New Strategies in Acute Myelogenous Leukemia: Leukemogenesis and Personalized Medicine

Ivana Gojo and Judith E. Karp

Abstract

Recent advances in molecular technology have unraveled the complexity of leukemogenesis and provided the opportunity to design more personalized and pathophysiology-targeted therapeutic strategies. Despite the use of intensive chemotherapy, relapse remains the most common cause for therapeutic failure in acute myelogenous leukemia (AML). The interactions between leukemia stem cells (LSC) and marrow microenvironment appear to be critical in promoting therapeutic resistance through progressive acquisition of genetic and epigenetic changes within leukemia cells and immune evasion, resulting in leukemia cell survival. With advances in genomic-sequencing efforts, epigenetic and phenotypic characterization, personalized therapeutic strategies aimed at critical leukemia survival mechanisms may be feasible in the near future. Here, we review select novel approaches to therapy of AML such as targeting LSC, altering leukemia/marrow microenvironment interactions, inhibiting DNA repair or cell-cycle checkpoints, and augmenting immune-based antileukemia activity.

Background

Acute myelogenous leukemias (AML) are a heterogeneous group of disorders that differ in their genotypic, phenotypic, and epigenetic characteristics, and in their net responses to antileukemic interventions. Despite the achievement of complete remission (CR) in substantial proportions of AML subgroups, relapse occurs in the majority and remains the most common reason for treatment failure.

Contrary to what might be expected for such a diverse group of diseases, the AML genome on average contains only 13 gene mutations, and the vast majority of patients with AML carry at least one pathogenic mutation affecting biologically relevant pathways, with unique patterns of mutual exclusivity and cooperation (1). Nonetheless, clonal complexity evolves from diagnosis through treatment and disease progression, at least in part due to selective pressure from chemotherapy (2, 3).

The ability to measure minimal residual disease (MRD) seems critical to determining optimal postinduction strategies that can eventually lead to disease eradication. Several AML subtypes have well-defined molecular aberrations and/or gene mutations, for example, NPM-1 or FLT-3, that permit the use of high-sensitivity molecular detection of the leukemic burden by reverse transcriptase quantitative (qRT)-PCR (4–8). Alternatively, in AMLs lacking such specific molecular hallmarks, qRT-PCR for WT1, a zinc-finger transcription factor that is preferentially overexpressed in patients with AML, may provide valuable information regarding MRD status. Several studies, including the recent European LeukemiaNet study, have found that the magnitude of WT1 log reduction following induction chemotherapy is an independent predictor of relapse (5, 9).

Flow cytometry provides an alternative method for detection of MRD based on the presence of aberrant cell surface marker expression. Detection of MRD by flow cytometry correlates with relapse (5). In addition, flow cytometry holds the promise to track residual leukemia stem cells (LSC). Although to date there is a limited consensus regarding LSC phenotypes, there are discrete markers reported to facilitate the isolation and identification of LSCs, including CD34, CD38, CD44, CD47, CD96, CD32, CD25, CD133, CD90, CD117, CD123, TIM-3, CLI-1, and ALDH1 (10, 11). As a case in point, Gerber and colleagues (12) used flow cytometry to assess aldehyde dehydrogenase (ALDH) expression in CD34+ cells, and identified a population of CD34+CD38− cells with intermediate ALDH activity that was 89% leukemic by FISH, reproducibly generated AML upon transplantation into mice, and was highly predictive of relapse.

If we are to combat AML more effectively, we must develop strategies that take into account the multiple factors contributing to leukemia pathogenesis and pathophysiology, including the LSC, its interaction with its surrounding bone marrow microenvironment, and the
development of net drug resistance over time. In this review, we discuss selected approaches that address aspects of both the leukemic clone and its supportive milieu.

