metabolic profiling. B, SIRT5 expression was assessed by immunoblot. C, Oxygen consumption rate (OCR) was measured in CMK cells on an Agilent Seahorse XFe96 Analyzer under basal conditions and under stress (for details, see Methods). Top, Representative experiment. Bottom, Means of three independent experiments. D, OCR was measured in CMK ± doxycycline for 72 hours and OCR was measured as in B. Top, Representative experiment. Bottom, means of three independent experiments. E, ECAR as a proxy for glycolysis was measured upon SIRT5 KD in CMK cells under basal conditions and stress. Top, Representative experiment. Bottom, Means of three independent experiments. F, OCI-AML3 cells expressing doxycycline-shSIRT5231/2321 were cultured ± doxycycline for 72 hours, and ECAR was measured as in D. Data represent the mean ± SEM from three independent experiments. Comparisons were performed with multiple unpaired t tests (*, P < 0.05; **, P < 0.01; ***, P < 0.001).
SIRT5 KD Induces Oxidative Stress in SIRT5-Dependent, but Not SIRT5-Independent, AML Cells

We next assessed the activation state of canonical signaling pathways, including stress-activated protein kinase, MAPK, S6 kinase, PI3K, STAT3, SHP2, and SRC, but found no evidence for SIRT5-dependent regulation (Supplementary Fig. S6A). AML cells with low spare respiratory capacity are susceptible to oxidative stress (19). To test whether cell death induced by SIRT5 KD is caused by increased oxidative stress, we measured mitochondrial superoxide by flow cytometry. SIRT5 KD increased superoxide in SIRT5-dependent cells, but not in SIRT5-independent cells (Fig. 5A-D). The superoxide increase preceded apoptosis and was partially rescued by vitamin E, but not other antioxidants (Fig. 5B and C; Supplementary Fig. S5F). SOD2 detoxifies mitochondrial superoxide to oxygen and hydrogen peroxide, which is converted to oxygen and water by catalase. We compared SOD2 expression in SIRT5-dependent and SIRT5-independent AML cells but found no differences (Supplementary Fig. S6C). However, ectopic SOD2 expression blunted the superoxide increase induced by SIRT5 KD in CMK cells, reduced apoptosis, and partially restored colony formation (Fig. 5E and F). Strikingly, SOD2 KD induced growth inhibition and apoptosis only in SIRT5-dependent cell lines (Fig. 5G and H). In contrast, ectopic expression of SOD1 failed to rescue SIRT5-dependent cell lines from the effects of SIRT5 KD (Supplementary Fig. S6D). In addition, measurement of SOD2 activity revealed no change after KD of SIRT5, suggesting that SOD2 is not a direct target of SIRT5 (Supplementary Fig. S6E). We next measured the NAD+/NADH ratio and GSH level as a measure of redox buffer capacity. Both NAD+/NADH and GSH decreased upon SIRT5 KD in SIRT5-dependent but not SIRT5-independent cell lines (Fig. 5I), suggesting that SIRT5-dependent AML cell lines require SIRT5 to reduce mitochondrial superoxide and maintain redox homeostasis to prevent apoptosis.

SIRT5 Regulates Glutamine Metabolism in SIRT5-Dependent AML Cells

To identify SIRT5-regulated metabolic pathways in AML cells, we performed untargeted metabolomics on SIRT5-dependent (CMK and SKM-1) and SIRT5-independent (OCI-AML and KG1a) cell lines expressing doxycycline-shSIRT5231/2312 at 36 and 48 hours after the addition of doxycycline. Steady-state levels of multiple metabolites were altered upon SIRT5 KD, often in opposite directions according to SIRT5 dependency (Supplementary Fig. S7A and S7B). Profound reductions in tri-carboxylic acid (TCA) cycle intermediates and amino acids were observed in SIRT5-dependent cell lines, while their concentrations were increased in SIRT5-independent cell lines. We used Ingenuity Pathway Analysis (IPA) to identify metabolic networks altered by SIRT5 KD and attribute metabolite alterations to pathways. We observed mostly consistent changes in TCA cycle metabolites, which were linked to SIRT5 (Supplementary Fig. S7C). IPA also identified potential upstream regulators, including GLS and α-ketoglutarate (Supplementary Fig. S7D).

At a global level, the pathways implicated by IPA were remarkably consistent, yet mostly regulated in opposite directions, in accord with the changes in total metabolite concentrations. Top IPA hits included RNA charging as well as alanine and serine metabolism (Supplementary Fig. S8).

GLS converts glutamine to glutamate, which is metabolized to α-ketoglutarate by glutamate dehydrogenase 1 (GLUD1) or aminotransaminases (GOT1/2, GPT2, and PSAT1). Recent studies have shown that SIRT5 promotes breast cancer by activating GLS and colorectal cancer by activating GLUD1 (54, 55). As previous work has shown that some AML cells are glutamine dependent and suggested a role for GLS in constraining de novo glutathione synthesis in AML, we hypothesized that SIRT5-dependent AML cell lines may require SIRT5 for regulating glutamine metabolism (24, 27, 56). To test this, we performed stable isotope metabolic tracing experiments using [13C5,15N2]-glutamine or [1,2,3-13C3]-glucose in SIRT5-dependent and SIRT5-independent cells. Glutamine abundance was much higher in SIRT5-dependent, but not SIRT5-independent, cell lines (Fig. 6A; Supplementary Fig. S9A). To ensure the metabolite changes are due to SIRT5 KD, but not cell death, cells were analyzed after 36 hours in doxycycline, when cell viability was >90%. Initial time course experiments were performed in SKM-1 cells. [1,2,3-13C3]-glucose tracing did not show significant changes in glycolytic flux upon SIRT5 KD, consistent with Seahorse experiments showing reduced ECAR only at relatively late time points (Fig. 4E; Supplementary Fig. S5B). The glutamine/glutamate ratio was markedly increased in SIRT5-dependent cells and further elevated upon SIRT5 KD (Fig. 6B). Glutamine abundance was much higher in SIRT5-dependent cells at baseline and altered by SIRT5 KD only in SIRT5-dependent cell lines. In addition, only SIRT5-dependent cell lines showed altered abundances of TCA cycle intermediates upon SIRT5 KD (Fig. 6C; Supplementary Fig. S9B). In light of the results above, we hypothesized that SIRT5-dependent AML cells require SIRT5 to regulate glutamine flux to sustain redox homeostasis and/or anabolism. To test this, we cultured SIRT5-dependent and SIRT5-independent cells with or without glutamine, and measured apoptosis. SIRT5-dependent cell lines were more sensitive to glutamine deprivation than SIRT5-independent cell lines (Fig. 6D). Moreover, glutamine withdrawal and SIRT5 KD were synergistic (Fig. 6E).

