Non-oncogene Addiction to SIRT5 in Acute Myeloid Leukemia

Meng Li and Ari M. Melnick

Summary: In this issue of Blood Cancer Discovery, Yan and colleagues discovered that mitochondrial deacetylase, SIRT5, is required in AML cells to support mitochondrial oxidative phosphorylation, maintain redox homeostasis, and drive glutaminolysis. The new SIRT5 inhibitor, NRD167, can efficiently target SIRT5 in AMLs at micromolar range and may constitute a novel therapeutic approach to improve clinical outcomes of patients with AML.

See related article by Yan et al. (4).

Acute myeloid leukemia (AML) is a blood cancer derived from the hematopoietic stem/progenitor cells, whereby leukemia-initiating cells (LIC) produce large numbers of leukemic blasts to destroy normal bone marrow functions, leading to disease related mortality. Many patients with AML can enter into clinical complete remission after standard chemotherapy treatments, but no more than 30% of patients survive longer than 5 years (1). Even though significant therapeutic improvements have been achieved in younger patients with AML with specific molecular features using cytotoxic agents directed toward mitochondrial processes, such as the BCL2 inhibitor venetoclax and the oxidative phosphorylation complex I inhibitor IACS-010759, for AML therapy (3). Hence, there are many opportunities to target functional hijacked by AML cells as a form of non-oncogene addiction (2, 3). Therefore, SIRT5 represents another mechanism enabling addition (2, 3). Hence, there are many opportunities to target such mechanisms to selectively disrupt AML dependencies on particular aspects of this metabolic process.

In this issue of Blood Cancer Discovery, Yan and colleagues carried out a cancer-focused shRNA screen searching for essential genes in primary human AML cells (4). SIRT5 scored as one of the top essential candidates from this screen of around 1,300 genes. One important reason why SIRT5 was selected in this study is because Sirt5 knockout mice have mild phenotypes, suggesting that strict SIRT5 dependency may be only related to disease (AML) phenotypes. SIRT5 is a member of the sirtuin protein family and localizes specifically in the mitochondria along with SIRT3 and SIRT4. Sirtuins were originally defined as NAD-dependent protein deacetylases. However, these three mitochondrial sirtuins possess different enzymatic activities due to structural differences in their enzyme pockets. SIRT5 is a protein deacetylase that removes malonyl, succinyll, and glutaryl groups, while SIRT3 works as a protein deacetylase and SIRT4 is mainly an ADP-ribosyltransferase (5).

SIRT5 was reported to play distinct roles in tumorigenesis in a context-dependent manner, but no study had explored its function in AML. Therefore, Yan and colleagues first validated that the dependency of SIRT5 was ubiquitous in most primary AML cases and AML cell lines, but not in normal cord blood cells. Depletion of SIRT5 in SIRT5-dependent AML cell lines eradicated leukemia cells in vivo but had minimal effect on SIRT5-independent cases. Bone marrow cells from SIRT5 knockout mice manifested delayed transformation into AML induced by canonical AML driver–mutant proteins, including MLL-AF9, BCR-ABL, and FLT3-ITD. These data are intriguing, as they indicate that SIRT5 functions as a novel form of non-oncogene addiction in many AMLs. Indeed, genetic profiling data showed that SIRT5 dependency in AML cells was not associated with any known somatic mutation. In contrast, Yan and colleagues found that depletion of mitochondrial DNA killed all SIRT5-dependent AML lines, while mitochondria were dispensable in SIRT5-independent lines. Thus, the dependence of SIRT5 was associated with AML’s strong dependence on mitochondria. Similarly, BCL2 was previously shown to sustain mitochondrial oxidative phosphorylation in AML cells regardless of specific somatic mutations. Therefore, SIRT5 represents another mechanism enabling mitochondrial activity to support AML progression. Previous proteomics study showed that SIRT5 knockout induced hypersuccinylation in hundreds of mitochondrial proteins including many enzymes in the tricarboxylic acid (TCA) cycle,

