malignancy (see figure). In addition to miR-21, other implicated miRNAs include mir-181ab1, which appears to dampen the expression of negative regulators of Notch such as Nrarp, thereby helping Notch clear the signaling threshold that is required for leukemogenesis; miR-451, a Dicer-independent miRNA that is repressed by Notch, an alteration that contributes to Notch’s ability to upregulate and sustain Myc expression; miR-193b-3p, which suppresses Notch-induced T-ALL development by repressing Myk, a “pioneer” transcription factor that dysregulates other oncogenes that contribute to T-ALL development; and numerous other “onco-miRNAs” targeting a who’s who of tumor suppressors in T-ALL, including Ikzf1, Pten, Phf6, Bim, Nf1, and Fbxw7, in addition to the aforementioned Pdcd4. This panoply of miRNAs may prove to be the tip of the proverbial noncoding RNA iceberg, as other recent papers have implicated long intervening noncoding RNAs, including some that are directly regulated by Notch, as participants in T-ALL pathogenesis. The challenge now is to translate these insights into new approaches that inform the diagnosis and improve the treatment of T-ALL and other blood cancers. An increasing number of diagnostic tests are coming on line that are centered on detection of specific miRNAs in situ, in tumor cell lysates, and free in blood.

Therapeutic miRNA targeting strategies also are in various stages of development, including agents that specifically target miR-21 or that are preferentially active in the tumor microenvironment. Much additional work is needed to determine if these (or any of the many other leads being pursued) can be brought to fruition, to the benefit of patients with T-ALL and other blood cancers.

**Conflict-of-interest disclosure:** The author declares no competing financial interests.

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**LYMPHOID NEOPLASIA**

**Comment on Dietrich et al, page 1005**

**New mutation in hairy cell leukemia**

**Tadeusz Robak and Piotr Smolewski MEDICAL UNIVERSITY OF LODZ**

In this issue of Blood, Dietrich et al make the first observation of the presence of deleterious CDKN1B mutation in 16% of patients with hairy cell leukemia (HCL). Furthermore, in the majority of patients, the CDKN1B mutation was clonal, suggesting that this mutation plays a role in the pathogenesis of HCL.

**HCL** is a rare subtype of B-cell chronic lymphoid leukemia, characterized by progressive pancytopenia, splenomegaly, and infiltrations of the bone marrow, liver, and spleen, with B lymphocytes possessing cytoplasmic projections that appear as fine hair-like microvilli. Over the last 5 years, significant progress has been made in the understanding of the molecular biology of this disease. In particular, the discovery of the BRAFV600E mutation provided a breakthrough in our understanding of

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the pathogenesis of HCL. Although the BRAFV600E mutation is clonally presented in almost 100% of classical HCL patients, it has been not identified in patients with other B-cell malignancies. In addition, 2 novel mutations in exon 11 of the BRAF gene were detected in BRAFV600E-negative cases of HCL. This understanding of the BRAFV600E mutation has provided a rationale for the diagnosis of HCL, with potential therapeutic implications. However, the pathogenesis of HCL, with potential therapeutic implications, has been studied in patients with other B-cell malignancies. In chronic lymphocytic leukemia, high levels of p27 protein stabilize cell cycle progression and allow cell cycle arrest. In contrast, lower levels of p27 protein stabilize cyclin D-CDK4/6 complexes and facilitate cell cycle progression.

Recent studies have shown that the CDKN1B gene may also play a role in the pathogenesis of other hematologic malignancies, including T-cell prolymphocytic leukemia (T-PLL), acute myeloid leukemia (AML), and lymphomas. An important role in the pathogenesis of T-PLL is played by CDKN1B haploinsufficiency.

In chronic lymphocytic leukemia, high levels of p27 are associated with rapid disease progression and poor outcome. However, CDKN1B mutations are very rare in these leukemias and other malignancies and do not coexist with BRAFV600E (see figure). Future studies should clarify whether the mutation of CDKN1B may contribute to the pathogenesis of HCL and what its impact on clinical outcome could be. In the highlighted study by Dietrich et al, the CDKN1B mutation was found to have no impact on clinical characteristics or response to standard therapy with purine analog. However, further analysis of the signaling pathways related to this mutation may allow a clearer understanding of this finding and its possible application in clinical practice, both as a prognostic factor and a specific therapeutic target.

In conclusion, Dietrich et al demonstrate that CDKN1B is inactivated in 16% of patients with classical HCL and that it is the second most commonly mutated gene in HCL. These observations strongly suggest that CDKN1B plays a potential role in the biology and pathogenesis of HCL, particularly in neoplastic cell cycle deregulation and tumor suppression.

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**MYELOID NEOPLASIA**

Comment on Barete et al, page 1009

**Cladribine for mastocytosis: benefits and risks**

**Cem Akin \nHarvard Medical School**

In this issue of Blood, Barete et al report the safety and efficacy of cladribine in 68 adult patients with mastocytosis. Cladribine (2-chlorodeoxyadenosine) is a purine analog that causes apoptosis in cells after phosphorylation intracellularly...
New mutation in hairy cell leukemia

Tadeusz Robak and Piotr Smolewski

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