

Exploring the Bone Marrow Microenvironment as a Therapeutic Barrier and Targetable Source of Crosstalk in Acute Myeloid Leukemia

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Abstract: Acute myeloid leukemia (AML) is an aggressive and genetically heterogeneous hematological malignancy characterized by the accumulation of immature myeloid blasts that disrupt healthy hematopoiesis. Despite advances in molecular profiling and targeted therapies, overcoming drug resistance and relapse remains a significant clinical challenge, resulting in poor long-term outcomes. Crucially, disease persistence is sustained not merely by intrinsic genetic lesions but by a highly adaptive bone marrow microenvironment (BMME) that functions as a therapeutic barrier. While the healthy niche tightly regulates hematopoietic stem cell maintenance, leukemic blasts co-opt stromal, vascular, and immune components to establish a sanctuary that fuels proliferation and shields the disease from cytotoxic stress. However, dissecting these reciprocal dependency mechanisms uncovers critical vulnerabilities, presenting a vital opportunity to develop novel targeted therapies. In this review, we discuss the architecture of the healthy BMME and its pathological AML-driven remodeling. We describe the role of specific signaling axes that govern AML-BMME crosstalk and evaluate targeted therapeutic strategies designed to uncouple these protective interactions. Finally, we highlight that current preclinical models lack the complexity of the BMME stromal components and its spatial organization, a limitation that continues to hinder clinical translation and delay the development of effective combination therapies.

Plain Language Summary: Acute Myeloid Leukemia (AML) is an aggressive blood cancer. It occurs when immature cells build up in the bone marrow, the soft tissue inside your bones where the body makes new blood. While many people respond well to initial treatment, the disease often returns because some AML cells survive by “hijacking” their surroundings.

This review explains how AML cells attach themselves to healthy bone marrow structures and send out chemical signals that force nearby healthy cells to protect them. This creates a shield that hides the cancer from both chemotherapy and the body's own immune system. Importantly, the review explores how we can target this communication to prevent the disease from returning.

A major challenge remains the difficulty of accurately modeling this complex environment in the laboratory. Current models often struggle to mimic the complex human bone marrow, which is why many drugs that appear promising in tests fail to help people in clinical trials. Therefore, the review highlights the need to use advanced models which allow researchers to more reliably test new strategies to disrupt the protective bone marrow environment.

The review concludes that the bone marrow acts as a single, connected shield rather than separate pieces. Because these parts work together to protect the cancer, blocking just one pathway is often not enough. Overcoming resistance requires new strategies that simultaneously target the leukemia cells and the multiple parts of the environment that support them.

Keywords: acute myeloid leukemia, bone marrow microenvironment, therapeutic resistance, targeted therapy

Introduction

Acute myeloid leukemia (AML) is an aggressive hematological malignancy characterized by the clonal expansion of myeloid progenitor cells with a blockade in differentiation.¹ This process is driven by leukemic stem cells (LSCs), a self-renewing subpopulation at the apex of the leukemic hierarchy that sustains the disease and often resists conventional therapy.² The resulting accumulation of immature blasts in the bone marrow (BM) disrupts normal hematopoiesis, giving rise to anemia, thrombocytopenia, and increased susceptibility to infections.³

Epidemiology, Genetics and Current Treatments

AML is the most common acute leukemia in adults, with an incidence of approximately 4.4 per 100,000 individuals in the United Kingdom (UK).⁴ Although AML mostly affects older people, with a median diagnosis age of 72 years, it can also occur in children (pediatric AML), which generally has a much improved prognosis.^{4,5} However, even with induction therapy achieving complete remission in most patients (60–80% in younger adults and 45–60% in older adults), long-term outcomes remain poor, with only 16.5% surviving beyond five years in the UK, largely due to relapse and the emergence of therapy resistance.^{4,6}

AML is a genetically heterogeneous disease, with recurrent mutations in NPM1, FLT3, DNMT3A, IDH1/2, RUNX1 and TP53.^{7,8} It is further characterized by translocation events that generate fusion oncogenes, most notably t(15;17) [PML-RARA], t(8;21) [RUNX1-RUNX1T1], inv(16) [CBFB-MYH11], inv(3) [GATA2-MECOM], t(6;9) [DEK-NUP214] and KMT2A rearrangements. This molecular diversity has major clinical implications for prognosis and therapy selection.⁹ Despite significant advances in molecular profiling and the introduction of targeted therapies, intensive induction therapy with cytarabine plus an anthracycline (“7+3”), followed by consolidation with further chemotherapy or hematopoietic stem cell transplantation (HSCT), has remained the mainstay for decades.^{9–11}

More recently, there has been a shift towards targeted therapies that exploit specific genetic vulnerabilities. Several classes of drugs have demonstrated significant clinical efficacy, particularly when combined with hypomethylating agents or chemotherapy: FLT3 inhibitors (midostaurin,^{12,13} gilteritinib¹⁴); IDH1/2 inhibitors (ivosidenib,^{15,16} enasidenib^{17–19}); and the B-cell lymphoma 2 (BCL-2) inhibitor venetoclax.^{20–26} Outcomes have also been improved in some patients through the incorporation of targeted agents into intensive chemotherapy, as seen with gemtuzumab ozogamicin (GO) in CD33-positive disease.²⁷

However, resistance mechanisms and relapse continue to challenge durable responses.²⁸ As a result of the significant challenges that persist, despite genetic stratification, attention is turning to the bone marrow microenvironment (BMME) as a contributor to therapeutic failure.^{29–32} AML blasts exploit the BMME to evade immune surveillance, gain a metabolic advantage, resist chemotherapy, and establish reservoirs of residual disease. However, despite significant promise in preclinical settings, niche-targeting strategies have yet to deliver a consistent clinical benefit (Table 1).

Scope of This Review

In this review, we discuss how AML cells interact with and reshape the BMME, highlighting that these interactions serve as essential mechanisms for leukemic survival while simultaneously offering opportunities for new targeted therapies. We also evaluate the current barriers to clinical translation of therapies targeting interactions between AML cells and the BMME, specifically addressing the inherent complexity and redundancy of the BMME and the technical limitations of existing model systems.

Bone Marrow Microenvironment

The BM is a complex and dynamic tissue responsible for maintaining lifelong hematopoiesis through a delicate balance between hematopoietic stem cell (HSC) self-renewal, proliferation, and differentiation.^{86–88} This process is tightly regulated by the BMME, which provides physical scaffolding, cellular interactions, and molecular signals essential for HSC maintenance and lineage commitment. In AML, this initially healthy, HSC-supportive niche is hijacked and remodeled to create a distinctly pathogenic BMME to favor disease progression and treatment resistance, a transition that can begin with early pre-leukemic mutations that facilitate clonal expansion and leukemogenesis.^{89,90} This pre-

Table 1 Clinical Trials Targeting Crosstalk Between Acute Myeloid Leukemia (AML) Cells and the Bone Marrow Microenvironment. This Table Summarizes Key Clinical Trials Investigating Therapeutic Strategies Designed to Disrupt the Protective Interactions Between AML Blasts and the Bone Marrow Microenvironment. The Trials are Categorized by the Specific Biological Signaling Axis or Niche Component Being Targeted, Including Adhesion Molecules, Chemokine-Mediated Retention, Intracellular Signaling Pathways, Metabolism, and Immune Checkpoints. Clinical Trial Identifiers (NCT Numbers) and Status Information Were Verified via ClinicalTrials.gov or the EU clinical trials register and are Accurate as of 1 April 2026.