lines (Fig. 4B–D; Supplementary Fig. SSA and SSB). Extracellular acidification rate (ECAR) as a measure of glycolysis was also reduced only in SIRT5-dependent cells, but changes tended to occur later (Fig. 4E and F; Supplementary Fig. SSC). As previous work has shown that SIRT5 KD induces mitophagy in breast cancer cells (52), we analyzed mitochondrial morphology but saw no obvious differences between SIRT5-dependent and -independent cell lines with or without SIRT5 KD (Supplementary Fig. SSD), and mitochondrial DNA copy numbers as assessed by qPCR for the mitochondrially encoded NADH-ubiquinone oxidoreductase core subunit 1 (ND1) were similar (Supplementary Fig. S5E). Chronic ethidium bromide exposure depletes mitochondrial DNA, allowing us to test whether OXPHOS is essential for viability (53). Derivative cell lines devoid of mitochondrial DNA are referred to as ρ0 cells. Repeated attempts to generate ρ0 derivatives from SIRT5-dependent lines failed (Supplementary Fig. S5F), while ρ0 cells were readily established from SIRT5-independent lines. KD of SIRT5 in these ρ0 lines had minimal effects on growth and viability, suggesting that independence of SIRT5 and OXPHOS cosegregate (Supplementary Fig. S5G and S5H).

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Figure 5. SIRT5 KD induces mitochondrial superoxide in SIRT5-dependent, but not SIRT5-independent, cell lines. A-D, KG1a cells (SIRT5-independent) and CMK cells (SIRT5-dependent) expressing doxycycline (dox)-shSIRT5231/232 were cultured for 96 hours ± 100 ng/mL doxycycline ± vitamin E (200 μmol/L). Following culture, cells were analyzed by FACS after staining with MitoSox dye to measure mitochondrial superoxide, annexin V (An V) to identify apoptotic cells positive for mitochondrial superoxide but negative for annexin V (multiple unpaired t tests). E, Percent CMK cells positive for annexin V. F, SIRT5 expression (immunoblot). G, CMK shSIRT5 cells expressing doxycycline-shSIRT5231/232 engineered to ectopically express SOD2 were cultured ± doxycycline for 72 hours. E, Left, percent MitoSox/annexin V/DAPI+ cells. Middle, percent annexin V+ cells. Right, colony formation. Comparisons were performed with paired t test. F, SOD2 expression (immunoblot). G, SIRT5-independent (KG1a, Marimo, OCI-AML3) and SIRT5-dependent (CMK, OCI-AML2, SKM-1) cell lines expressing doxycycline-inducible shSOD2 were cultured in 100 ng/mL doxycycline. Left, viable cells (MTS assay) after 96 hours. Comparisons were performed with multiple paired t test. Middle, apoptosis (annexin V staining) in SIRT5-independent cells. Right, apoptosis (annexin V staining) in KG1a cells. H, Immunoblot analysis of SOD2 expression shown for KG1a and OCI-AML2 cells. I, NAD+/NADH ratio was measured by GLO assay in SIRT5-independent (OCI-AML3, KG1a) and SIRT5-dependent (OCI-AML2, CMK, SKM-1) cell lines expressing doxycycline-shSIRT5231/232 at 24 to 72 hours after addition of 100 ng/mL doxycycline. Data represent the mean ± SEM from three independent experiments. Comparisons were performed with multiple unpaired t tests (*, P < 0.05; **, P < 0.01; *** P < 0.001).
A Small-Molecule SIRT5 Inhibitor Selectively Inhibits Cell Proliferation, Metabolism, and Colony Formation of AML Cells

To assess the potential of targeting SIRT5 catalytic activity in AML, we tested several published SIRT5 inhibitors in cell proliferation assays of AML cells and normal controls but found them indiscriminately toxic or inactive (52, 57). To overcome this limitation, we synthesized a prodrug of SIRT5 inhibitor 1 (SS11) named ethyl 3-(3-((S)-6-((((S)-1-(cyclobutylamino)-3-(1H-indol-3-yl)-1-oxopropan-2-yl)amino)-5-((3-fluorophenyl)sulfonamido)-6-oxo-hexyl)thioureido)propanato) (NRE139; Fig. 7A; Supplementary Fig. S10). The parent inhibitor, SS11, inhibits SIRT5 with an IC_{50} of 110 nmol/L in a published
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Figure 7. A small-molecule SIRT5 inhibitor, NRD167, recapitulates SIRT5 KD effects on AML cells. A, Structures of SIRT5 inhibitor 1, NRE139, and NRD167. B, HEK cells expressing FLAG-SOD1 were treated with NRD167 for 18 hours. SOD1 immunoprecipitates were probed with anti–succinyl-lysine 122 serum. One representative experiment is shown. C and D, Two SIRT5-dependent (OCI-AML2; SKM-1) and two SIRT5-independent (KG1a; Marimo) cell lines were treated with graded concentrations of SIRT5 inhibitor 1, NRE139, and NRD167 for 72 hours. C, Viable cells were quantified by MTS assay, and IC50 values were calculated. D, Apoptosis was quantified by FACS for annexin V and DAPI. E, Cells were treated with NRD167 for 24 hours, and OCR and ECAR were determined by Seahorse. (continued on next page)

biochemical assay (58) but exhibits no activity in cell-based assays. Presumably, SS11 does not enter cells, partly due to a negatively charged carboxylate moiety. We modified SS11 by masking the carboxylate as the corresponding ethyl ester NRE139, enabling cellular uptake. Inside the cell, NRE139 is converted into SS11 by ubiquitous esterases. In addition, we included the structurally closely related prodrug NRD167 (Fig. 7A). To confirm that NRD167 is cell permissive and inhibits SIRT5 catalytic activity, HEK293 cells expressing FLAG-tagged SOD1 were treated with vehicle or NRD167 (10 μmol/L) for 18 hours. FLAG-tagged SOD1 was immunoprecipitated, followed by immunoblotting with an antibody raised against SOD1 succinyl-lysine 122, a documented SIRT5 target (59, 60). Succinylation of SOD1 at lysine 122 was increased in the presence of NRD167 (Fig. 7B). The effect of SS11, NRE139, and NRD167 was compared against SIRT5-dependent (OCI-AML2; SKM-1) and SIRT5-independent cell lines (KG1a and Marimo). As expected, SS11 was inactive. NRE139 and NRD167 selectively inhibited cell proliferation and induced apoptosis in SIRT5-dependent cells, with minimal effects on SIRT5-independent cells. NRD167 was more...
potent than NRE139, inhibiting proliferation of SIRT5-dependent cell lines with an IC_{50} of 5 to 8 μmol/L and inducing >80% apoptosis at 5 to 10 μmol/L (Fig. 7C and D), and was chosen for further evaluation. Globally NRD167’s effects on OXPHOS and ECAR, as assessed by Seahorse, resembled those of SIRT5 KD (Fig. 7E), suggesting that inhibition of SIRT5 catalytic activity is sufficient to reproduce the metabolic consequences of SIRT5 KD, although subtle differences were noted such as a decrease in ECAR with NRD167 in KG1a cells and preserved spare oxidative capacity in SKM-1 cells. Next, NRD167 was tested against CD34+ cells from patients with AML and CB CD34+ cells in colony assays (n = 3 each; Fig. 7F). Reduction of colony formation was significantly more pronounced in AML versus CB samples (6.25 μmol/L: 70% ± 8.6% vs. 102% ± 4.4%, P = 0.03; 12.5 μmol/L: 62% ± 6.7% vs. 92% ± 7.9%, P = 0.044). Cells from sample 17-268 were treated ex vivo with NRD167 for 72 hours and then injected into NSG-SGM3 mice. The survival of mice injected with NRD167 for 72 hours. These data implicate SIRT5 catalytic activity as a potential therapeutic target in AML.