On the Horizon

Targeting LSCs and marrow microenvironment

LSC-directed therapies. LSCs share many properties with normal hematopoietic stem cells (HSC) such as self-renewal, quiescence, and resistance to traditional cell-cycle-dependent chemotherapeutic agents (13). An ability to target LSCs offers a possibility of eradicating AML at its roots. Such eradication, however, requires the ability to exploit differences between LSCs and HSCs in terms of dependence on specific survival pathways, alterations in the genetic, epigenetic and metabolic landscapes, and immunophenotypes. As new drugs are developed to selectively target the abnormalities responsible for leukemia initiation and perpetuation, there may be an opportunity to eradicate LSC clones before acquisition of additional mutations renders them resistant to therapy (Table 1).

Several pathways appear to promote LSC survival preferentially. NF-κB, a transcription factor that promotes cell growth and inhibits apoptosis, is constitutively activated in LSCs (14). Parthenolide induces LSC apoptosis via NF-κB inhibition and increases in reactive oxygen species (ROS), and decreases engraftment of LSCs but not HSCs in mice (15). The proteasome inhibitor bortezomib produces an anti-NF-κB effect by inhibiting the degradation of IκB. Bortezomib given with traditional induction chemotherapy produced encouraging results (CR 65%; DFS and OS of 7.4 and 17.5 months) in newly diagnosed elderly patients with AML (16). Whether or not this is a consequence of more effective LSC eradication will require further studies. The PI3K/AKT/mTOR pathway is frequently upregulated in AML and plays a central role in multiple key survival processes within the cells such as in regulation of formation of ROS, modulation of Bcl-2 family proteins, upregulation of NF-κB, and self-renewal of LSCs through the Wnt/β-catenin pathway.

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Abbreviations: BITE Ab, bispecific T-cell engager Ab; CAR, chimeric antigen receptor T cells; DART, dual affinity retargeting molecule.
Novel Approaches to AML Therapy

Interactions between CXCL12 (stromal cell derived factor alpha-1) and its receptor CXCR4 on leukemia cells contribute to LSC homing to the microenvironment. CXCR4 expression is increased on AML cells, particularly in FLT3-mutated AML, and is associated with poor outcome (33). Anti-CXCR4 mAb given to NOD/SCID mice engrafted by human AML decreased the numbers of AML cells in blood, bone marrow, and spleen, but did not affect homing of HSCs (34). CXCR4 inhibitors are currently in clinical studies in AML (NCI01120457, NCT01352650, and NCT01160354). Plerixafor, a small-molecule antagonist of CXCR4, mobilizes AML cells into peripheral blood in which they are more sensitive to chemotherapy. Plerixafor in combination with chemotherapy produced CR in 46% of patients with relapsed/refractory AML, and correlative studies demonstrated 2-fold increased mobilization of leukemia cells into peripheral blood (35). Adhesion of LSCs to the bone marrow microenvironment promotes survival, self-renewal, and resistance to therapy. Interaction between VLA-4 on the surface of leukemia cells and fibronectin on stromal cells activates prosurvival pathways and contributes to MRD persistence (36). Another adhesion molecule, CD44, promotes LSC homing to microenvironmental niches by mediating cell–cell and cell–extracellular matrix interactions through binding to hyaluronan (37).

Leukemia progression may promote hypoxia in the bone marrow niche, leading to overexpression of hypoxia-inducible factor-1α (HIF1α), which promotes leukemia cell quiescence as well as recruitment and retention of leukemia cells through activation of CXCL12–CXCR4 signaling (38). Targeting HIF1α transcription factor and its downstream target CIAX is now amenable to pharmacologic inhibition. The hypoxia-activated prodrug PR-104 demonstrated clinical activity in patients with AML but produced prolonged myelosuppression at higher doses (39). Nonetheless, because HSCs and LSCs use overlapping pathways of microenvironmental protection, it will be important to examine the safety and selectivity of these novel agents.