Target	Therapy	Monotherapy/Additional Agents or Treatment	Phase	Trial ID	Status/Outcome	Ref.
<i>Adhesion</i>						
FAK	Defactinib	Decitabine/cedazuridine	Phase I	NCT05636514	Recruiting	N/A
E-selectin	Uproleselan (GMI-1271)	In combination with mitoxantrone, etoposide and cytarabine (MEC) or fludarabine, cytarabine and idarubicin (FAI)	Phase III	NCT03616470	Terminated: Failed primary OS endpoint for ITT population; increase in mOS of 21.1 months primary refractory AML population.	[33]
		Daunorubicin, Cytarabine	Phase II/III	NCT03701308	Active, not recruiting	N/A
<i>Chemokine-mediated retention</i>						
CXCR4	Plerixafor (AMD3100)	Decitabine	Phase I	NCT01352650	Completed: ORR 43% (CR 35%); mOS 11.2 months. MTD 810 µg/kg for monotherapy.	[34]
		Sorafenib, Filgrastim	Phase I	NCT00943943	Completed: ORR 36%; 4 patients achieved CR. MTD established at 400 mg.	[35]
	Motixafortide (BL-8040)	Cytarabine	Phase IIa	NCT01838395	Completed: Well tolerated; composite CR rate of 28.6% (39.1% in expansion phase). mOS 8.4 months.	[36]
CXCL12/CXCR4	Dociparstat sodium (DSTAT/CX-01)	Azacitidine	Phase I	NCT02995655	Completed: ORR 20%; mOS 205 days. One AML patient achieved CR. No additional toxicity.	[37]
		Cytarabine, Idarubicin (7+3)	Phase II	NCT02873338	Completed: Composite CR rate was 89% in the high-dose group (0.25 mg/kg/h) vs 58% in the 7+3 control. Statistically significant improvement in EFS (P = 0.019).	[38]
<i>JAK/STAT signaling</i>						
JAK1/2	Ruxolitinib (INCB018424)	Monotherapy	Phase I/II	NCT01251965	Terminated: Lack of clinical benefit.	[39]
		Monotherapy	Phase II	NCT00674479	Completed: Well tolerated; composite CR rate of 16% (2 CR, 1 CRi).	[40]
		Venetoclax, Azacitidine	Phase I	NCT03874052	Arm 1 (Ruxolitinib + Venetoclax): Composite CR 10%; median OS 3.7 months. 23% alive after 1 year. Arm 2: Recruiting	[41]
		Decitabine	Phase I/II	NCT02257138	Completed: MTD not reached (doses up to 50mg BID tested). Well tolerated with an ORR of 45% in Phase I and 61% in Phase II. mOS was 6.9 months for the overall cohort (8.4 months for Phase II patients).	[42]
		Standard APL protocols	Phase III/IV	NCT04446806	Unknown: Primary study endpoint was the incidence of DS and severe DS. Successfully reduced early mortality by mitigating DS.	[43]
		Post allogenic stem cell transplantation	Phase II	NCT03286530	Active, not recruiting: Lower rates of cGVHD; 2 year OS 76%.	[44]
		CART123 cells	Phase I	NCT06768476	Active, not recruiting	N/A

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Table I (Continued).

Target	Therapy	Monotherapy/Additional Agents or Treatment	Phase	Trial ID	Status/Outcome	Ref.
STAT3	OPB-111077	Monotherapy	Phase I	NCT03197714	Completed: MTD not reached. No CRs observed, but 3 patients achieved PR. 25% discontinued due to adverse events.	[45]
		Decitabine, venetoclax	Phase Ib	NCT03063944	Completed: MTD not reached (up to 250 mg).	[46]
FLT3/JAK2	Pacritinib	Cytarabine with daunorubicin or decitabine (7+3)	Phase I	NCT02323607	Completed: MTD not formally defined due to early termination; DLTs observed at 100 mg.	[47]
IL-6R	Tocilizumab	Cytarabine, idarubicin (7+3)	Phase I	NCT04547062	Completed: MTD not reached; CR achieved in 4 patients and CRi in 4 patients.	[48]
<i>PI3K/AKT/mTOR signaling</i>						
PI3K p110 Δ	Idelalisib (CAL-101)	Monotherapy	Phase I	NCT00710528	Completed: Interim report shows no response observed in AML patients. DLTs observed.	[49]
PI3K	Buparlisib (BKM120)	Monotherapy	Phase I	NCT01396499	Completed: MTD established at 80 mg/day; mOS 75 days.	[50]
PI3K/mTOR	Gedatolisib (PF-05212384)	Monotherapy	Phase II	NCT02438761	Terminated: Lack of clinical benefit.	[51]
	Dactolisib (BEZ235)	Monotherapy	Phase I	NCT01756118	Completed: DLTs at 400 mg incompatible with prolonged treatment.	[52]
mTOR	Rapamycin/Sirolimus	Cytarabine	Phase II	NCT00235560	Completed: 44% (4/9 pts) achieved PR.	[53]
		Decitabine	Phase II	NCT02109744	Completed: Did not meet primary endpoint of improvement over decitabine alone; Composite CR 33%.	[54]
		Cytarabine, idarubicin (7+3)	Phase I	NCT01822015	Completed: MTD established (12 mg load / 4 mg daily); 64% composite CR rate. mOS was 16 months.	[55]
	Temsirolimus	Clofarabine	Phase II	2007-005374-31	Completed: 8% CR, 13% CRi. mOS was 4 months (9.1 months for responders).	[56]
	Everolimus (RAD001)	Cytarabine, daunorubicin	Phase Ib	NCT01074086	Completed: MTD not reached (up 70 mg); 68% CR rate achieved in relapsed AML. mOS was 19.5 months.	[57]
AKT	Uprosertib (GSK2141795)	Monotherapy	Phase II	NCT01907815	Terminated: Lack of clinical benefit.	[58]
	Afuresertib	Monotherapy	Phase I	NCT00881946	Completed: MTD established at 125 mg/day. Treatment failure in 5/9 AML patients (4 were not assessed).	[59]
G protein-coupled receptor DRD2	ONC201	Venetoclax	Phase I/II	NCT02392572	Recruiting	
		Post-allogenic stem cell transplant maintenance	Phase I	NCT03932643	Completed: No DLTs, 2 year RFS 65% and OS 70%.	[60]
<i>Angiopoietin/Tie2 signaling</i>						
Ang-1/2	Trebananib	Cytarabine	Phase Ib	NCT01555268	Completed: Well tolerated with some DLTs (mucositis, ataxia). Limited efficacy: 1 PR and 4 SD observed out of 24.	[61]
BCR-ABL1/Tie2/VEGFR-2	Rebastinib	Monotherapy	Phase I	NCT00827138	Completed: MTD established at 150 mg BID. Safe profile but no clinical response observed in AML patients.	[62]

Wnt/ β -catenin signaling						
CBP/ β -catenin complex	PRI-724	Cytarabine	Phase I/II	NCT01606579	Completed (no additional information available).	N/A
β -catenin	CWP232291	Monotherapy	Phase I	NCT01398462	Completed: MTD defined at 257 mg/m ² ; low efficacy.	[63]
GSK-3	LY2090314	Ranitidine pretreatment	Phase II	NCT01214603	Completed: Safe; no CR or PR observed.	[64]
COX1/COX2	Sulindac	Sulindac	Phase II	NCT01843179	Withdrawn: Lack of funding.	N/A
COX2	Celecoxib	Celecoxib	Phase I	NCT03878524	Terminated: Low accrual.	N/A
Notch signaling						
y-secretase	MK-0752	Monotherapy	Phase I	NCT00100152	Terminated: Only 1 AML patient enrolled. Well tolerated below 300 mg/m ² .	[65]
NF- κ B signaling						
BCL-2	Venetoclax	Azacitidine	Phase III	NCT02993523	Completed: mOS 14.7 months vs 9.6 months in control (P<0.001). CR+CRi rate 66.4% vs 28.3%.	[26]
26S proteasome	Bortezomib	Decitabine	Phase II	NCT01420926	Completed: No benefit from adding bortezomib.	[66]
		Cytarabine, daunorubicin (7+3)	Phase I/II	NCT00742625	Completed: Treatment was tolerable. CR 65%; CRp 4%. For patients with CR and subsequent alloHCT at 24 months DFS and OS were 54% and 52%, for patients without alloHCT were 19% and 36%.	[67]
		Sorafenib tosylate	Phase III	NCT01371981	Active, not recruiting	N/A
		CPX-351	Phase I/II	NCT07008638	Recruiting	[68]
VEGF signaling						
VEGFR-1 VEGFR-2, VEGFR-3, c-kit, and PDGFR- β .	Axitinib (AG-013736)	Monotherapy	Phase II	NCT00071006	Completed: No response in AML patients.	[69]
VEGFR-1 VEGFR-2, VEGFR-3	Cediranib (AZD2171)	Monotherapy	Phase II	NCT00475150	Completed: No response in AML patients.	[70]
VEGF	Bevacizumab	Cytarabine, daunorubicin	Phase II	NTR904	Completed: No improvement in outcome. CR rate 65% in both arms. 12-month EFS 30% vs 33% in control.	[71]
		Cytarabine, mitoxantrone	Phase II	NCT00015951	Completed: ORR 48%; CR 33%. Median OS for CR patients 16.2 months.	[72]
Metabolism						
Causes DNA crosslinking in hypoxia	Evofofamide (TH-302)	Monotherapy	Phase I	NCT01149915	Completed: MTD 460 mg/m ² (daily infusion) and 330 mg/m ² (continuous infusion). Combined ORR 6% (2 CR/CRi, 1 PR). DLTs included grade 3 esophagitis, stomatitis, and hyperbilirubinemia.	[73]
Mitochondrial Complex I	IACS-010759	Monotherapy	Phase I	NCT02882321	Terminated: Lack of efficacy.	[74]
PDH and OGDH	Devimistat (CPI-613)	Cytarabine, mitoxantrone, etoposide, fludarabine, filgrastim	Phase III	NCT03504410	Terminated: Lack of efficacy.	[75]

(Continued)

Table I (Continued).