**DISCUSSION**

We discovered that SIRT5 KD reduced colony formation by >25% to 100% in 80% of primary AML samples and 77% of AML cell lines, while colony formation by normal CD34+ cells was unaffected. Genetic absence of SIRT5 impairs transformation of primary hematopoietic cells by AML-associated oncogenes in vitro, and absence of SIRT5 attenuates myeloid leukemia in vivo. Similar to BCL2, SIRT5 dependence is not associated with particular genotypes, and extends to p53- and N/KRAS-mutated cells, suggesting that targeting SIRT5 may be effective in these challenging cases.

Through a combination of steady-state measurements and metabolic tracing with stable isotope-labeled substrates, we identified a role for SIRT5 in regulating glutaminolysis in multiple SIRT5-dependent cell lines. Decreased glutaminolysis upon SIRT5 KD in SIRT5-dependent, but not -independent, cells, was accompanied by an increase in mitochondrial superoxide that preceded apoptosis, and was partially rescued by vitamin E or ectopic SOD2. Consistent with a critical role for this pathway, SIRT5-dependent AML cell lines were highly sensitive to SOD2 KD. In striatonigral neurons of Sirt5−/− mice challenged with the reactive oxygen species (ROS) inducer MTPT, SOD2 expression decreases much more than in Sirt5+/− controls, although the mechanism for this is unknown (42). In contrast, SIRT5 KD had no effect on SOD2 expression in AML cells. While SIRT3 has been shown to positively regulate SOD2 by lysine deacetylation (61), there is no evidence that deacetylation of any SOD2 lysines is controlled by SIRT5 (34, 35, 37, 38). Consistent with this, SOD2 activity was unaffected by SIRT5 KD in OCI-AML2 cells, suggesting that the increase in superoxide is caused by an alternative mechanism. Regardless, our data implicate glutamine metabolism in maintaining redox homeostasis in AML cells, adding to previous evidence pointing to glutamine as an AML vulnerability (23, 24, 26, 27, 56). We have now identified SIRT5 as a master regulator of this process in AML. SIRT5 may regulate glutamine metabolism at several levels and in a cell type-specific manner. In colorectal cancer, SIRT5 was shown to activate GLUD1 through deglutarylation, thereby increasing α-ketoglutarate concentrations (54). In contrast, SIRT5-dependent desuccinylation of GLS K158 in breast cancer protects GLS from ubiquitination at K158 and subsequent degradation (55). Similar to the latter study, we find that SIRT5 KD increases the glutamine/glutamate ratio in SIRT5-dependent, but not SIRT5-independent, AML cell lines, consistent with positive regulation of GLS by SIRT5. Strikingly, [15C]-glutamine at steady state is much higher in SIRT5-dependent compared with SIRT5-independent cell lines, suggesting fundamental differences in glutamine uptake. However, RNA sequencing shows comparable expression of the main glutamine transporter SLC1A5, and additional studies are needed to clarify the underlying...
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300-fold increased stoichiometry in Sirt5>lysine succinylation sites are identified, including K97 with respiratory chain complex proteins (34, 37). In complex V, 12 corresponding to the presence of SIRT5-regulated lysines in remains possible that SIRT5 directly regulates OXPHOS, which was previously associated with increases in OXPHOS ionylation of succinate dehydrogenase (SDH; complex II), hypothesis via glutaminolysis, SIRT5 may participate in glutathione synthesis via glutaminolysis, SIRT5 may participate in glutathione synthesis via glutaminolysis or selectivity over other sirtuins, or are peptide based with insufficient cell permeability (39). To the best of our knowledge, no clinical SIRT5 inhibitors have been reported to date. We have identified NRD167 as a potent, cell-permeant SIRT5 inhibitor that overcomes several of the limitations of previous SIRT5 inhibitors. While NRD167’s limited bioavailability precludes in vivo studies, inhibition of SIRT5 catalytic activity with NRD167 mirrors the phenotypic consequences of SIRT5 KD, selectively inhibiting AML over CB CD34+ cells and SIRT5-dependent over SIRT5-independent AML cell lines. These data provide a strong rationale for the development of clinical SIRT5 inhibitors to treat AML.

METHODS

Patient Samples

This study was approved by the University of Utah Institutional Review Board, based on the recommendations of the Belmont Report, and all patients provided written informed consent to protocol 45880 before donating samples. Mononuclear cells (MNC) or CD34+ cells were isolated from blood or BM of patients with newly diagnosed (N = 48), relapsed/refractory AML (N = 5), and one unknown using Ficoll-Paque Premium (GE Healthcare) and an AutoMACS Pro Separator (Miltenyi Biotec). Twelve samples (unique patients) were used in the initial shRNA screen and 51 in subsequent experiments. For clinical and molecular diagnostic details, see Supplementary Table S1.

shRNA Library Screen

Lentiviral shRNA Library. A custom pooled shRNA library targeting leukemia-related genes was provided by Cellecta (http://www.cellecta.com). This library contains 10,091 shRNAs targeting 1,287 genes associated with leukemia, as well as positive and negative control shRNAs (Supplementary Table SS). The shRNA constructs were designed in a pRSI16 Clonal Barcode vector containing a puromycin-resistant gene (Puro) and a red fluorescent protein (RFP) marker (TagRFP). Each shRNA was linked to a unique 8-bp barcode identifiable by sequencing. The pooled shRNA library was received as packed lentiviral particles. The titer of the leukemia library stocks was determined by the manufacturer as 1.56 × 109 U/mL.

Infection of Primary AML Cells. MNCs were cultured at up to 5 × 10⁶ cells/mL in RPMI supplemented with 10% FBS (Sigma-Aldrich), 2 mmol/L L-glutamine, 100 U/mL penicillin/streptomycin plus CC100 (StemCell Technologies), GM-CSF (10 ng/mL), and G-CSF (10 ng/mL; PeproTech). At 48 hours, cells were diluted to 10⁷/mL and distributed into 6-well plates at 2 mL/well. shRNA lentiviral particles were added, targeting a multiplicity of infection (MOI) of 0.3, followed by the addition of polybrene (2 μg/mL) and HEPES buffer (Invitrogen; 10 mM). The cells were centrifuged at 1,800 rpm for 90 minutes at 32°C. Following centrifugation, the plates were kept in a humidified incubator at 5% CO2 and 37°C. The medium was...
replaced with fresh medium at 12 to 18 hours after transduction. At 72 hours after transduction, the cells were pooled and RFP+ cells quantified by flow cytometry (Becton-Dickinson (BD) FACS Aria II).