Novel treatments based on improved understanding of AML biology

Epigenetic therapies. Global epigenetic modulators such as DNA methyltransferase (DNMT) or histone deacetylase (HDAC) inhibitors are associated with reduction but not eradication of LSCs (40). The identification of recurring unique mutations in epigenetic modifiers and overall epigenetic profiles opens the possibility of developing more effective inhibitors. Mutations such as IDH1/IDH2 or DNMT3 appear to be leukemia initiating and may contribute to initial LSC expansion (41, 42). IDH mutations lead to production of 2-hydroxyglutarate (2-HG) that inhibits histone and DNA methyltransferases, resulting in increased DNA methylation and blocked cellular differentiation (43). Small-molecule inhibitors of IDH2 (AG-6780 and AG-221) reduce 2-HG levels, increase differentiation, and produce survival benefit in xenograft models (44, 45). AG-221 is currently in phase I testing (NCT01915498). The presence of DNMT3 mutations may be associated with an increased...
response to hypomethylating agents, as reported in a small number of patients with AML treated with decitabine (46). DNMT3 mutations occur early in leukemogenesis (41), raising the possibility that DNMT3 inhibitors could be used selectively, not only in initial therapy, but also as maintenance or to target MRD following chemotherapy in DNMT3-mutated leukemias.

**Increasing the DNA-damaging efficacy of chemotherapy.**

Cytarabine remains the single most effective drug for therapy of AML and there are ongoing efforts to identify strategies to enhance its activity. CPX-351 is a liposomal encapsulation of cytarabine and daunorubicin at a 5:1 molar concentration ratio that provides optimal synergistic activity (45). A randomized phase II study of CPX-351 versus 7+3 in older adults with newly diagnosed AML resulted in improved CR rates (66.7% vs. 51.2%) with survival advantage noted in patients with secondary AML (12.1 vs. 6.1 months), leading to a phase III study in this population (NCT01696084; ref. 47).

Incorporation of cytarabine into DNA activates Chk1, a serine/threonine kinase, which stabilizes stalled replication fork, induces S phase arrest, and diminishes cytarabine toxicity. Depletion of Chk1 either by siRNA (48) or selective Chk1 inhibitor SCH900776 (MK8776; ref. 49) can overcome S phase checkpoint activation and enhance cytarabine cytotoxicity in AML. In a phase I study, SCH900776 given with timed sequential cytarabine produced CR in 33% of patients with relapsed/refractory AML, and increased H2Ax phosphorylation in marrow blasts consistent with unrepaired DNA damage (50). A randomized phase II study comparing cytarabine plus MK8776 to cytarabine alone is ongoing in patients with relapsed or refractory AML (NCT01870596). Several other cell-cycle checkpoint inhibitors have shown preclinical or clinical activity in AML.

![Cell-cycle checkpoint inhibitors in AML](image)

