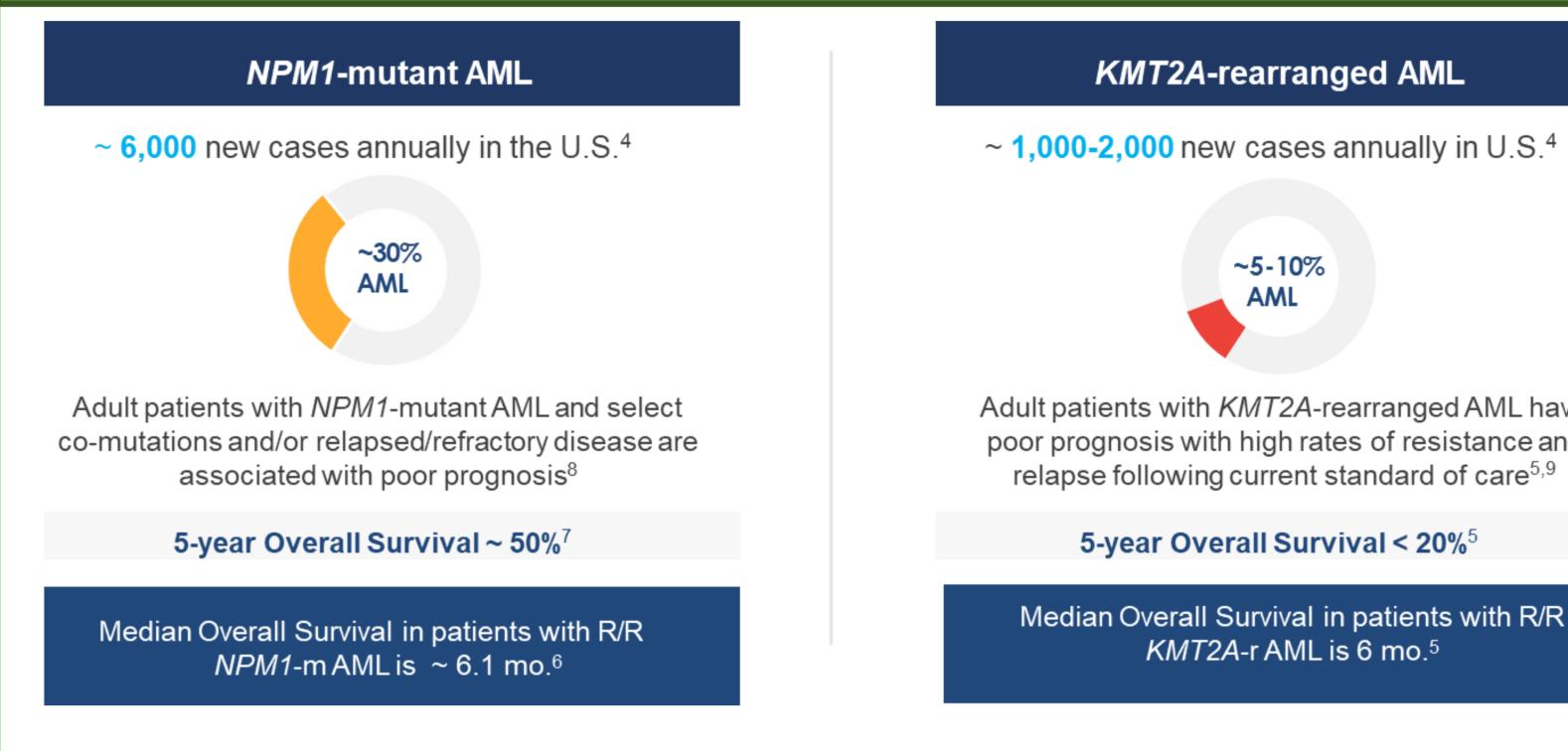
KOMET-008: A Phase 1 Study to Determine the Safety and Tolerability of Ziftomenib Combinations for the Treatment of KMT2A-rearranged or NPM1-mutant Relapsed/Refractory Acute Myeloid Leukemia