Target	Therapy	Monotherapy/Additional Agents or Treatment	Phase	Trial ID	Status/Outcome	Ref.
CD38	Daratumumab	Monotherapy	Phase II	NCT03067571	Terminated: Lack of efficacy.	N/A
		Fludarabine, melphalan	Phase I	NCT06287944	Recruiting	N/A
		Cytarabine, idarubicin	Phase I	NCT05749276	Not yet recruiting	N/A
<i>Immune checkpoint</i>						
PD-1/PD-L1	Pembrolizumab (MK-3475)	Cytarabine	Phase II	NCT02768792	Completed: ORR 46%; composite CR (primary endpoint) 38%. mOS 11.1 months (13.2 months for refractory/early relapse).	[76, 77]
		Given post-autologous stem cell transplant; Fludarabine, Melphalan	Phase II	NCT02771197	Completed: 2-year LFS 48.4% (met primary endpoint of >25%). 2-year OS 68%. Cumulative incidence of relapse 46%.	[78]
		Cytarabine and idarubicin or daunorubicin	Phase II	NCT04214249	Active, not recruiting	[79]
	Tislelizumab	Azacitidine or Decitabine + CAG regimen	Phase II	NCT04541277	Unknown status: ORR 63% (14 CR/Cri, 3 PR). mOS 9.7 months and EFS 9.2 months.	[80, 81]
CTLA-4	Ipilimumab	Decitabine	Phase I	NCT02890329	Active, not recruiting: MTD/RP2D of ipilimumab established at 10 mg/kg.	[82]
	Sabatolimab	Venetoclax, Azacitidine	Phase II	NCT04150029	Terminated: Due to negative results in other trials.	[83, 84]
CD33	CAR-NK cell therapy	Preconditioning (Fludarabine, Cytosin)	Phase I	NCT05008575	Unknown status: 6 of 10 patients achieved MRD-negative CR by day 28. No grade 3–4 AEs observed except marrow suppression. No cases of ICANS or GVHD; one case of grade 2 CRS.	[85]

Abbreviations: AE, Adverse events; APL, Acute Promyelocytic leukemia; BID, Bis in die (twice a day); cGVHD, Chronic graft-versus-host disease; CR, Complete remission; Cri, CR with insufficient recovery of blood counts; CRS, Cytokine release syndrome; DLT, Dose limiting toxicity; DS, Differentiation Syndrome; EFS, Event free survival; GVHD, Graft-versus-host disease; ICANS, Immune effector cell-associated neurotoxicity syndrome; ITT, Intent-to-treat; mOS, Median overall survival; MTD, Maximum tolerated dose; N/A, Not available; OGDH, α -ketoglutarate dehydrogenase; ORR, Overall response rate; OS, Overall survival; PDH, Pyruvate dehydrogenase; PR, Partial Response; RFS, Relapse-free survival; RP2D, Recommended Phase II dose; SD, Stable disease.

leukemic remodeling creates a dysfunctional environment that facilitates the clonal expansion of mutated cells over healthy progenitors.⁹¹ By providing a selective advantage to these early clones, the remodeled niche actively contributes to the clonal evolution and eventual leukemogenic transformation of the disease.^{92–96} Therefore, understanding the physiological role of individual components and interactions within the BMME, and how they are manipulated in AML, can shed light on how we may re-sensitize leukemic cells to treatment.³²

Healthy Niche

Two major anatomical niches are recognized within the BM: the endosteal and the vascular niches, although increasing evidence supports significant functional overlap between these compartments.⁹⁷ The endosteal niche, rich in osteoblasts, supports HSC quiescence and self-renewal partly via stromal Wnt/ β -catenin and Notch signaling.^{90,98–101} In contrast, the vascular niche, situated near sinusoids and arterioles, is formed predominantly by endothelial cells that secrete growth factors including stem cell factor (SCF), C-X-C motif chemokine 12 (CXCL12; also known as stromal cell-derived factor 1 or SDF-1), and Transforming Growth Factor Beta 2 (TGF- β 2) to promote HSC activation, proliferation, and differentiation.^{90,98,99} Genetic lineage-tracing studies have shown that SCF derived specifically from arterial endothelial cells is essential in HSC maintenance.^{98,99}

Within these niches, mesenchymal stromal cells (MSCs) form a central component of the stromal compartment and are multipotent progenitors capable of differentiating into osteoblasts, adipocytes, and chondrocytes, thereby contributing to the structural and functional organization of the BM niche.^{102,103} The majority of MSCs are situated within the perivascular space of the BMME, in close association with blood vessels, and are characterized by the expression of leptin receptor (Lepr), Nestin (Nes), or NG2 (Cspg4), which distinguish overlapping subsets with distinct HSC-supportive roles.^{86,99,102,104,105} CXCL12-abundant reticular (CAR) cells are an MSC subset, which largely correspond to Lepr⁺ perivascular MSCs. CARs form extensive structural and functional scaffolds that coordinate HSC localization, anchor them in place and mediate their quiescence.¹⁰⁶

Fibroblasts are a mesenchymal population within the BM that is distinct from MSCs and contribute to the composition of a healthy BMME network.^{90,107} Although distinguishing fibroblasts from BM-MSCs remains challenging due to the absence of definitive surface markers, transcriptomic analysis has identified multiple subsets, including subsets expressing CXCL12 and ANGPT1, indicating a potential for direct regulation of the BMME.⁹⁰

In addition to the key regulatory cell types mentioned above, there is an emerging picture of less well studied BMME components that may have significant functional roles in normal BMME composition and signaling. Adipocytes, once considered inert space fillers, are now recognized as active contributors to hematopoietic support through the production of factors such as SCF.^{108,109} Non-myelinating Schwann cells help preserve HSC dormancy by regulating sympathetic innervation and TGF- β activation.¹¹⁰ Megakaryocytes have also been implicated in regulating HSC proliferation; for example by releasing thrombopoietin (TPO) which can stimulate platelet production as well as supporting HSC growth.¹¹¹

The immune compartment forms another integral part of the BMME, establishing a complex interplay between immune effectors and this specialized niche. Neutrophils, macrophages, T cells, and natural killer (NK) cells are distinct populations that mediate HSC fate by regulating processes such as retention, differentiation, and quiescence.¹¹²

These diverse cellular populations are surrounded by highly specialized extracellular matrix (ECM) that provides both structural support and a delivery mechanism for instructive biochemical and biomechanical cues essential for HSC regulation.^{113,114} The ECM is composed of glycoproteins such as laminins, fibronectin, and osteopontin, together with various collagens and proteoglycans. Collectively, these components form an organized scaffold that anchors niche cells and shapes gradients of cytokines and growth factors within the BMME. Beyond biochemical signaling, the physical properties of the ECM, such as stiffness and topography, act as potent biophysical regulators of HSC fate through mechanotransduction pathways, influencing differentiation.¹¹⁵

AML Niche

This balance of physical and biochemical cues that is carefully maintained in health is disrupted in malignancy. In AML, the BMME is co-opted and remodeled into a malignant niche that promotes leukemic cell survival, proliferation, and

