Editorial
The Landscape of Blood Cancer Research Today—and Where the Field Is Headed ...............1
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IN THIS ISSUE
Highlighted research articles.......................... 5

NEWS IN DEPTH
Q&A: Carl June on CAR T-cell Therapy .................8

VIEWS
In The Spotlight
Soil and Seed: Coconspirators in Therapy-Induced Myeloid Neoplasms .................. 10
K. Shannon and D.C. Link
See article, p. 32

MEF2D Fusions Drive Oncogenic Pre-BCR Signaling in B-ALL ....... 18
T. Sadras and M. Müschen
See article, p. 82

Deciphering the Clonal Origin of Relapsed Acute Lymphoblastic Leukemia in Children ....... 21
S. Ogawa
See article, p. 96

The Genomic Landscape of HIV-Associated Plasmablastic Lymphoma ..................... 23
R. Küppers
See article, p. 112

REVIEW
Epitranscriptomics in Hematopoiesis and Hematologic Malignancies ............ 26
M. Rosselló-Tortella, G. Ferrer, and M. Esteller

Cytotoxic Therapy–Induced Effects on Both Hematopoietic and Marrow Stromal Cells Promotes Therapy-Related Myeloid Neoplasms ....... 32
Précis: Genotoxic therapy-induced persistent damage to non-hematopoietic tissues promotes myeloid leukemia development by conferring advantage to p53-deficient preleukemic clones and driving acquisition of additional lesions in DNA damage response genes.
See commentary, p. 10

Persistence of Drug-Resistant Leukemic Stem Cells and Impaired NK Cell Immunity in CML Patients Depend on MIR300 Antiproliferative and PP2A-Activating Functions ................. 48
Précis: Differential regulation of MIR300 targets by TUG1 lncRNA promotes CML leukemic progenitor survival while retaining cell cycle arrest, and blocking MIR300-TUG1 interaction eliminates quiescent leukemic stem cells.
See commentary, p. 13

Monosomic Loss of MIR15A/MIR16-1 Is a Driver of Multiple Myeloma Proliferation and Disease Progression .............. 68
Précis: MIR15A/MIR16-1 deletion promotes multiple myeloma (MM) initiation and progression in mice, identifying it as a key tumor suppressor gene associated with human chromosome 13 loss in MM.

See commentary, p. 16

Targeting MEF2D-fusion Oncogenic Transcriptional Circuitries in B-cell Precursor Acute Lymphoblastic Leukemia


Précis: MEF2D fusion protein reprograms B-ALL transcriptional circuits, establishing self-reinforcing regulatory network dependent on pre-BCR and SREBF1, which can be exploited to therapeutically target a fusion-driven leukemia.

See commentary, p. 18

Mutational Landscape and Patterns of Clonal Evolution in Relapsed Pediatric Acute Lymphoblastic Leukemia


Précis: The landscape of mutations and clonal evolution trajectories in pediatric ALL reveal relapse-fated, drug-resistant subclones present at diagnosis and expanded by therapy.

See commentary, p. 21

Genomic Characterization of HIV-Associated Plasmablastic Lymphoma Identifies Pervasive Mutations in the JAK–STAT Pathway


Précis: Jak-STAT, Ras, Notch pathway genes and CD44 are frequently mutated in HIV-associated PBL, and together with transcriptomic features distinguish the disease from closely related B-cell cancers.

See commentary, p. 23

The labs of John Dick, Roland Kuiper, Charles Mullighan join forces to characterize mechanisms of relapse in a large cohort of pediatric ALL through the power of high-resolution genomics. They report that in most cases, relapse-associated mutations can be traced to a subclone already present at diagnosis. Taken from treatment-naïve patients, these subclones display drug resistance in mouse xenografts. The relapse-fated subclones carry genomic alterations known to drive resistance, and expand in patients following therapy. Clones persisting through serial relapses display hypermutation suggestive of increased immunogenicity. Genomic patterns revealed in this analysis may help identifying personalized therapies least prone to relapse. For details, please see the article by Waanders and colleagues on page 96 and a joint publication in the April issue of Cancer Discovery.