**Culture and Selection.** At 48 hours after the infection of the AML cells, HS-5 human stromal cells (a kind gift of Dr. Beverly Torok-Storb, University of Washington, Seattle, WA; ref. 46) were plated in 6-well plates at 3 × 10^5 cells/well and cultured for 24 hours in RPMI1640 medium supplemented with 10% FBS. At this point, the infected AML cells were layered on top of the adherent HS-5 cells, without additional cytokines. The medium was changed every 24 hours. To avoid depleting the cytokines produced by HS-5 cells, half of the medium was removed from each well and pooled. The AML cells were spun down, and the supernatant was removed. Next, the cells were resuspended in fresh medium, and an equal volume of the previously pooled medium was redistributed to each well. After 7 to 9 days of coculture, the AML cells growing in suspension were removed and pooled. To quantitatively collect all AML cells attached to HS-5 cells, the cells were trypsinized and sorted for RFP+ on a BD FACS Aria II. The sorted RFP+ cells were combined with the remaining AML cells, pelleted, and stored for subsequent DNA extraction.

**DNA Extraction and Sequencing of Barcodes.** The cell pellets were resuspended in Qiagen Buffer P1 supplemented with 100 µg/mL RNase A (Qiagen) at a concentration of 10^7 cells/mL and mixed with 1/20 volume of 10% SDS followed by incubation for 5 minutes at room temperature. Next, cells were sheared by passing through a 22-gauge syringe needle. DNA was extracted with phenol/chloroform as reported previously (72). Sequence reads from an Illumina HiSeq were converted into barcode counts and deconvoluted by Cellecta, with subsequent merging of gene-target information. The entire final set of sequences consisted of 10,091 uniquely barcoded shRNA targeting 1,287 loci. Most genes (1,110) were targeted by eight barcodes, and the remainder by five to seven barcodes.

**Bioinformatics Analysis.** We analyzed the read reduction for all shRNA probes across all samples compared with the total reads observed for each shRNA in a simultaneously run plasmid sample (control). We initially analyzed the abundance of barcodes corresponding to survival-critical genes (as identified previously by Cellecta across multiple and diverse cell lines) included as positive controls but found the fold changes of these genes to be subtle, consistent with a general trend across the entire library. On the basis of this, we conjectured that giving greater weight to frequently recurring, highly ranked shRNAs (ranked by fold reduction compared with plasmid) across samples would increase the likelihood for identifying genes critical for leukemic cell survival and/or proliferation due to their recurrence across multiple samples. Barcode counts for each sample were normalized to the number of reads in a simultaneously assessed plasmid sample, and the relative barcode depletion was estimated by calculating the ratio of measured shRNA plasmid input with barcode output counts, adding 20 to numerator and denominator to mitigate high ratios resulting from low read counts. As such, each gene’s depletion, also referred to as fold change, is estimated as (plasmid_input gene + 20)/ (barcode_count gene + 20). Degrees of depletion were rank partitioned into percentiles for each sample. Candidate genes were prioritized by requiring that at least two of their shRNAs were ranked in the top two-percentile depletion in at least two samples among the set of 12. Sequence reads that did not correspond to known barcodes from the shRNA library were not counted toward the tally for any gene locus. Finally, genes were tallied and ranked for the total number of AML samples within this remaining set. Additional statistical calculations, including ranking of fold reductions, were performed in SAS ver. 9.1 (SAS Institute, Inc.).

**IPA**

Pathway-associated gene analyses were generated using commercially available software (Qiagen; https://digitalinsights.qiagen.com/products-overview/discovery-insights-portfolio/analysis-and-visualization/qiagen-IPA/). For pathway analysis, metabolite lists were uploaded as exp.log ratio [Kyoto Encyclopedia of Genes and Genomes (KEGG) and Human Metabolome Database (HMDB), identification numbers] into the IPA server. The IPA function Core Analysis/Metabolomics Analysis was used for the enriched pathway identification. In addition, IPA includes an upstream regulator analysis to determine whether the observed metabolic perturbations are associated with a particular upstream regulator. P values, calculated from the right-tailed Fisher exact test, reflect whether the number of overlapping metabolites associated with a particular pathway or upstream regulator is greater than expected by chance. For upstream regulator analysis, both direct and indirect relationships between metabolites and their targets were considered. The overall activation/inhibition status of the upstream regulator was determined from the level of consistency in the observed up or down changes of the metabolites. The strength of evidence was statistically represented by z-score.

**Statistical Methods**

Prism 8 (GraphPad) was used to perform all statistical analysis. For the comparisons of two groups, data were presented as mean ± SEM and analyzed by t test. For the comparisons of median survival, Kaplan-Meier curves were analyzed by the log-rank (Mantel-Cox) test. Cellular IC_{50} values were calculated by nonlinear regression analysis. P < 0.05 was considered to be statistically significant.

**Doxycycline-Inducible shRNA Constructs**

For initial validation, the two SIRT5-targeting shRNAs with the highest depletion during the screening (shSIRT2311 and shSIRT2312) were inserted into a doxycycline-inducible vector (pRSRT16-U6tet-shCMV-TetR-2A-TagRFP-2A-Puro, Cellecta) containing the wild-type tetracycline repressor (tetR), which blocks transcription unless 100 ng/mL doxycycline is added. Constructs were packaged and used individually for infection. Cells were sorted for RFP-positive cells. For primary cells, the shRNA-induced suppression of SIRT5 was assessed by measuring mRNA transcripts using SYBR Green– and SIRT5-specific primers (Supplementary Table S6) in a CFX96 Real-Time System (Bio-Rad). For cell lines, the KD of SIRT5 was assayed by immunoblotting.

**CRISPR**

**SIRT5 Guide RNA/Cas9 Expression Vector Construction.** The Lenti-CRISPR-v2-PURO plasmid was purchased from Addgene (#52961, a gift from Peng Zhang, Broad Institute, Cambridge, MA; http://n2t.net/addgene:52961; RRID:Addgene_52961; ref. 73). The puromycin-resistant gene was removed and replaced with ZsGreen1 using restriction-enzyme cloning to produce Lenti-CRISPR-v2-ZsGreen. Three 20-bp guide sequences (gRNA-A: 5′-CATCGATGAGCTGCACCGC-3′, gRNA-B: 5′-GTTCCGACCTTCAGAGGAC-3′ and gRNA-C: 5′-AAGCACAATGCTACATCTC-3′) targeting SIRT5 were selected from a published database of predicted high-specificity protospacer adjacent motif (PAM) target sites for human SIRT5. In addition, a nontargeting oligo control was cloned (5′-TGACATCAATTATACATCAT-3′). Complementary oligos were designed with 5′- and 3′-overhangs for cloning and purchased from Invitrogen. Each pair of oligonucleotides was annealed at a concentration of 10 µmol/L in annealing buffer. The Lenti-CRISPR-v2-ZsGreen plasmid was digested with BamBI (New England BioLabs) to remove the filler and gel purified. Each pair of oligonucleotides (790 pg) was ligated in the Lenti-CRISPR-v2-ZsGreen vector (50 ng) using QuickLigase and transformed in OneShot chemically competent Stbl3 cells (Invitrogen) using the manufacturer’s protocol. Clones were expanded in liquid culture,
and the extracted DNA plasmids (Qiagen) were verified by Sanger sequencing. The four plasmids created in this fashion were as follows: Lentiviral-pCR-v2-ZsGreen1-SIRT5-A, Lentiviral-pCR-v2-ZsGreen1-SIRT5-B, Lentiviral-pCR-v2-ZsGreen1-SIRT5-C, and Lentiviral-pCR-v2-ZsGreen1-Control-OLIGO.