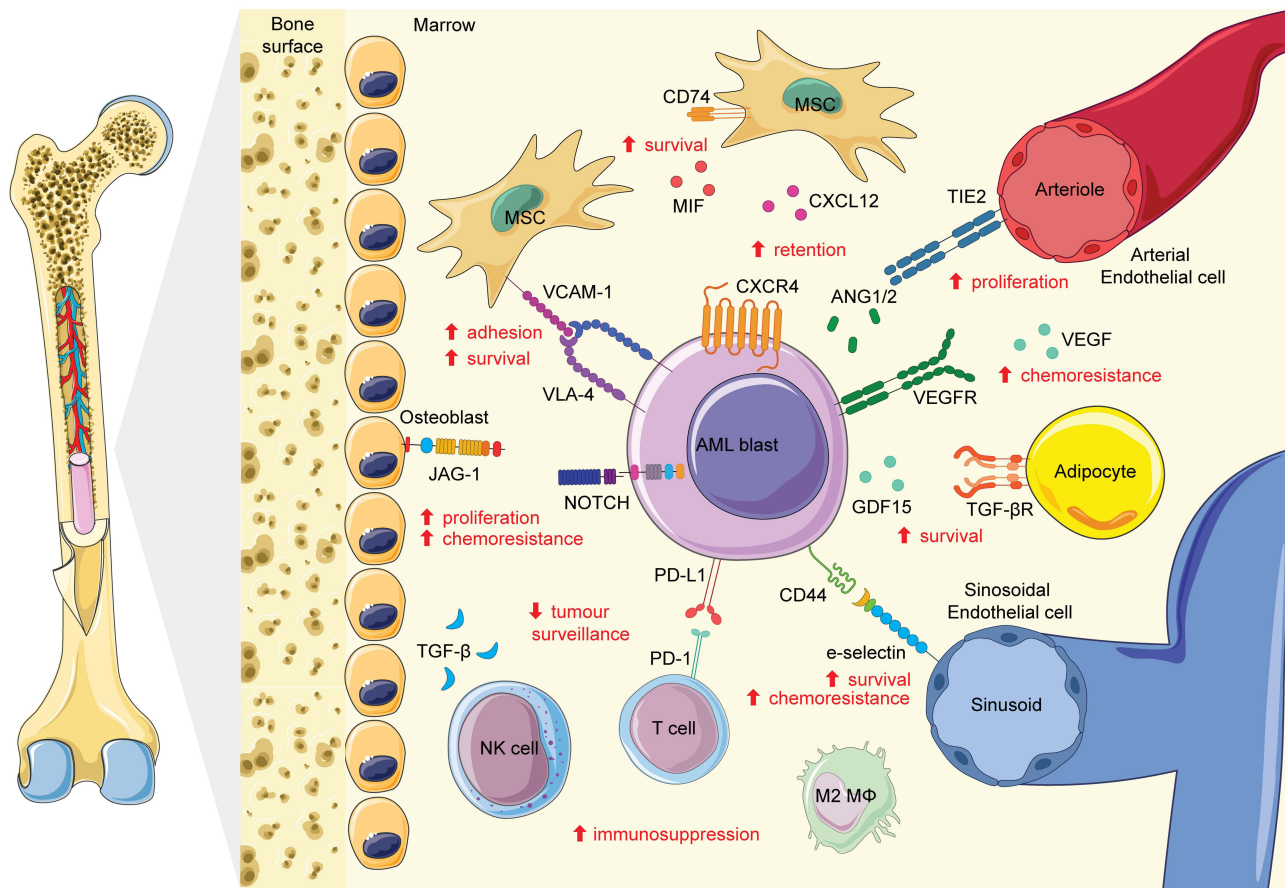


Figure 1 The bone marrow microenvironment as a therapeutic barrier and source of pro-survival crosstalk in acute myeloid leukemia (AML). AML blasts interact with niche-resident mesenchymal stromal cells (MSCs), osteoblasts, adipocytes and endothelial cells (arterial and sinusoidal) through adhesion and signaling axes including VCAM-1/VLA-4, CXCL12/CXCR4, E-selectin/CD44, JAG1/Notch. AML-derived factors such as MIF, ANG1/2 and GDF15 further engage receptors on BMME cells (CD74, TIE2 and TGF- β R), reinforcing reciprocal crosstalk between leukemic and stromal compartments. These interactions promote blast adhesion, retention within the niche, proliferation and resistance to chemotherapy. In parallel, the immune landscape is driven towards an immunosuppressive state; TGF- β released by AML cells impairs NK cell surveillance, while PD-L1/PD-1 checkpoint engagement and M2 macrophage polarization facilitate immune evasion. M2 macrophages abbreviated to M2 M Φ . Red arrows and text indicate the predominant functional outcomes of each interaction. Some parts of image adapted from Servier Medical Art (<https://smart.servier.com/>), licensed under CC BY 4.0 (<https://creativecommons.org/licenses/by/4.0/>).

therapy resistance while impairing normal hematopoiesis.⁹¹ Recent evidence indicates that these changes can occur early in disease evolution, with a “pre-leukemic” niche emerging before overt transformation. Profiling of the pre-leukemic BMME has revealed an altered state, characterized by a loss of endothelial cells and reduced collagen deposition by fibroblasts, suggesting that microenvironmental dysfunction may precede and facilitate malignant progression.⁸⁹ Once established, AML cells further manipulate cellular adhesion pathways and soluble factors within the niche to reinforce protection from chemotherapy, thereby promoting resistance and relapse.³⁰ Examples of the extensive interactions between AML and the BMME discussed in this review are summarized in Figure 1, highlighting the complexity of this protective niche. By co-opting native BMME signaling to drive retention, proliferation, and survival, AML blasts evade therapeutic intervention, underscoring the critical need to consider this remodeled niche when assessing novel targets.

Adhesion-Mediated Interactions and Resistance

AML blasts interact closely with stromal and endothelial cells through adhesion molecules that activate pro-survival signaling and promote resistance to chemotherapy. Integrins represent a prominent family of these receptors, consisting of heterodimeric transmembrane proteins composed of α and β subunits.¹¹⁶ While leukemic cells express various integrin combinations, the β 1-integrin subfamily has been shown to be essential for anchoring blasts to the extracellular matrix

and stromal cells. β 1-integrin signaling through the Very Late Antigen-4 (VLA-4; α 4 β 1 integrin)–Vascular Cell Adhesion Molecule 1 (VCAM-1) axis, has been shown to enhance AML blast survival. Specifically, the overexpression of VLA-4 on AML cells and VCAM-1 on stromal cells have been shown to trigger nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B)-dependent signaling that protects them from cytotoxic stress.¹¹⁷ Engagement of CD44 enhances VLA-4 activation and avidity on AML cells, strengthening adhesion to VCAM-1-expressing stromal cells and promoting resistance to chemotherapy.¹¹⁸ These leukemia-supporting mechanisms can provide novel therapeutic targets, as disrupting these interactions through blocking CD44, either alone or in combination with focal adhesion kinase (FAK) blockade, re-sensitizes AML cells to treatment *in vitro*.¹¹⁹

Although direct targeting of the VLA-4–VCAM-1 axis has not yet yielded an approved therapy for AML, the anti-VLA-4 monoclonal antibody natalizumab, approved for multiple sclerosis, demonstrates the pharmacological feasibility of this approach.¹²⁰ Furthermore, integrin-targeted agents have entered clinical evaluation in other malignancies,¹²¹ while dual targeting of FAK and CD44 is yet to progress further than *in vitro* studies,¹¹⁹ FAK inhibition with defactinib is currently being investigated in combination with ASTX727 (decitabine/cedazuridine) in a phase I clinical trial (NCT05636514).

To secure residence within the vascular niche, AML cells exploit endothelial adhesion molecules, such as E-selectin. In the healthy BMME, E-selectin expressed on sinusoidal endothelium regulates HSC homing and quiescence.^{122–124} In AML, engagement of E-selectin on BM endothelium activates pro-survival signaling in leukemic blasts and contributes to chemotherapy resistance. Conversely, uproleselan (GMI-1271), a glycomimetic which binds to E-selectin preventing cancer cell binding, reduces blast adhesion, mobilizes them into circulation, and enhances treatment efficacy *in vivo*.¹²⁵

In a Phase III clinical trial of patients with relapsed or refractory AML (NCT03616470), uproleselan showed an acceptable safety profile and signs of clinical activity, but the study did not achieve its primary overall-survival endpoint. Pre-specified subgroup analyses suggested potential benefit in refractory disease, with few treatment-related toxicities.³³ An ongoing study (NCT03701308) is evaluating daunorubicin and cytarabine with or without uproleselan as induction therapy for patients aged \geq 60 years.

Overall, although the biological rationale for disrupting adhesion is strong, the translation into clinical benefit has proven challenging (summarized in Table 1). The inability of single-agent adhesion inhibitors to consistently improve patient outcomes indicates that AML cells rely on a complex network of retention signals rather than a single physical anchor. This suggests that the protective capacity of the BMME is not solely dependent on direct cell-to-cell contact but is likely reinforced by soluble factors. To fully understand niche-mediated retention, one must also consider the role of chemokine gradients which, much like adhesion molecules, actively tether leukemic blasts to their protective microenvironment.