Aaron D. Goldberg,¹ Daniel Corum,² Julie Ahsan,² Kun Nie,² Tom Kozlek,² Mollie Leoni,² and Stephen Dale² ¹Memorial Sloan Kettering Cancer Center, New York, NY; ²Kura Oncology, Inc., Boston, MA

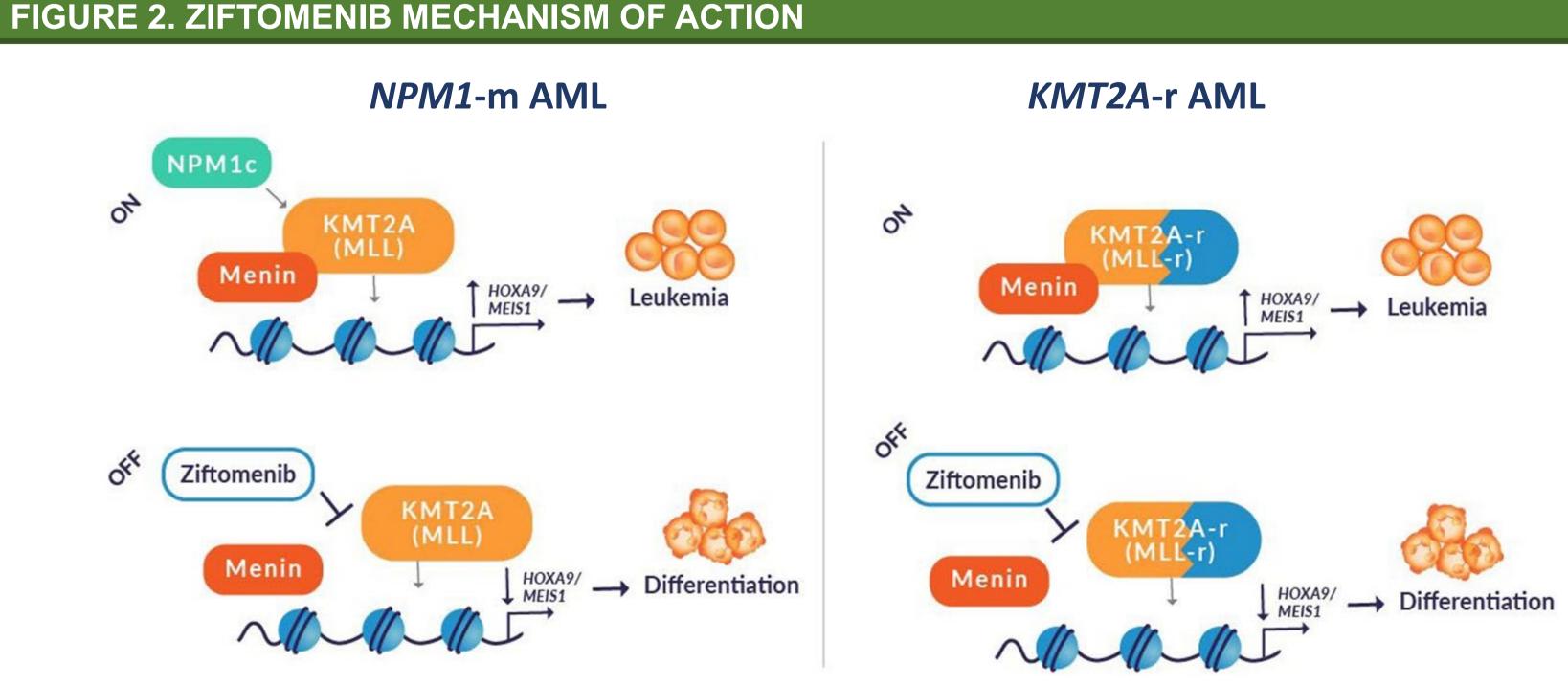
BACKGROUND

- Relapsed/refractory (R/R) acute myeloid leukemia (AML) with nucleophosmin 1 (NPM1) mutations or lysine[K]specific methyltransferase 2A (KMT2A) rearrangements represent a high unmet need, with no currently approved targeted therapies (Figure 1).¹⁻³
- There are approximately 6,000 new cases of NPM1-mutant (NPM1-m) AML and 1,000 to 2,000 new cases of KMT2A-rearranged (KMT2A-r) AML each year in the United States.⁴
- Adult R/R AML patients harboring NPM1 mutations or KMT2A rearrangements have poor prognoses, with median overall survivals of approximately 6 months (Figure 1).^{5,6}

FIGURE 1. NPM1-m AND KMT2A-r AML



- NPM1-m and KMT2A-r AML subtypes are dependent on the protein-protein interaction between menin and histonelysine-N-methyltransferase 2A (KMT2A), a central regulator of target genes driving leukemic transformation in AML subtypes (Figure 2).¹⁰⁻¹²
- [•] Ziftomenib is an oral investigational drug that is a potent and selective inhibitor of the protein-protein interaction between menin and KMT2A (Figure 2).¹⁰⁻¹²
- Preclinical studies have demonstrated that ziftomenib effectively triggers myeloid differentiation and produces antileukemic effects in NPM1-m and KMT2A-r AML cellular and in vivo models.^{13,14}
- Furthermore, the antitumor activity of menin inhibitors in preclinical models of *KMT2A*-r and *NPM1*-m AML is enhanced by the addition of FLT3 inhibitors such as gilteritinib.^{15,16}
- In an ongoing Phase 1/2 study (KO-MEN-001; NCT04067336) in patients with heavily pre-treated R/R AML, ziftomenib 600 mg monotherapy was well tolerated and demonstrated meaningful clinical activity in NPM1-m AML, with a complete remission (CR) rate of 35.0% (n=20), and in KMT2A-r AML, with a composite CR rate of 16.7% (n=18).¹⁷