**Lentivirus Production.** Lentiviral-pCR-v2-ZsGreen1-SIRT5 plasmids were transfected into a stochiometric mixture (21 μg) in HEK293T/17 cells using Lipofectamine 2000 and Plus Reagent (Invitrogen) together with pPAX2 (15 μg) and pVSV-g (10 μg) to generate lentiviral particles. The virus was concentrated with PEG and stored at −80°C.

**Generation of SIRT5 Knockout Cell Line.** 5 × 10^4 cells were plated in a 6-well plate in standard media in the presence of polybrene (8 μg/mL) and infected at high MOI. Four days after infection, the cells were sorted for ZsGreen1 expression and expanded in culture for 1 week. Subsequently, the cells were single-cell sorted in 96-well plates and cultured in RPMI media for 2 to 3 weeks. When single-cell colonies were formed and covered more than 50% of the well area, the cells were transferred to 12-well plates for expansion. Again, the cells were verified for ZsGreen1 expression, and only pure population clones were further analyzed. The clones obtained in this manner were processed for RNA/DNA extraction and for protein expression analysis.

**Effects of SIRT5 Knockout on Leukemogenicity.** Mouse BM cell lines transduced with leukemia-associated oncogenes (1 × 10^6 cells/dish) were plated in duplicate in methylcellulose medium without cytokine (Methocult M3231, StemCell Technologies) to detect cytokine-independent CFU-GM colonies.

For immunoblotting, cells were lysed in RIPA lysis buffer containing phosphatase and proteinase inhibitors (Cell Signaling Technology) with freshly added phenylmethylsulfonyl fluoride (PMSF; 2 mmol/L). Protein lysates were boiled in Laemmli sample buffer for 5 to 10 minutes and separated on Tris-glycine/SDS-PAGE gels (BioRad), followed by transfer to nitrocellulose membranes. For antibodies used in immunoblotting experiments, see Supplementary Table S7. Images were collected with an Odyssey Fluorescent Imaging System (LI-COR) or a Bio-Rad ChemiDoc and quantified with ImageJ.

**Plasmids**

Plasmids were obtained from various sources. For complete information, see Supplementary Table S8.

**Mitochondrial Protein Fractionation**

Cells (1 × 10^9) were pelleted, washed, and resuspended in 4 mL sucrose buffer [250 mM sucrose, 1 mM EDTA, 10 mM Tris-HCl (pH 7.4), filtered at 0.2 μm] with PMSF (2 mM/L) and kept on ice for 15 minutes until the cells expanded as visualized under a microscope. The cell suspension was pulled through an 18-gauge needle and expelled onto the wall of a 50-mL tube through a 26-gauge needle. This process was repeated 15 to 20 times, and break-up of cells was ascertained by inspection under a light microscope. The suspension was then centrifuged at 1,200 × g for 5 minutes at 4°C, and 200 μL of the supernatant was set aside for analysis of total protein. The remaining supernatant was centrifuged at 12,000 × g for 10 minutes at 4°C. Of this supernatant, 200 μL was set aside for analysis of cytosolic protein. The pellets (mitochondria) were washed one to two times with 1 mL sucrose buffer, and then lysed in 2× Laemmli sample buffer, incubated at 100°C for 6 minutes, and stored at −80°C.

**Superoxide Dismutase Activity Assay**

Superoxide dismutase activity was measured in OCI-AML2 cells 36 hours after the addition of doxycycline with the Superoxide Dismutase (SOD) Colorimetric Activity Kit (Invitrogen) using

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**Cell Culture**

**AML Cell Lines.** AML cell lines (Supplementary Table S4) were grown in RPMI1640 medium (Invitrogen) containing 10% FBS, 2 mmol/L l-glutamine, and 100 U/mL penicillin/streptomycin. In the case of OCI-AML5, TF-1, UT-7, M-07e cells, GM-CSF (10 ng/mL) was added to the culture medium. Cell lines were authenticated using the GenePrint 24 Kit (Promega) and DSMZ Online STR Analysis was added to the culture medium. Cell lines were confirmed for Mycoplasma negativity using the MycoAlert Mycoplasma Detection Kit (Lonza).

**Short-term Liquid Culture of Primary AML and CB CD34+ Cells.** FACS-sorted RFP+ CD34+ cells were plated at 5 × 10^2 to 10^3 cells/well in 96-well plates in RPMI supplemented with 10% FBS and cytokines [for AML: CC100, GM-CSF (10 ng/mL), and G-CSF (10 ng/mL); for CB: CC100 only, ± doxycycline (100 ng/mL)], for 3 to 5 days.

**Cell Proliferation Assays**

Cells were seeded in triplicate in 96-well plates (5–9 × 10^3 cells/well) ± doxycycline (100 ng/mL). Viable cells were measured using CellTiter 96 AQueous One Solution MTS Reagent (Promega) on an Epoch microplate spectrophotometer (BioTek Instruments).

**Colony-Forming Assays**

**AML Cell Lines.** Cells were seeded in duplicate at 0.1–0.2 × 10^3 cells/dish in MethoCult H4230 (StemCell Technologies) ± 100 ng/mL doxycycline or in the presence and absence of graded concentrations of NRD167. Colonies were counted 7 to 10 days after planting.

**Primary AML and CB CD34+ Cells.** FACS-sorted RFP+ (AML patient cells: 2–4 × 10^3 cells/dish; CB: 1–10^3 cells/dish) were plated in duplicate in MethoCult H4230 with CC100, GM-CSF (10 ng/mL), and G-CSF (10 ng/mL; AML cells) or CC100 only (CB), ± doxycycline (100 ng/mL). For inhibitor studies, nontransduced cells were plated with graded concentrations of NRD167. Colonies were scored after 10 to 15 days. AML colony-forming assays were considered informative if an average of at least 15 colonies/dish was present in the control (no doxycycline).

**Mouse BM Cell**

**Effects of SIRT5 Knockout on Leukemogenicity.** Mouse BM cells transduced with leukemia-associated oncogenes (1 × 10^6 cells/dish) were plated in duplicate in methylcellulose medium without cytokine (Methocult M3231, StemCell Technologies) to detect cytokine-independent CFU-GM colonies.