Chemokine-Mediated Retention

In the normal marrow, the CXCL12/CXCR4 axis directs HSC homing,^{126,127} however, AML cells co-opt this signal to anchor themselves within the protective niche and maintain quiescence.^{128,129} Interestingly, this provides a link between AML genetic heterogeneity and the BMME as frequently occurring mutations in AML, such as TET2 and FLT3-ITD, have been correlated to aberrant CXCL12/CXCR4 signaling, effectively locking LSCs within the niche.^{130,131}

Plerixafor (AMD3100), a CXCR4 antagonist blocking the CXCL12 signal, originally used for stem cell mobilization in lymphoma and myeloma, has been tested in clinical trials for AML.¹³² While it successfully mobilizes AML cells out of the protective BM niche into the peripheral blood, where they are more susceptible to cytotoxic agents, translating this mobilization into improved long-term survival has been difficult (NCT01352650 and NCT00943943).^{34,35} Alternative agents such as dociparstat sodium (DSTAT or CX-01), which is derived from heparin and alters the activity of the CXCL12/CXCR4 axis, has shown encouraging responses when combined with azacitidine in a Phase I trial (NCT02995655),³⁷ as well as promising complete remission (CR) and event-free survival (EFS) rates in a recent Phase II trial when added to induction therapy (NCT02873338).³⁸ Similarly, motixafortide (BL-8040), another high-affinity CXCR4 inhibitor, has shown efficacy in combination with cytarabine in a Phase IIa clinical trial (NCT01838395).³⁶

Several alternative methods of drug delivery to target this axis are also being considered in preclinical research. For example, M-E5-Dox integrates a chemically synthesized CXCR4 antagonistic peptide and the cytotoxic drug, doxorubicin, using DSPE-mPEG2000 micelles, allowing CXCR4 downregulation alongside targeted doxorubicin uptake.¹³³ These strategies aim to improve efficacy by simultaneously disrupting the protective niche and delivering cytotoxic payloads.

In summary, although pharmacological CXCR4 inhibition can transiently mobilize AML cells and enhance short-term chemosensitivity, clinical outcomes indicate that mobilization alone is insufficient to overcome durable niche protection (Table 1). The microenvironment does not merely hold AML cells in place; it engages them in reciprocal signaling that actively promotes survival and drug resistance. Therefore, to fully overcome niche protection, internal signaling cascades sustained by these stromal interactions must also be addressed.

Beyond Adhesion and Retention: Targeting Niche-Derived Signaling

While adhesion molecules physically anchor AML cells within the marrow, their long-term survival and resistance to therapy depend on a complex network of intracellular signaling pathways. AML cells do not merely passively receive these signals; they actively engage in bidirectional crosstalk with stromal components to generate a self-sustaining, protective environment.⁹⁰

JAK/STAT Signaling

In AML, Janus kinase/signal transducers and activators of transcription (JAK/STAT) signaling acts as a major conduit for stromal-derived inflammatory cues, reinforcing pro-survival and anti-apoptotic responses in leukemic cells that compromise therapeutic efficacy.^{134–138} The JAK/STAT pathway is a central regulator of hematopoiesis, immune response, and cell survival.¹³⁹ While intrinsic activating mutations (such as JAK2 V617F) are only identified in a small subset of patients, the JAK/STAT pathway is frequently activated in AML via extrinsic signals from the BMME.¹³⁴ For example, leukemic blasts stimulate MSCs to upregulate the secretion of interleukin-6 (IL-6) and metalloproteinase-14 (MMP14). This leads to activation of the JAK/STAT pathway in the blasts, driven directly by IL-6 and indirectly via the MMP14-dependent release of prostaglandin E2 (PGE2) from MSCs.^{135–137} The resulting phosphorylation of STAT3 and STAT5 drives the expression of pro-survival BCL-2 family proteins; this axis establishes a high apoptotic threshold that confers chemoresistance.¹³⁸

Strategies to disrupt JAK/STAT signaling are under active clinical investigation (Table 1). Ruxolitinib, a selective inhibitor of the AKT site on both JAK1 and JAK2, has been explored as a monotherapy, and in combination with venetoclax and/or decitabine, but showed specific potential as a second-line therapy for differentiation syndrome in acute promyelocytic leukemia (APL) (NCT03874052, NCT01251965, NCT00674479, NCT02257138 and NCT04446806).^{39–43} Ruxolitinib is also being investigated for limiting relapse after allogeneic stem cell transplantation (NCT03286530),⁴⁴ as well as in combination with CART123 cells for relapsed or refractory disease (NCT06768476). Agents targeting this pathway less directly showed some preliminary anti-leukemic activity, including OPB-111077, which disrupts mitochondrial oxidation and STAT3 phosphorylation, as well as pacritinib, a dual FLT3/JAK2 inhibitor, which was explored for patients with FLT3 mutations (NCT03197714, NCT03063944 and NCT02323607).^{45–47}

Tocilizumab, a humanized monoclonal antibody targeting the IL-6 receptor (IL-6R), was recently evaluated in the phase I TOCILAM study. In this trial, the addition of tocilizumab to standard “7+3” induction chemotherapy was found to be safe, with no dose-limiting toxicities observed and encouraging complete remission (CR) rates (NCT04547062).⁴⁸ IL-6 blockade with tocilizumab was also explored in the post-transplant setting in a phase II trial to mitigate IL-6-driven inflammation and reduce the risk of graft-versus-host disease (GVHD) following stem cell transplantation but it did not provide significant reduction in GVHD and/or survival benefit (NCT03434730).¹⁴⁰ Collectively, the critical role of JAK/STAT signaling in mediating stromal protection, combined with emerging signs of clinical efficacy, validates the continued pursuit of pharmacological strategies targeting this pathway.

PI3K/AKT/mTOR Signaling

Activated by direct contact with stromal cells or soluble factors such as CXCL12, Phosphoinositide 3-kinase (PI3K), protein kinase B (AKT) and mechanistic target of rapamycin (mTOR) (PI3K/AKT/mTOR) signaling contributes to the therapeutic barrier maintained by the BMME, promoting AML survival and resistance.^{129,141} Evidence highlights a reciprocal interaction where AML blasts induce the downregulation of methyltransferase-like 3 (METTL3) in MSCs; this triggers AKT activation in the stroma and directs MSCs toward adipogenic differentiation, creating a lipid-rich niche that fuels cancer cell survival.^{142,143}

Effective targeting of the pathway in a clinical setting has proven challenging (Table 1). First-generation PI3K inhibitors, such as idelalisib (CAL-101), which inhibits the PI3K δ isoform, showed no meaningful response in AML, while the pan-PI3K inhibitor buparlisib (BKM120) demonstrated only modest efficacy with significant toxicity (NCT00710528 and NCT01396499).^{49,50} Similarly, dual targeting with inhibitors of both PI3K and mTOR (eg gedatolisib, dactolisib) have largely failed as single agents due to lack of therapeutic response and poor tolerance (NCT02438761 and NCT01756118).^{51,52}

Complexes of mTOR, such as mTORC1, are activated within osteoblastic niches, acting via IL-6 to promote AML cell growth, providing rationale for mTOR-directed therapies to target this interaction.¹⁴⁴ The mTOR inhibitors rapamycin/sirolimus, temsirolimus and everolimus have shown limited single-agent activity, though some benefit has been observed in combination with chemotherapy (NCT00235560, NCT02109744, NCT01822015, 2007–005374-31 and NCT01074086).^{53–57} Similarly, direct AKT inhibitors (eg uposertib, afuresertib) have also been largely ineffective (NCT01907815 and NCT00881946).^{58,59} However, novel strategies are emerging such as ONC201, an imipridone that antagonizes DRD2 and activates mitochondrial ClpP to downstream inactivate AKT and ERK, is currently being evaluated in combination with venetoclax (NCT02392572). It was found to be well tolerated and had encouraging early responses as maintenance therapy to prevent post-transplant relapse (NCT03932643).⁶⁰ Together, these findings indicate that PI3K/AKT/mTOR signaling in AML reflects a microenvironmentally reinforced survival state, driven by convergent niche-derived signals rather than a discrete oncogenic dependency, helping to explain the limited clinical efficacy of direct pathway inhibition and underscoring the need for combinatorial or context-dependent therapeutic strategies.

Angiopoietin/Tie2 Signaling

Angiopoietin/Tie2 signaling serves as a vascular therapeutic barrier in AML within the BMME, stabilizing endothelial niches and reinforcing pro-survival cues, which drives disease progression and protects leukemic cells from cytotoxic and targeted therapies.^{145–147} Leukemic blasts have been shown to overexpress angiopoietin-1 (Ang-1), which engages Tie2 receptors on endothelial cells to subvert the vascular niche and promote cancer cell proliferation.¹⁴⁵

Consequently, disruption of this signaling network has been explored as a therapeutic strategy (Table 1).^{145,148} In preclinical studies, the dual Tie2/p38 MAPK inhibitor pexmetinib (ARRY-614) demonstrated the ability to abolish AML cell proliferation.¹⁴⁹ However, whilst this agent has been well tolerated and has shown efficacy in myelodysplastic syndromes (MDS), it has not yet progressed to the clinical setting for AML (NCT00916227).¹⁵⁰ Conversely, other inhibitors of this pathway have entered clinical evaluation but yielded modest results. For instance, trebananib, a peptibody that neutralizes Ang-1 and Ang-2, and the switch-control tyrosine kinase inhibitor, that specifically targets Tie2, as well as VEGFR-2 and BCR-ABL, have both been tested in clinical trials for AML, but demonstrated limited efficacy as monotherapies or in combination with chemotherapy (NCT01555268 and NCT00827138).^{61,62} Collectively, these findings suggest that Angiopoietin/Tie2 signaling functions primarily to stabilize a permissive vascular niche rather than acting as a leukemia-specific driver, helping to explain the limited clinical efficacy of Tie2-targeted monotherapies in AML.