- This encouraging preliminary clinical activity and safety/tolerability profile of ziftomenib support its clinical investigation in combination with standard therapies, which may lead to improved outcomes for these genetically defined AML patients.
- KOMET-008 (KO-MEN-008; NCT06001788) is a Phase 1 clinical trial being conducted to evaluate the safety and preliminary clinical activity of ziftomenib in combination with standard-of-care (SOC) therapies in patients with R/R NPM1-m or KMT2A-r AML.



AML, acute myeloid leukemia; KMT2A-r, lysine[K]-specific methyltransferase 2A-rearranged; HOXA9, homeobox A9; MEIS1, meis homeobox 1; MLL, menin-mixed-lineage leukemia; MLL-r, MLL-rearranged; NPM1c, cytoplasmic NPM1; NPM1c, cytoplasmic nucleophosmin 1; NPM1-m, nucleophosmin 1mutant; XPO1, exportin 1

- Adult patients with KMT2A-rearranged AML have poor prognosis with high rates of resistance and relapse following current standard of care^{5,9}
- Median Overall Survival in patients with R/R *KMT2A*-r AML is 6 mo.⁵

BACKGROUND (CONT) ZIFTOMENIB MECHANISM OF ACTION

- Genetic rearrangements of KMT2A lead to aberrant expression of homeobox (HOX) genes and their DNA-binding cofactor *MEIS1*, which leads to proliferation, stemness and differentiation block of bone marrow cells.^{11,18,19}
- Rearrangements involving KMT2A alter the gene's normal histone methyltransferase function, maintaining is preserved throughout all KMT2A fusion proteins.^{11,18,20} Likewise, the leukemic gene expression program is dependent on NPM1-m interacting with menin and wild-type KMT2A.^{1,2,11}
- Inhibition of the menin–KMT2A interaction disrupts the assembly of oncogenic KMT2A wild-type or fusion complexes on chromatin and studies have demonstrated that menin inhibition downregulates HOX and MEIS1 transcription leading to differentiation of leukemic blasts.^{10,18}