**Real-Time Quantitative RT-PCR**

RNA was purified with the RNeasy Kit by Qiagen, and cDNA was synthesized with iScript RT Supermix by Bio-Rad. Sirtuin family members 1 to 7 were analyzed with TaqMan Fast Advanced Master Mix (Applied Biosystems) and probe assays from Life Technologies (Supplementary Table S6). Routine monitoring of SIRT5 following induction of shRNA was performed with SsoFast EvaGreen Supermix by Bio-Rad.

**Immunoblot Analysis**

For immunoblotting, cells were lysed in RIPA lysis buffer containing phosphatase and proteinase inhibitors (Cell Signaling Technology) with freshly added phenylmethylsulfonyl fluoride (PMSF; 2 mmol/L). Protein concentration was measured using the Bradford method. Protein lysates were boiled in Laemmli sample buffer for 5 to 10 minutes and separated on Tris-glycine/SDS-PAGE gels (BioRad), followed by transfer to nitrocellulose membranes. For antibodies used in immunoblotting experiments, see Supplementary Table S7. Images were collected with an Odyssey Fluorescent Imaging System (LI-COR) or a Bio-Rad ChemiDoc and quantified with ImageJ.
Retroviral Transduction of Mouse BM Cells

Sirt5+ or Sirt5− littermates were injected with 5-FU (Fresenius Kabi; 100 μg/g of body weight). Four to five days later, BM cells were harvested from 5-FU–primed mice and cultured overnight in DMEM (Invitrogen) supplemented with 15% FBS, 15% WEHI, murine IL3 (7 ng/mL), murine IL6 (12 ng/mL), and murine SCF (56 ng/mL; PeproTech, for all mouse cytokines). Half of BM cells were then transduced with pMSCV-GFP retrovirus for expression of leukemia-associated oncogenes by two rounds of spinoculation with 10 μg/mL polybrene and HEPEs (10 mmol/L) at 2,500 rpm for 90 minutes at 32°C. Oncogenes tested were BCR-ABL1210, FL3-ITD, MLL-AP9, RUNX1-RUNX1T1/NSR3112, and MPP1115. Transduced cells were used in colony assays or transplantation models.

BM Transplantation


cells sorted from transduced C57BL/6 Sirt5+ or Sirt5− BM 48 hours after first infection. Five thousand GFP+Lin+ cells plus 3 × 10^6 irradiated BM cells from Sirt5+ or Sirt5− donors, respectively, were injected into lethally irradiated Sirt5+/− recipient mice (two doses of 450 rad, 4 hours apart). For maintenance of identical genetic background, all recipients were 6 to 11 weeks old and gender-matched Sirt5− littermates from the same colony. Mice were monitored by daily inspection, weekly body weight measurement, weekly complete blood counts, and weekly FACS for GFP. Moribund animals (see xenograft studies) were sacrificed and subjected to detailed autopsy, FACS analysis, and histology as appropriate.

MILL-AF9.

Following transduction, 3 × 10^4 cells/mouse were injected into lethally irradiated Sirt5− recipient mice (two doses of 450 rad, 4 hours apart). For maintenance of identical genetic background, all recipients were 6 to 11 weeks old and gender-matched Sirt5− littermates from the same colony. Mice were monitored as described above. For secondary transplants, 5,000 GFP+Lin+ cells sorted from the BM of primary recipients were injected into secondary Sirt5+/− recipients, with 3 × 10^5 untransduced BM cells from Sirt5+ or Sirt5− donors, respectively, for support. Mice were followed as described above for BCR-ABL1210.

Quantification of Mitochondrial DNA Copy Number

Analysis of mitochondrial DNA copy number was performed by comparing expression of the mitochondrial encoded gene NADH Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1) with the nuclear encoded gene Hemoglobin Dehydrogenase 1 (ND1).
and 2.5 mmol/L CaCl₂, and incubated with annexin V-APC (BD Biosciences). After 15 minutes, 4,6-diamidino-2-phenylindole (DAPI; Sigma-Aldrich) was added to 2 μg/mL and fluorescence was measured on a LSRFortessa (BD Biosciences) flow cytometer and analyzed with FlowJo analysis software (Treestar; ref. 62).

**GSH Measurement**

Cells were seeded in duplicate in white, opaque-walled 96-well plates (8 × 10⁴ cells/well) ± doxycycline (100 ng/mL) for 24, 48, and 72 hours. NAD/NADH and GSH were measured using luminescence-based assays according to the manufacturer’s instructions (NAD/ NADH-Glo, and GSH-Glo, Promega) on a Synergy HT microplate spectrophotometer (BioTek Instruments).

**Global Metabolic Profiling**

Oxygen consumption and glycolysis of intact cells were measured using XF Cell Mito Stress Test Kit and Glycolysis Stress Test Kit on a Seahorse XFe96 Analyzer (Agilent) at the Metabolic Phenotyping Core Facility at the University of Utah (Salt Lake City, UT) according to the manufacturer’s instructions. Briefly, Seahorse XPF96 microplates were first coated with 20 μL/well of Cell-TAK adhesive (Corning) at 22.4 μg/mL in 0.1 mol/L NaHCO₃ (pH 8.0) for 20 minutes at room temperature to increase adherence of AML cells. Next 1–1.5 × 10⁵ cells/well were attached to the plate by centrifugation at 200 × g for 3 minutes without brakes. After spinning, cells were rested at 37°C for 30 to 40 minutes in a CO₂-free incubator before analyzing. XF Base medium (DMEM without sodium bicarbonate; Agilent) was used for all experiments. Depending on the experiment, XF base medium was supplemented with either 2 mmol/L glucose (for glycolytic stress test) or pyruvate (1 mmol/L), glucose (10 mmol/L), and glutamine (2 mmol/L) for Mito Stress Test) on the day of assay and adjusted to 7.4 with 1 N NaOH at 37°C. Respiration was measured under basal conditions, with sequential addition of 1 μmol/L oligomycin (ATP synthase inhibitor), 1 μmol/L carbonic anhydrase p-trifluoromethoxyphenyldrazone ( FCCP, mitochondrial oxidative phosphorylation uncoupler), and 0.5 μmol/L rotenone and antimycin A (electron transport chain complex I and III inhibitors). Glycolysis was measured under basal conditions, with sequential addition of 10 mmol/L glucose, 1 μmol/L oligomycin, and 50 mmol/L 2-deoxy-glucose (hexokinase inhibitor).