Wnt/ β -Catenin Signaling

Wnt/ β -catenin signaling represents a niche-remodeling component of the BMME as a therapeutic barrier in AML, promoting osteogenic skewing and stromal states that indirectly reinforce leukemic cell survival and chemoresistance.¹⁵¹

Osteoblasts derived from patients with AML exhibit elevated levels of β -catenin activation, a feature clinically correlated with poor prognosis and reduced treatment response.¹⁵² Mechanistically, the interaction between AML blasts and MSCs leads to the release of the pro-inflammatory mediator PGE2 from MSCs, which subsequently drives β -catenin expression.¹⁵³

Therapeutic targeting of this pathway has proved challenging (Table 1). Direct inhibition strategies have failed to demonstrate efficacy in clinical trials (eg NCT01606579 and NCT01398462)⁶³ and alternative approaches aimed at stabilizing β -catenin through inhibition of Glycogen Synthase Kinase-3 (GSK-3) with inhibitors such as LY2090314, have likewise been explored with limited efficacy in patients with AML (NCT01214603).^{64,154,155} Targeting upstream regulators has also been explored, but the inhibition of the cyclooxygenase-1/2 (COX1/2) axis with the non-steroidal anti-inflammatory drugs sulindac and celecoxib did not translate clinically, with trials ultimately abandoned due to lack of funding and low accrual (NCT01843179 and NCT03878524).^{156,157} Despite promising preclinical data, this consistent lack of translational success highlights that Wnt signaling within the leukemic niche operates predominantly through microenvironmental remodeling rather than direct leukemic cell dependency, underscoring why tumor-intrinsic pathway inhibition has failed to overcome this component of the therapeutic barrier.^{158–160}

Notch Signaling

Notch signaling acts as another niche-remodeling element creating a therapeutic barrier, where AML cells activate this pathway within MSCs to drive aberrant osteogenic differentiation, which results in the accumulation of osteoprogenitors and pre-osteoblasts.¹⁶¹ This remodeled niche not only enhances leukemic cell growth and therapy resistance, but also compromises the support of normal HSCs.¹⁶¹ Consistent with this, BM-MSCs derived from patients with AML exhibit upregulated Notch1 and its ligand Jagged1 (JAG1), as well as increased expression of the downstream target gene HES1. Together, these findings confirm active Notch signaling within components of the AML BMME. Concurrently, activation of Notch1 within the AML blasts themselves further supports leukemic proliferation and chemoresistance.^{162,163}

Therapeutic strategies targeting this axis have shown promise in preclinical models. In particular, synergistic apoptosis induction has been observed when FLT3 tyrosine kinase inhibitors (TKIs) are combined with γ -secretase inhibitors (GSIs), such as DAPT and RO4929097, which block Notch activation.¹⁶⁴ However, clinical translation has been limited (Table 1); only GSI MK-0752 has been tested in AML patients, where it yielded poor response rates (NCT00100152).⁶⁵ These limitations have promoted interest in alternative approaches to targeting notch ligand-specific interactions. For instance, JAG1 inhibition has been shown in vitro to restore healthy hematopoiesis and ameliorate anemia, thrombocytopenia, and immune dysregulation driven by the β -catenin/JAG1/Notch1 axis in AML osteoblasts.¹⁶⁵ Similarly, inhibitors of JAG1 and JAG2, such as CTX014, show preclinical promise; they have been shown to sensitize tumors to T-cell-mediated killing.¹⁶⁶ In summary, the Notch pathway represents an attractive therapeutic target for disrupting the leukemic niche, yet further clinical evaluation is required to translate this into therapeutic benefit.

NF- κ B Signaling

The NF- κ B pathway is a critical mediator of inflammation and cell survival, that is frequently hijacked through stromal interactions within the leukemic niche.^{117,167,168} Constitutive activation of NF- κ B in AML cells drives the expression of anti-apoptotic proteins, including BCL-2 and B-cell lymphoma-extra large (BCL-XL), thereby promoting cell survival and resistance to cytotoxic stress.¹⁶⁹ Due to the on-target toxicities associated with NF- κ B-directed treatment, focusing on downstream mediators is a more attractive option.¹⁷⁰ The NF- κ B-driven increase in anti-apoptotic proteins has been successfully exploited clinically, through the BCL-2 inhibitor, venetoclax, in combination with the hypomethylating agent azacitidine; a regimen that has established a new standard of care for patients who are ineligible for intensive chemotherapy (NCT02993523).²⁶

Beyond direct BCL-2 inhibition, strategies targeting upstream regulators of NF- κ B have also been explored (Table 1). For example, stabilization of the NF- κ B inhibitor, I κ B α , using the proteasome inhibitor MG-132, either alone or in combination with idarubicin, effectively promoted leukemic cell death in preclinical models; however, this specific approach has not yet translated to clinical practice due to low bioavailability, specificity and stability of the drug.^{171–173} An alternative proteasome inhibitor bortezomib, which inhibits the degradation of I κ B α , reducing NF- κ B activity has

been evaluated in several AML trials with mixed results in older populations.¹⁷³ While its combination with decitabine did not enhance outcomes (NCT01420926),⁶⁶ adding it to daunorubicin and cytarabine (NCT00742625) successfully improved remission rates.⁶⁷ Currently, bortezomib is being assessed in newly diagnosed patients: a Phase III trial is investigating its combination with sorafenib tosylate (NCT01371981), and a Phase I/II study (NCT07008638) is evaluating it with CPX-351 for patients harboring TP53 mutations.⁶⁸ In summary, the notable success of venetoclax, alongside encouraging findings of manipulating the upstream members of the NF- κ B, as well as its critical role in AML pathogenesis, highlights this pathway as a compelling target for further clinical investigation.

TGF- β

Transforming growth factor-beta (TGF- β) plays a multifaceted role in the leukemic niche, contributing to chemoresistance while actively remodeling microenvironmental components, including endothelial and Natural Killer (NK) cells.^{174–176} Notably, the activity of TGF- β is significantly elevated in the BM of patients with relapsed AML, impairing NK cell function and compromising innate tumor surveillance.¹⁷⁴ Niche remodeling extends further to BM adipocytes. AML cells secrete growth differentiation factor 15 (GDF15), which signals through the GDF15/TGFBRII/FOXC1/TRPV4 axis to alter adipocyte metabolism by reducing Ca²⁺ influx, and ultimately enhance leukemic cell survival.^{177,178}

Pharmacological targeting of the TGF- β pathway has shown promise in related myeloid malignancies. For example, the TGF- β 1 receptor inhibitor, galunisertib, has demonstrated clinical efficacy for MDS (NCT02008318),¹⁷⁹ however, application in AML remains to be established. TGF- β receptor targeting molecules have also been explored as a way of disrupting adipocyte-mediated survival support within the AML BMME, although results have been variable. For example, the TGF- β receptor I inhibitor LY-2109761 has shown mixed effects in preclinical AML models.^{178,180,181} Conversely, restoring downstream signaling through pharmacological activation of TRPV4 in BM adipocytes using the agonist 4aPDD has yielded promising preclinical results,¹⁷⁸ suggesting that targeting downstream effectors of the TGF- β axis may represent a more tractable therapeutic strategy.

IL-8

Interleukin-8 (IL-8) expression within the leukemic niche is driven by complex bidirectional crosstalk between AML blasts and stromal cells.^{182,183} AML-derived migration inhibitory factor (MIF) activates CD74 and downstream PKC β signaling in MSCs, triggering IL-8 overexpression. This promotes MSC migration towards AML cells, releasing CXCL12 and facilitating leukemic cell survival.¹⁸⁴ This inflammatory state is further reinforced by osteoblast-derived signals and the hypoxic conditions characteristic of the BMME.^{182,185} Pre-clinical pharmacological disruption of this axis, either through PKC β inhibition (using agents such as Ro-31-8220, Go6976, or enzastaurin) or direct blockade of CD74 and IL-8, has been shown *in vitro* to abolish this stromal-mediated protection.¹⁸⁴

Clinically, activation of the IL-8/CXCR2 pathway correlates with adverse outcomes in AML. Preclinical investigation of SB332235, which binds to and blocks CXCR2 activation, shows that it can suppress AML cell proliferation and induces cell cycle arrest.¹⁸⁶ Although several CXCR1/CXCR2 inhibitors, including reparixin and SCH-527123, as well as IL-8-neutralising antibodies, have been evaluated in other disease settings,^{187–189} their therapeutic efficacy in AML has not yet been tested clinically.