STUDY DESIGN

- KOMET-008 is a 2-part dose-escalation (Phase 1A) and expansion (Phase 1B) clinical trial to evaluate the safety, tolerability, and preliminary clinical activity of ziftomenib when combined with SOC regimens for the treatment of either NPM1-m or KMT2A-r R/R AML
- escalation within each cohort will occur independently following a rule-based approach based on a i3+3 design to select ziftomenib doses for expansion/validation in Phase 1B (Figure 3).
- Study objectives/endpoints and key inclusion and exclusion criteria are shown in Table 1 and Table 2, respectively.

FLAG-IDA, fludarabine, cytarabine (Ara-C), granulocyte-colony stimulating factor (G-CSF), and idarubicin; LDAC, low-dose cytarabine.

FIGURE 3. KOMET-008 STUDY DESIGN

PHASE 1 Ziftomenib Combination Clinical Trial in Patients with NPM1-m OR KMT2A-r Relapsed/Refractory AML

SCREENING	PHASE 1A DOSE ESCALATI
<image/>	 Arm A: R/R NPM1-m A Ziftomenib and: FLAG-IDA (Cohort A-4) LDAC (Cohort A-2) Gilteritinib (Cohort A-3) patients with a docum <i>FLT3</i> co-mutation) Arm B: R/R KMT2A-r A Ziftomenib and: FLAG-IDA (Cohort B-4) LDAC (Cohort B-2)

AML, acute myeloid leukemia; FLAG-IDA, fludarabine, cytarabine, granulocyte-colony stimulating factor, and idarubicin; *KMT2A*-r, lysine[K]-specific methyltransferase 2A-rearranged; LDAC, low-dose cytarabine; NPM1-m, nucleophosmin 1-mutant; R/R, relapsed or refractory.

REFERENCES

1. Li X, Song Y. J Hematol Oncol. 2021;14:56; 2. Kühn MW, et al. Cancer Discov. 2016;6:1166-81; 3. Matthews AH, et al. Cancers (Basel). 2022;14(23):5906; 4. Surveillance, Epidemiology, and End Results Program. 2023. https://seer.cancer.gov/statfacts/html/amyl.html; 5. lssa GC, et al. Blood Cancer J. 2021;11:162; 6. Venugopal S, et al. ASH Abstract 2287, 2021; 7. Angenendt L, et al. J Clin Oncol. 2019;37(29):2632-2642. 8. Döhner H, et al. Blood. 2017;129:424-447; 9. Vetro C, et al. Cancer Genet. 2020;240:15-22 10. Grembecka J, et al. Nat Chem Biol. 2012;8:277-84; 11. Klossowski S, et al. J Clin Invest. 2020;130:981-97; 12.Shi A, et al. Blood. 2012;120:4461-9; 13. Fiskus W, et al. Leukemia. 2022;36:2729-33; 14. Rausch J, et al. Haematologica. 2023;108:2837-2843; 15. Dzama MM, et al. Blood. 2020;136:2442-2456. 16. Miao H, et al. *Blood.* 2020;136:2958–2963; 17. Fathi A. *Hemasphere.* 2023;7(Suppl):e19161da. 18. Krivtsov AV, et al. *Cancer Cell.* 2019;36:660-73; 19. Thorsteinsdottir, et al. Mol. Cell. Biol. 2001;21:224–234. 20. Krivtsov AV, Armstrong SA. Nat Rev Cancer. 2007;7:823-33.