**Steady-state Metabolomics**

**Cell Culture and Sample Preparation.** SIRT5-dependent cell lines (CMK and SKM-1) and SIRT5-independent cell lines (OCI-AML3 and KG1α) expressing doxycycline-shSIRT52311/2312 were harvested after culturing ± doxycycline (100 ng/mL) for 36 and 48 hours, and washed twice in cold PBS. Samples were aliquoted into five 1.5-mL tubes (replicates) with 8–12 × 10⁶ cells/tube, and snap-frozen in liquid nitrogen. Cell numbers were equal for each cell line at each time point ± doxycycline. For metabolite extraction, 450 μL of cold 90% methanol solution containing an appropriate amount of internal standard (1 μg of d₄-succinic acid) was added to each sample tube. Each tube was vortexed thoroughly, sonicated for 3 minutes, and incubated at −20°C for 1 hour. After incubation, the sample tubes were centrifuged at 20,000 × g for 5 minutes at 4°C. The supernatant was transferred from each sample tube into labeled microcentrifuge tubes. A quality control sample was created by removing approximately 15% volume of the collected supernatant from each sample and mixing it in a single tube. Simultaneously to the extraction of samples, process blanks were prepared in the same manner as real sample but substituting deionized water for sample.

**Gas Chromatography–Mass Spectrometry Analysis.** All gas chromatography–mass spectrometry (GC-MS) analysis was performed with a Waters GCT Premier mass spectrometer fitted with an Agilent 6890 gas chromatograph and a Gerstel MPS2 autosampler. Dried samples were suspended in 40 μL of a 40 mg/mL O-methoxylamine hydrochloride (MOX) in pyridine and incubated for 1 hour at 30°C. To autosampler vials was added 25 μL of this solution; 40 μL of N-methyl-N-trimethylsilyl trifluoroacetamide was added automatically via the autosampler and incubated for 60 minutes at 37°C with shaking. After incubation, 3 μL of a fatty acid methyl ester standard (FAMES) solution was added via the autosampler and then 1 μL of the prepared sample was injected to the gas chromatograph in the split mode with the inlet temperature held at 250°C. A 10:1 split ratio was used for analysis. The gas chromatograph had an initial temperature of 95°C for 1 minute, followed by a 40°C/minute ramp to 110°C and a hold time of 2 minutes. This was followed by a second 5°C/minute ramp to 250°C, a third ramp to 350°C, and then a final hold time of 3 minutes. A 30 m Phenomex ZBS–5 MSi column with a 5 μm long guard column was employed for chromatographic separation. Helium was used as the carrier gas at 1 mL/minute. Because of the high amounts of several metabolites, the samples were analyzed once more at a 10-fold dilution. Data were collected using MassLynx 4.1 software (Waters). Metabolites were identified, and their peak area was recorded using QuanLynx. These data were transferred to an Excel spreadsheet (Microsoft). Metabolite identity was established using a combination of an in-house metabolite library developed using pure purchased standards and the commercially available NIST library.

**LC-MS Analysis.** Prior to analysis, samples and process blanks were transferred to PTFE autosampler vials. Quality control samples were tested in four technical replicates, and the order of actual samples was randomized. An Agilent 6550 UPLC-QTOF (Agilent Technologies, Inc.) run in both positive and negative modes was used for analysis. Separation was achieved using a Sequant zic-pHILIC 2.1 × 100 mm column (Millipore Sigma) with Phenomenex Krudkatcher (Phenomenex). An internal concentration of 90% ACN (buffer A) and 10% 10 mM/L ammonium carbonate in dDH₂O (buffer B) was held for 1 minute at a flow rate of 0.3. A was decreased to 20% over 20 minutes and held for 2 minutes. A was returned to starting conditions over 2 minutes, and the system was allowed to re-equilibrate for 6 minutes between runs at a flow rate of 0.4 mL/minute. Data were collected using MassHunter 7.0 software (Agilent). Molecular features were identified using MassHunter ProFinder 8.0, and their peak area was recorded using MassHunter Quant 7.0. These data were transferred to an Excel spreadsheet (Microsoft). Metabolite identity was established using a combination of an in-house metabolite library developed using pure purchased standards and the METLIN library. Altered metabolites were identified, and statistical analysis was performed using Mass Profiler Professional (Agilent).

**Metabolic Flux**

SKM-1 cells expressing doxycycline-shSIRT52311/2312 were cultured in RPMI medium ± 100 ng/mL doxycycline. At 28, 32, or 35 hours after doxycycline addition, cells were spun down and resuspended in either RPMI medium (no l-glutamine, 21870-076, Gibco) supplemented with [1³C₅,1⁵N₂]-l-glutamine (final concentration: 2 μmol/L; CNLM-1275-H-0.1, Cambridge Isotope) or RPMI medium (no glucose, 11879–020, Gibco) supplemented with 1,2,3–¹³C₃ glucose (final concentration: 11 mmol/L; 720127; Sigma-Aldrich) ± doxycycline for 1, 4, and 8 hours, for a total time of 36 hours ± doxycycline. Cells were then harvested and washed three times with cold PBS, counted and aliquoted into 1.5-mL tubes with 1–2 × 10⁶ cells/tube, four replicates/sample/time point. Cells were then snap-frozen and stored in liquid nitrogen and shipped on dry ice to the University of Colorado (Aurora, CO). Metabolites were extracted from frozen cell pellets at 2 × 10⁶ cells/mL of ice-cold lysis/extraction buffer (5:3:2 MeOH:MeCN:H₂O) as described previously (69, 74). Following...
centrifugation, samples were randomized, and 10 μL of supernatants were injected into a Thermo Vanquish UHPLC coupled online to a Thermo Q Exactive mass spectrometer operating in positive and negative ion modes (separate runs). Metabolites were separated on a 5-minute C18 gradient as described previously (74). Instrument stability was assessed via injections of technical replicate samples every 10 runs and ensuring a peak area coefficient of variation of <10%. Metabolite assignments and peak area integrations were performed using Mavan (Princeton University, Princeton, NJ) in conjunction with the KEGG database following conversion of raw files to the .mzXML file type using RawConverter. Stable isotope tracing data was plotted in Prism 8 (GraphPad).

**Experimental Methods and Materials for Organic Synthesis**

All reagents and solvents were of analytic grade and used without further purification as obtained from commercial suppliers. Anhydrous solvents were obtained from a PureSolv-system. Reactions were conducted under an atmosphere of argon or nitrogen whenever anhydrous solvents were used. All reactions were monitored by thin-layer chromatography (TLC) using silica gel-coated plates (analytic SiO2−60, F−254). TLC plates were visualized under UV light and by dipping in either (i) a solution of potassium permanganate (10 g/L) in water (v/v) followed by heating with a heat gun. Vacuum liquid chromatography was performed with silica gel 60 (particle size 15−40 μm). After column chromatography, appropriate fractions were pooled and dried at high vacuum (<2 mbar) for at least 12 hours to give obtained products in high purity (>95%) unless otherwise stated. Evaporation of solvents was carried out under reduced pressure at a temperature below 40°C. UPLC−MS analyses were performed on a Phenomenex Kinetex column (1.7 μmol/L, 50 × 2.0 mm) using a Waters Acquity ultra-high-performance liquid chromatography (UPLC) system. Gradient A with eluent I (0.1% HCOOH in H2O) and eluent II (0.1% HCOOH in MeCN) rising linearly from 0% to 95% of H2 during t = 0.00−5.20 minutes was applied at a flow rate of 0.6 mL/minute. Preparative reverse-phase high-performance liquid chromatography (HPLC) purification was performed on a C18 Phenomenex Luna column (3 μmol/L, 100 Å, 50 × 4.60 mm) using an Agilent 1100 LC system equipped with a diode array UV detector and an evaporative light scattering detector (ELSD). Gradient B using eluent III (H2O/MeCN/TFA, 95:5:0.1) and eluent IV (0.1% TFA in MeCN) was applied isocratically at 95% during t = 5−45 minutes and then isocratically at 95% during t = 45−50 minutes was applied at a flow rate of 20 mL/minute. Analytic HPLC was performed on a C18 Phenomenex Luna column (3 μmol/L, 100 Å, 50 × 4.60 mm) using an Agilent 1100 series system equipped with a diode array UV detector.