**Figure 1.** Cell-cycle checkpoint inhibitors in AML. Cell cycle is controlled by successive activation of cyclin–cyclin-dependent kinases (CDK). Cell-cycle checkpoints serve to stop progression of the cell cycle in response to DNA damage, to allow time for DNA repair and to preserve genomic integrity. The p53-dependent G1–S checkpoint blocks initiation of DNA replication. p53 is frequently altered (mutations or losses) in patients with complex karyotype AML. Inhibitors of HDM2 (RG7112, RO5503781, and MK-8242) are in clinical studies in AML alone or in combination with cytarabine and have a potential to be effective in leukemia cells that retain wild-type p53. Tumors that are defective in p53 function rely on an intact S phase and G2 checkpoint. Depending on the type of genotoxic stress, either ataxia-telangiectasia–mutated (ATM) protein kinases or ataxia-telangiectasia–related (ATR) protein kinases are activated leading to activation of Chk1 and Wee1 kinases that inactivate Cdk1 resulting in intra S phase and G2–M arrest, allowing time for DNA repair. Inhibition of Chk1 (MK8776) and Wee1 (MK1775) sensitizes leukemia cells to cytarabine cytotoxicity in preclinical studies and the combination of Chk1 inhibitor and cytarabine is in a phase II testing in AML. Synergistic activity has been described for Chk1 and Wee1 inhibition in leukemia cells. Plk1 and Aurora kinases are critical for centrosome maturation and proper formation of the mitotic spindle, and also play a role in chromosome segregation and cytokinesis. Plk1 inhibitor (volasertib) and Aurora B kinase inhibitor (AZD1152) have shown promising clinical activity in patients with AML when given with low-dose cytarabine. In addition, several pan CDK inhibitors (flavopiridol and dinaciclib) have been explored as a therapeutic strategy in AML. Flavopiridol in combination with cytarabine and mitoxantrone (FLAM) is in a phase III testing for newly diagnosed AML.
Recent attention has focused on blocking negative regulatory signals to activate T-cell–mediated antitumor immunity (Table 2). CTLA-4 and PD-1, members of the CD28 family, are the key inhibitory receptors that limit T-cell activation. CTLA-4 is expressed on activated T cells and Tregs and binds CD80/CD86 ligands on antigen-presenting cells (APC). On effector T cells, CTLA-4 is able to outcompete CD28 for access to the immune synapse, thereby limiting costimulation (61, 63). The anti–CTLA-4 inhibitory mAb ipilimumab was approved by the FDA after clinical studies in advanced melanoma demonstrated remarkable activity (64). CTLA-4 blockade by mAb enhances AML-specific T-cell responses in vitro (65), and CTLA-4 polymorphism has been associated with AML relapse (66). Ipilimumab is now being evaluated in patients with relapsed MDS/AML (NCT01757639) or following allogeneic stem cell transplantation (NCT01822509).

PD-1 is expressed on the surface of activated T cells, B cells, NK cells and monocytes in response to inflammation and binds two ligands: PD-L1 and PD-L2. PD-L1 is expressed on hematopoietic and nonhematopoietic cells and is overexpressed on multiple tumors, including AML blasts, whereas PD-L2 is mainly restricted to APCs (61, 67, 68). Leukemia-specific T-cell immunity and survival upon AML challenge was increased in PD-1 knockout mice or in wild-type mice upon PD-L1 blockade using mAb (69). PD-1 expression is increased in peripheral blood T cells in patients with leukemia compared with healthy donors (70). PD-1/PD-L1 pathway blockade has shown promising activity in solid tumors (71, 72) and is now being investigated in clinical trials in AML in combination with a dendritic cell–based vaccine (NCT01096602). Additional non-CD28/B7 family T-cell inhibitory receptors such as LAG-3 and TIM3 have also been identified as potential therapeutic targets.

Immunosuppressive Tregs are defined by their expression of FoxP3 transcription factor and have been implicated as major contributors to the defective immune response in AML. Patients with AML have a greater Treg frequency at diagnosis relative to normal control subjects, their Tregs more potently suppress the effector T cells, and those with greater numbers of Tregs appear to have a relatively poor clinical outcome (62, 73, 74). In mice, Tregs accumulate at leukemia sites and impede the activity of CTLs, whereas their removal, alone or in combination with PD-L1 blockade, results in increased frequency of CTL at tumor sites and improves the efficacy of adoptive therapy (75, 76). Clinical studies are investigating whether responses to tumor vaccines can be augmented in patients with AML following Treg depletion using metronomic cyclophosphamide or/and anti-IL2 receptor (CD25) antibodies (NCT01513109, NCT01842139), or whether immunomodulatory drugs such as pomalidomide may reduce Tregs following induction chemotherapy (NCT02029950).