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Figure 1. Schematic description how SIRT5 is proposed to work in normal HSCs (A) and AML LICs (B), and how treatment against SIRT5 may affect AML cells (C). A, Normal HSCs rely on glycolysis as main energy source to prevent mitochondria producing excessive ROS which may induce differentiation. SIRT3, maybe also SIRT5, can help HSCs scavenge ROS, maintain HSC self-renew, and prevent differentiation. B, AML LICs depend on active oxidative phosphorylation, which may generate more ROS. SIRT5 is required to promote oxidative phosphorylation via glutaminolysis and suppress mitochondrial ROS production in AMLs. SIRT5 and SIRT3 may cooperate to maintain normal mitochondrial protein acylation levels. For example, SIRT3 protects AML cells from oxidative stress via deacetylating SOD2. However, SIRT3 expression decreases with aging, so SIRT5 may become more critical in old AML patients. C, Targeting mitochondrial function with SIRT5 inhibitor, NRD167, leads to hyper-acylations in mitochondria and kills AML cells by inducing oxidative stress as well as inhibiting oxidative phosphorylation which may mimic the therapeutic effects like venetoclax. Additional targeting of SIRT3/SOD2 regulation may further increase the efficacy of NRD167 against AMLs mitochondrial dependency. Gray, red, and purple arrows show repressed, activated, and interfered reactions, respectively. Black lines represent deacylations and blue lines stand for drug targeting effects. The solid lines indicate direct regulations, whereas the dashed lines indicate indirect regulations.

ketone, and fatty acid metabolic pathways, all of which could affect downstream oxidative phosphorylation (5). Indeed, the authors confirmed that depletion of SIRT3 led to a profound decrease of oxygen consumption rate and inhibition of the central carbon metabolic pathway in SIRT5-dependent AML cells. As oxidative phosphorylation is one of the critical metabolic hallmarks in AML stem cells, these metabolic actions of SIRT5 may be critical for self-renewal of AML LICs.

It is critical for AML LICs to prevent excessive production of ROS from the oxidative phosphorylation, which may otherwise impair self-renewal and trigger differentiation and cell death (2). SIRT5 was reported to protect cells from ROS by desuccinylating superoxide dismutase 1 (SOD1) and enzymes generating NADPH as reducing power. In this study, Yan and colleagues observed that loss of SIRT5 induced mitochondrial ROS and cell death in SIRT5-dependent AML cells. Addition of vitamin E and ectopic expression of SOD2, instead of SOD1, could partially rescue the SIRT5 knockdown effects. It is still a mystery how SIRT5 depletion induces ROS production because no direct connection was discovered between SIRT5 and SOD2. However, as it is known that SIRT3 can deacetylate SOD2 to increase its activity, it is possible that SIRT5 and SIRT3 may coordinate together to protect AML cells from ROS damage. This is consistent with recent findings showing that SIRT5 and SIRT3 can compensate for each other’s loss of function in specific biological conditions (6). SOD2 activity induced by SIRT3 deacetylation is required for aged HSCs to maintain their self-renewal ability. AMLs can thus hijack the activity of SIRT3 to support oxidative phosphorylation and SOD2 to facilitate chemoresistance (7).

Interestingly, the expression of SIRT3 gradually decreases with age, but no such change is observed in SIRT5 expression, which may point to the importance of SIRT5 in scavenging ROS in aged AML cells (Fig. 1B).

On the other hand, the authors found that SIRT5-dependent AML cells more efficiently converted glutamine into glutamate as a source for anaplerotic metabolism. This enhanced glutaminolysis may be the result of SIRT5 desuccinylating its substrate glutaminase (GLS). Untargeted metabolomic profiling accordingly showed that SIRT5 loss of function resulted in reduced abundance of TCA cycle and amino acid metabolites. These metabolic changes may be explained by the diverse deacetylation activities of SIRT5. Yan and colleagues observed increased expression of protein succinylation, malonylation, and even acetylation in SIRT5-depleted AML cells, which indicates that these posttranslational modifications may have an important functional impact on the respective metabolic enzymes. CMK cells (SIRT5-dependent) showed more profound increase of acylation than KG1a cells (SIRT5-independent), so it might be possible to characterize SIRT5’s deacetylated targets as a putative biomarker to determine the dependency of SIRT5 in AML cases. Such effects on metabolism-associated posttranslational modifications have also been documented as being regulated by SIRT3. Proteomics studies showed that lysine acetylation and succinylation are most frequently observed in mitochondrial proteins, and some proteins can be regulated by both
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