VEGF

Vascular Endothelial Growth Factor (VEGF), a signaling protein involved in angiogenesis, is markedly upregulated in endothelial cells following exposure to the cytotoxic drug, cytarabine.¹⁹⁰ In co-culture AML blasts develop resistance to cytarabine, which can be partly resensitized through targeting the VEGF receptor.¹⁹⁰ Despite the rationale that this endothelial support limits treatment efficacy for AML blasts, clinical trials evaluating VEGF receptor inhibitors (such as axitinib and cediranib), or direct VEGF sequestration with bevacizumab, have provided limited benefit (Table 1), regardless of whether they were administered concurrently with or following chemotherapy (NCT00071006, NCT00475150, NTR904 and NCT00015951).^{69–72,191}

Although multi-targeted tyrosine kinase inhibitors, including sunitinib and sorafenib, possess anti-VEGF activity, their clinical and pre-clinical utility in AML has been largely restricted to FLT3-mutant disease rather than inhibition of

angiogenic signaling (NCT00783653, NCT01254890 and NCT02728050).^{192–194} Similarly, aflibercept, a decoy VEGF receptor that prevents ligand binding, demonstrated potent anti-leukemic synergy with chemotherapy in preclinical models but failed to successfully translate into the clinical setting.¹⁹⁵ This may suggest that VEGF is a bystander rather than offering a causative change in therapy resistance.

Metabolic Crosstalk Within the Leukemic Niche

As indicated above, the bidirectional relationship between AML cells and the BMME extends beyond structural and signaling support to include a complex metabolic interplay. AML cells actively remodel the niche to promote their own metabolic reprogramming, thereby supporting survival, proliferation, and resistance to therapy.¹⁹⁶ These metabolic interactions are currently being exploited through various niche-targeted therapeutic interventions undergoing evaluation in both preclinical studies and clinical trials (Table 1).

Although the BMME maintains high vascular density, it remains inherently hypoxic.¹⁹⁷ This condition is further exacerbated in AML through increased vascular leakiness.¹⁹⁸ This low oxygen state is not merely a byproduct of the disease but a functional advantage, as it actively promotes AML cell survival and proliferation. Attempts to exploit this environment have led to the development of TH-302 (evofosfamide), a hypoxia-activated prodrug.¹⁹⁹ TH-302 induces DNA damage upon metabolism in low-oxygen conditions and showed promise in preclinical models, but this success failed to translate into clinical efficacy (NCT01149915).^{73,199}

The environmental constraints of the BMME, coupled with the differentiation status of the cells, dictate the specific metabolic dependencies of AML cells. While rapidly dividing blasts tend to rely on glycolysis, primitive LSCs are more dependent on mitochondrial oxidative phosphorylation (OXPHOS) for survival.^{200–203} Indeed, co-culture of AML cells with BM-MSCs induced metabolic shift toward glycolysis in AML cells, via CXCL12/CXCR4/mTOR signaling, inducing protection against cytarabine.²⁰⁴ Targeting this pathway with plerixafor or directly inhibiting glycolysis using 2-Deoxy-D-glucose (2-DG) and diclofenac increased chemosensitivity.

Similar challenges have emerged when targeting AML cells dependent on mitochondrial OXPHOS. Utilising inhibitors such as IACS-010759 (a BH3 mimetic) and CPI-613 (devimistat, a non-redox active analog of the OXPHOS cofactor lipoic acid) has yielded disappointing results in humans.^{75,205} A phase I clinical trial for IACS-010759 was terminated due to ineffectiveness and adverse effects (NCT02882321).⁷⁴ While CPI-613 failed to demonstrate additional benefit (NCT03504410).⁷⁵ Crucially, there is evidence that interactions between AML cells and MSCs within the BM can actively enhance OXPHOS, further driving chemoresistance.²⁰⁶

This metabolic flexibility is fuelled by a bidirectional exchange of metabolites between the BM stroma and AML cells, which may be an additional source of therapeutic targets. For instance, AML cells induce MSCs to secrete acetate which they take up via gap junctions to fuel the tricarboxylic acid cycle (TCA) cycle and lipid biosynthesis.²⁰⁷ Similarly, AML blasts trigger metabolic reprogramming in adipocytes to activate lipolysis.^{208,209} This generates fatty acids that are utilised by leukemic cells via fatty acid-oxidation (FAO) to produce the energy required for proliferation. While a detailed review of BMME adipocyte-driven FAO is beyond the current scope, its role as a therapeutic target has been documented extensively elsewhere.²¹⁰

In addition to the exchange of metabolites, there is also active exchange of mitochondria from MSCs through tunnelling nanotubes to AML cells, increasing proliferation and resistance to therapy.^{211,212} AML cells are also able to increase mitochondrial biogenesis within MSCs.²¹³ The anti-CD38 monoclonal antibody daratumumab has been shown to inhibit this mitochondrial transfer; however, it has demonstrated limited efficacy as a monotherapy in a clinical trial (NCT03067571).²¹⁴ Further trials combining daratumumab with chemotherapy are currently recruiting (NCT06287944 and NCT05749276). Evidence further suggests that mitochondrial transfer is not limited to MSCs, as it also occurs between AML blasts and other BM resident cells, including endothelial cells and macrophages.^{215,216}

Immune Evasion in the BMME

Within the BM, AML blasts actively drive immune niche remodeling to shield themselves from immune surveillance, thereby contributing a critical immunological component to the therapeutic barrier. This protection is orchestrated

through the coordinated activity of stromal cells and immune-modulatory pathways that suppress anti-leukemic immune responses and promote disease persistence, representing potential targets for personalized therapy.²¹⁷

Immune Checkpoint Inhibition

AML cells and LSCs exploit immune checkpoint pathways, such as PD-1/PD-L1, CTLA-4 and TIM-3 to evade immune detection, primarily through suppression of B and T cell activity.²¹⁷ Beyond immune suppression, recent evidence suggests that PD-L1 also exerts intrinsic effects within AML cells, regulating cell cycle progression, proliferation, and apoptosis via downstream signaling pathways including PI3K/AKT.²¹⁸

Therapeutic targeting of the PD-1/PD-L1 axis, using monoclonal antibodies such as pembrolizumab, nivolumab, and atezolizumab, is well-established in solid tumors and is now being actively evaluated in AML (Table 1). Early clinical studies have demonstrated potential benefits, including reductions in graft-versus-host disease (GVHD) following allogeneic transplantation and improved responses in relapsed/refractory disease settings (NCT02768792, NCT02771197 and NCT04541277).^{76–78,80,81} A phase II trial is currently investigating the addition of pembrolizumab to standard induction chemotherapy (cytarabine plus idarubicin or daunorubicin) (NCT04214249).⁷⁹

Alternative immune checkpoint targets are also being explored (Table 1). Ipilimumab, a CTLA-4 blocking antibody, was investigated in a successful phase I trial in combination with nivolumab²¹⁹ and is currently being assessed in combination with decitabine for relapsed/refractory AML (NCT02890329).⁸² However, not all checkpoint-directed strategies have shown the same promise. For instance, while sabatolimab (a TIM-3 receptor inhibitor) demonstrated acceptable safety and tolerability in combination with venetoclax and azacitidine, its phase II trial (NCT04150029) was terminated following the failure of other TIM-3 inhibitor trials to meet their primary endpoints.^{83,84,217}

Blockade of growth differentiation factor 15 (GDF-15) has been shown to synergize with PD-1 inhibition in solid tumors (NCT04725474).²²⁰ Similarly, antibodies targeting T cell immunoreceptor with Ig and ITIM domains (TIGIT), an inhibitory immune checkpoint receptor expressed on T cells and NK cells that suppresses cytotoxic function through engagement of ligands such as CD155, have demonstrated clinical benefit in combination with atezolizumab in non-small cell lung cancer (NCT03563716).²²¹ However, evaluation in the context of AML remains at an early stage. Looking forward, emerging targets such as these, from solid tumor oncology, may hold relevance for AML.