**NREI39**

The Boc group in S1 (Supplementary Fig. S10) was removed by iPr2SiH (0.3 mL, 1.5 mmol) and TFA (5 mL, 65.3 mmol) added to a solution of S1 (870 mg, 1.35 mmol) in CH2Cl2 (7.5 mL). The reaction mixture was stirred at ambient temperature for 1.5 hours and was then concentrated in vacuo. Eksa TFA was removed by coevaporation with CH2Cl2/toluene (1:1, 2 × 100 mL), CH2Cl2/heptane/CH3OH (1:1:0.06, 2 × 100 mL), and CH2Cl2/CH3OH (1:0.06, 100 mL), affording an off-white solid, tentatively assigned as the resulting TFA salt (UPLC-MS t R 1.29 minutes, m/z 544.2; [M+H] +, C27H35N5O4SF2; Calcd 544.2), which was used without further purification. A solution of HC19-alanine tbutyl ester (50 mg, 0.32 mmol) and iPr2NET (85 μL, 0.49 mmol) in anhydrous CH2Cl2 (8.0 mL) was added dropwise (5 minutes) to a solution of S2 (Supplementary Fig. S10; 87 mg, 0.31 mmol) in anhydrous CH2Cl2 (4.0 mL) at 0°C. The reaction mixture was stirred at 0°C for 10 minutes and was then concentrated under reduced pressure. The crude residue and the TFA salt of the Boc-protected derivative of compound S1 (98 mg, ∼0.15 mmol) were dissolved in anhydrous DMF (4.0 mL). Then, iPr2NET was added (129 μL, 0.56 mmol), and the reaction mixture was stirred overnight at ambient temperature and was then concentrated under reduced pressure. Preparative reverse-phase HPLC purification of the crude residue afforded the desired ester NREI39 (Supplementary Fig. S10) (37 mg, 17% from S1) as a colorless fluffy material after lyophilization.

1H NMR (600 MHz, DMSO-d6) Δ 10.80 (d, J = 2.4 Hz, 1H, NH indole), 8.09 (d, J = 8.6 Hz, 1H, NH indole), 8.05 (d, J = 7.9 Hz, 1H, H1 indole), 7.51−7.47 (m, 2H, H2 indole, H3 indole), 7.43 (s, 1H, NH indole), 7.39−7.33 (m, 3H, H4 indole, H5 indole, NH(CH2CO2Et)), 7.31 (dd, J = 8.1, 0.9 Hz, 1H, H7 indole), 7.05 (ddd, J = 8.1, 7.0, 1.1 Hz, 1H, H6 indole), 7.01 (d, J = 2.3 Hz, 1H, H2 indole), 6.96 (ddd, J = 8.0, 6.9, 1.0 Hz, 1H, H5 indole), 4.26−4.21 (m, 1H, H3 indole), 4.13−4.02 (m, 3H, CH2CH2CH2, H1 Cyclobutyl), 3.76 (td, J = 8.6, 5.5 Hz, 1H, H4 indole), 3.59 (br s, 2H, CH2CH2CH2CO2Et), 3.20 (br s, 2H, CH2CH2CH2CO2Et), 2.61−2.55 (m, 2H, H2 Cyclobutyl), 2.54 (t, J = 6.7 Hz, 2H, CH2CO2Et), 2.33−2.03 (m, 3H, H2 Cyclobutyl), 1.98−1.93 (m, 2H, H2 Cyclobutyl), 1.84−1.74 (m, 1H, H1 Cyclobutyl), 1.68−1.60 (m, 1H, H5 Cyclobutyl), 1.49 (m, 2H, H3 Cyclobutyl), 1.49−1.27 (m, 4H, H2 Cyclobutyl, H3 Cyclobutyl), 1.23−1.13 (m, 4H, H2 Cyclobutyl, H3 Cyclobutyl), 1.05 (ddt, J = 17.0, 12.9, 4.0 Hz, 1H, H1 Cyclobutyl), 1.01 (m, 1H, H2 Cyclobutyl).

13C NMR recorded at 100 MHz, 1H NMR and 13C NMR recorded at 600 and 151 MHz, respectively, for NREI39 (Supplementary Fig. S10; 87 mg, 0.15 mmol) in deuterated solvent as internal standard ([M+H] +, C27H35N5O4SF2; Calcd 544.2). Metabolites were removed in CH2Cl2 (1.5 mL) at 0°C. The reaction mixture was stirred at ambient temperature for 0.5 hours and was then concentrated under reduced pressure. The crude residue and the TFA salt of the Boc-protected derivative of compound S1 (98 mg, ∼0.15 mmol) were dissolved in anhydrous DMF (4.0 mL). Then, iPr2NET was added (129 μL, 0.56 mmol), and the reaction mixture was stirred overnight at ambient temperature and was then concentrated under reduced pressure. Preparative reverse-phase HPLC purification of the crude residue afforded the desired ester NREI39 (Supplementary Fig. S10) (37 mg, 17% from S1) as a colorless fluffy material after lyophilization.

Nuclear magnetic resonance (NMR) spectra were recorded either on a maXis G3 quadrupole time-of-flight (TOF) mass spectrometer ( Bruker Daltonics) equipped with an electrospray ionization (ESI) source or on an Agilent 1290 UHPLC equipped with a diode array detector and coupled to Agilent 6550 QTOF mass spectrometer operated in positive electrospray or on a Bruker Solarix WR by either matrix assisted laser desorption/ionization, or ESI. Nuclear magnetic resonance (NMR) spectra were recorded either on a Bruker Avance III HD equipped with a cryogenically cooled probe (1H NMR and 13C NMR recorded at 600 and 151 MHz, respectively) or on a Bruker Avance III (1H NMR, 13C NMR, and 19F NMR recorded at 400, 101, and 377 MHz, respectively). All spectra were recorded at 298 K unless otherwise stated. Chemical shifts are reported in ppm relative to deuterated solvent as internal standard ([M+H] +, C27H35N5O4SF2; Calcd 544.2). Assignments of NMR spectra are based on two-dimensional correlation spectroscopy (COSY, HSQC, and HMBC spectra).

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Authors’ Contributions


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REFERENCES


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