Conclusions

The therapeutic armamentarium for AML is evolving as we increase our basic understanding of the diverse factors that play into leukemogenesis and leukemia cell biology. Given the complex interactions between AML cells and the many components of their environment, it is reasonable to surmise that the future of AML therapy lies in the combination of molecularly selective agents with traditional cytotoxics and/or with each other throughout induction and postinduction therapies. Such multidirected approaches have the potential to overcome AML cell resistance by targeting crucial leukemic cell pathways and critical cellular

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### Table 2. Select immunotherapeutic strategies

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<td>CD28/B7 family receptors</td>
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<td>CTLA-4 (cytotoxic T lymphocyte antigen-4)</td>
<td>Ipilimumab&lt;sup&gt;a&lt;/sup&gt;</td>
<td>CTLA-4 blockade enhances AML-specific T-cell responses; CTLA-4 polymorphism associated with relapse (65, 66).&lt;sup&gt;a&lt;/sup&gt; Clinical study in relapsed AML and after alloHSCT.</td>
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<td>Nivolumab, MK-3475&lt;sup&gt;a&lt;/sup&gt;, CT-011&lt;sup&gt;a&lt;/sup&gt;, Nivolumab, MK-3475&lt;sup&gt;a&lt;/sup&gt;, CT-011&lt;sup&gt;a&lt;/sup&gt;, MEDI0680, BMS-936559, MEDI4736, MPDL3280A</td>
<td>PD-L1 is expressed on AML blasts; PD-1 expression increased on circulating T cells in leukemia patients; leukemia-specific T-cell immunity and survival upon AML challenge increased in PD-1 knockout mice or upon PD-L1 blockade (61, 69, 70).&lt;sup&gt;a&lt;/sup&gt; Clinical study of CT-011 and vaccine; and MK-3475 in MDS.</td>
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<tr>
<td>Non-CD28/B7 family receptors</td>
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<td>LAG-3 (lymphocyte activation gene-3)</td>
<td>BMS-986016, IMP321 mAb, TIM-3 fusion protein</td>
<td>No studies in AML. Galectin-9 is expressed on AML cells; coexpression of TIM-3 and PD-1 identifies exhausted T cells in mice with advanced AML and increases during AML progression; combined blockade of TIM-3/PD-L1 had an additive effect in improving survival of AML-bearing mice (77).</td>
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<td>TIM-3/galectin-9 (T-cell immunoglobulin domain and mucin domain 3)</td>
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<td>IDO (Indoleamine 2,3-dioxygenase)</td>
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<td>IDO overexpressed in AML cells, predicts poor prognosis, depletes tryptophan, thus limiting T-cell proliferation and stimulating Treg accumulation (78–80).&lt;sup&gt;a&lt;/sup&gt; Clinical study in MDS.</td>
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<td>CD25 is overexpressed in AML, predicts poor prognosis, depletes tryptophan, thus limiting T-cell proliferation and stimulating Treg accumulation. Several clinical studies of anti-CD25 plus vaccine and chemotherapy plus immunomodulatory drugs ongoing in AML.</td>
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<td>Targeting NK cells</td>
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<td>Triplebody (SPM2)</td>
<td>Increased patient’s NK cell cytolytic activity against AML cells ex vivo (84). Reversed MDSC immunosuppression of NK cells and induced CD33&lt;sup&gt;a&lt;/sup&gt; MDS and MDSC target cell lysis ex vivo (85).</td>
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<td>CD16 &lt;sup&gt;x&lt;/sup&gt; CD33</td>
<td>CD16 &lt;sup&gt;x&lt;/sup&gt; CD33 bispecific killer cell engager (BiKE)</td>
<td>CD16 &lt;sup&gt;x&lt;/sup&gt; CD33 bispecific killer cell engager (BiKE)</td>
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<sup>a</sup>Therapeutics in clinical studies in AML and MDS.
and humoral components of the bone marrow microenvironment, thereby preventing AML clonal expansion and survival. The successful introduction of diverse molecularly targeted agents into the clinic will require standardization of molecular tests, development of predictive biomarkers of response, proper timing, and integration with current therapies.

Disclosure of Potential Conflicts of Interest

I. Gojo is a consultant/advisory board member for Boehringer Ingelheim. No potential conflicts of interest were disclosed by the other author.

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