BMME Shaping Response to Cellular Immunotherapies

The efficacy of cellular immunotherapies in AML, such as Chimeric Antigen Receptor (CAR) T-cells, is frequently constrained by the immunosuppressive BMME, which limits effector cell persistence, function and target engagement. To overcome this barrier, novel “dual-targeting” CAR-T cells strategies have been developed that simultaneously target AML blasts and immunosuppressive niche components. Examples include CAR constructs directed against CD123 and NKG2D ligands, designed to not only eliminate leukemic cells but also monocyte-like myeloid-derived suppressor cells (M-MDSCs) and alternatively activated (M2) macrophages that contribute to immune evasion.²²²

Despite these advances, CAR-T cell therapy in relapsed/refractory AML has historically been associated with limited efficacy and significant off-target toxicity, reflecting the lack of tumor-specific antigens and persistent microenvironmental immunosuppression.²²³ CAR-engineered natural killer (CAR-NK) cells offer a potential alternative, by retaining anti-leukemic activity while exhibiting a more favorable toxicity profile. Notably, CD33-targeted CAR-NK cells, adapted from CAR-T constructs, have recently demonstrated preliminary efficacy and safety in a phase I clinical trial (NCT05008575).⁸⁵

Challenges in Modeling the BMME and AML Interactions

The intricate and dynamic crosstalk between AML blasts and the protective BMME represents a significant barrier to the successful translation of targeted therapies. While the biological rationale for disrupting microenvironmental support is compelling, faithfully reproducing these complex interactions in preclinical models remains a formidable challenge, which contributes to the gap between experimental promise and clinical efficacy. The various experimental platforms used to study these interactions, ranging from simplified cell cultures to advanced humanized systems, are summarized in Figure 2.

Standard preclinical studies historically relied on immortalized AML cell lines cultured in suspension. Although these models facilitate the high-throughput interrogation of defined AML subtypes based on morphology, genetic mutations, and immunophenotypes, they fail to capture the cellular heterogeneity, spatial organization, and context dependence observed in patient disease.^{224,225} Two-dimensional (2D) co-culture systems incorporating stromal components (such as MSCs or endothelial cells) have therefore been developed to model niche-mediated protection more accurately.²²⁶ However, even these adaptations remain limited by the absence of native three-dimensional (3D) architecture and bio-mechanical cues that are integral to the BMME.

To better recapitulate this structural complexity, a range of 3D culture models have been introduced. While these systems offer important conceptual advances, their widespread adoption has been limited by significant technical barriers; they often require labor-intensive preparation, specialized biomaterials, and lengthy optimization periods. As a result, reproducibility across laboratories remains limited, reflected in the relative paucity of follow-up studies utilizing these specific models once initially described.^{227–232}

In vivo murine models remain the gold standard for investigating leukemogenesis within a largely intact physiological niche.²²⁶ Nevertheless, fundamental species-specific differences impose important limitations. The reliance on immunocompromised hosts to permit human AML engraftment, together with the presence of a murine-specific stromal compartment, results in the absence or distortion of key immunological, cytokine and cell-cell interactions. These discrepancies likely contribute to the high attrition rate of therapies that show promise in murine models but fail to translate into meaningful clinical benefit.^{34,233,234}

To address these challenges, increasing efforts are focused on the development of more representative, “humanized” preclinical models. Approaches such as mice engrafted with functional human immune systems, aim to restore aspects of the immune context lacking in conventional xenografts.²³⁵ Ultimately, progress in this area will depend on the generation of experimental platforms that more accurately reflect both the intrinsic heterogeneity of AML, and the multifaceted, adaptive nature of the human BMME thereby enabling more reliable evaluation of niche-targeted strategies.

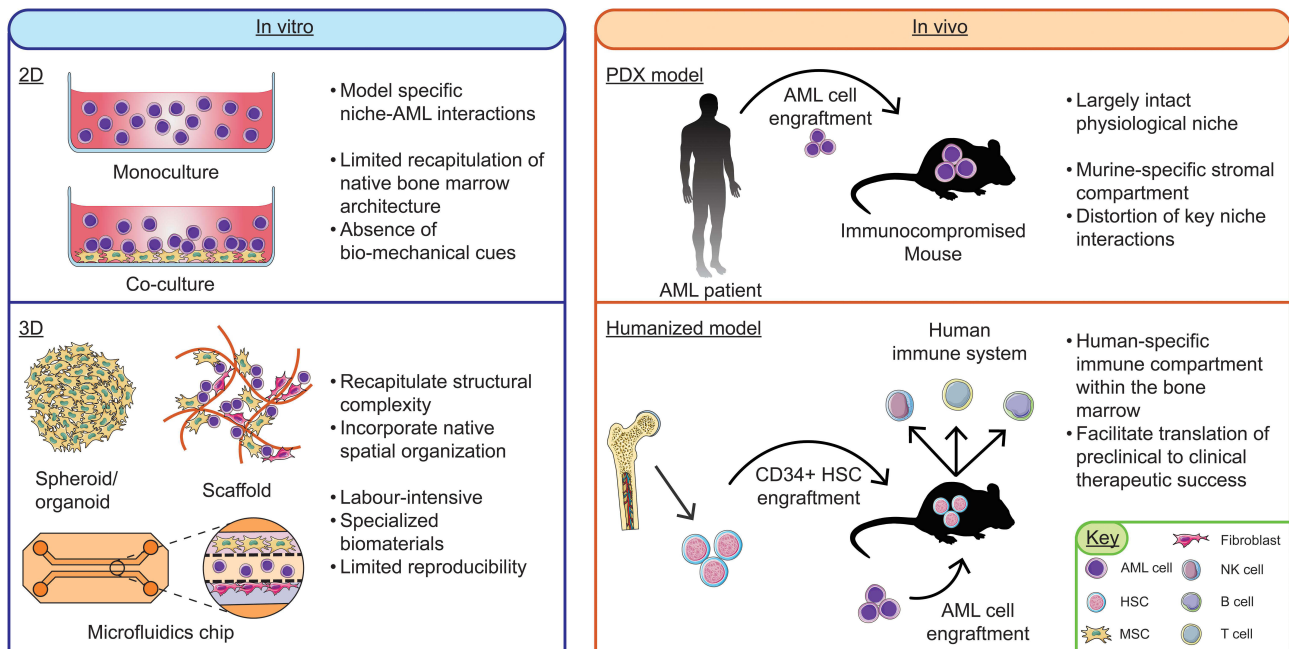


Figure 2 Methodological landscape of preclinical AML models. Left: In vitro platforms ranging from 2D monocultures and co-cultures (with mesenchymal stromal cells (MSCs) or fibroblasts) to 3D systems. While 2D models offer high reproducibility, 3D platforms (spheroids, organoids, scaffolds, and microfluidic chips) are utilized to better recapitulate the structural complexity, extracellular matrix (ECM) organization, and biomechanical cues of the bone marrow microenvironment (BMME). Right: In vivo murine models for translational validation. Patient-derived xenograft (PDX) models utilize immunocompromised mice to facilitate engraftment, though murine-specific stroma can distort human niche-mediated resistance. Humanized models involve the engraftment of human CD34+ hematopoietic stem cells (HSCs) to generate a human-specific immune compartment (T, B, and NK cells), facilitating more accurate clinical translation of novel therapeutics. Some parts of image adapted from Servier Medical Art (<https://smart.servier.com/>), licensed under CC BY 4.0 (<https://creativecommons.org/licenses/by/4.0/>).

Conclusion

AML is sustained not only by intrinsic genetic lesions but also by a highly dynamic and adaptable BMME that actively promotes leukemic cell survival, immune evasion, and therapeutic resistance. As outlined in this review, AML blasts engage in extensive bidirectional crosstalk with stromal, vascular, and immune compartments through a complex network of adhesion-dependent interactions, soluble factors, and reciprocal signaling pathways, collectively establishing a permissive niche that undermines the efficacy of otherwise rational targeted therapies.

Despite substantial advances in delineating these mechanisms, clinical translation of strategies aimed at disrupting niche-mediated support has remained limited (Table 1). This reflects both inherent redundancy and plasticity of microenvironmental support networks and the ongoing difficulty of modeling their complexity in preclinical systems. Together, these observations indicate that the BMME functions as an integrated therapeutic barrier rather than a collection of independent, targetable pathways. Consequently, effective disruption of niche-mediated protection is unlikely to be achieved through single-pathway inhibition alone. Future therapeutic strategies will instead need to employ rational, context-aware combination strategies that simultaneously target leukemic cells and key components of their supportive microenvironment, informed by disease stage, molecular subtype and treatment timing. Such strategies represent a critical step toward eliminating the reservoirs of residual disease that drive clinical relapse, thereby improving long-term survival and cure rates for patients with AML.

Disclosure

The authors report no conflicts of interest in this work.

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