ACKNOWLEDGEMENTS

The KOMET-008 clinical trial is sponsored by Kura Oncology, Inc. Medical writing and editorial assistance were provided by Troy A. Baudino, PhD, Kura Oncology.

elevated HOX expression and sustaining the hematopoietic differentiation blockade, while the menin-binding motif

• During Phase 1A, the ziftomenib dose will be escalated with gilteritinib, FLAG-IDA, or LDAC in separate geneticallydefined cohorts (NPM1-m and KMT2A-r). Initially, 6 patients will be treated at DL1 within the respective cohort. Dose

PHASE 1B DOSE VALIDATION/EXPANSION

-3; for mented

AML

combination from the dose escalation phase (Phase 1A) will be examined in the dose validation phase (Phase 1B) • Up to 15 patients will be enrolled per cohort at the dose level chosen for validation

At least 1 dose level for each

STUDY DESIGN (CONT TABLE 1. KEY OBJECT

Objectives **Primary**

Determine safety and tolera

Secondary **Evaluate clinical activity**

Evaluate survival and disea

Characterize the PK of zifto metabolites when administer

Evaluate the PK of gilteritini administered concurrently with ziftomenib

^aCR, CRc, or MLFS rate determined using the ELN 2022 criteria. AE, adverse event; AUC_(0-last), area under the concentration-time curve from time zero to the time of the last quantifiable concentration after dosing; AUC_(tau), area under the concentration-time curve over a dosing interval; BM, bone marrow; C_{max}, maximum plasma concentration; CR, complete remission; CRc, composite complete remission; CRh, complete remission with partial hematologic recovery; CRi, complete remission with incomplete hematologic recovery; DLT, dose-limiting toxicity; EFS, event-free survival; ELN, European Leukemia Network; HSCT, hematopoietic stem cell transplant; MFC, multiparameter flow cytometry; MLFS, morphologic leukemia-free state; MRD, measurable residual disease; NCI-CTCAE, National Cancer Institute Common Terminology for Adverse Events; NGS, nextgeneration sequencing; OS, overall survival; PCR, polymerase chain reaction; T_{max} , time to maximum plasma concentration; zifto, ziftomenib.

TABLE 2. KEY INCLUSION AND EXCLUSION CRITERIA Inclusion Criteria

therapy

- Documented NPM1-m or KMT2A-r AML
- etc)
- ECOG performance status: 0, 1, or 2
- Adequate and stable renal, hepatic, and cardiac function

Exclusion Criteria

- Clinically active CNS leukemia
- Active and uncontrolled infection
- approximately 5 minutes of each other

^aPer WHO Classification of Hematolymphoid Tumors (5th Edition). AML, acute myeloid leukemia; APML, acute promyelocytic leukemia; CNS, central nervous system; ECOG, Eastern Cooperative Oncology Group; ELN, European Leukemia Network; FLT3, FMS-like tyrosine kinase 3; HIV, human immunodeficiency virus; HMA, hypomethylating agents; *KMT2A*-r, lysine[K]-specific methyltransferase 2A-rearranged; MDS, myelodysplastic syndromes; *NPM1*-m, nucleophosmin 1-mutant; R/R, relapsed/refractory; WHO, World Health Organization.

SUMMARY



-)		
IVES AND ENDPOINTS		
	Endpoints	
rability	 Rate of DLT per dose level 	
	 Descriptive statistics of AEs per the NCI-CTCAE v 5.0 	
	 CR for FLAG-IDA, LDAC combinations in patients with KMT2A-r or NPM1-m R/R AML 	
	 CR/CRh in combination with gilteritinib in NPM1-m patients with a documented FLT3 mutation 	
ase control outcomes	 CRc (CR+CRi+CRh) and MLFS rates¹⁵ 	
	 OS and 6-month OS 	
	 Median EFS and 6-month EFS 	
	 Duration of remission 	
	 MRD assessment in BM by flow cytometry and molecular analysis (PCR, NGS) 	
	 Proportion of patients that undergo HSCT 	
	 Rate of transfusion independence 	
omenib and tered in combination	 Cmax, Tmax, AUC(0-last), AUC(tau) 	
nib when with ziftomenib	 Cmax, Tmax, AUC(0-last), AUC(tau) 	

Adults (\geq 18 years of age) diagnosed with AML^a who relapsed following or were refractory (R/R) to \geq 1 prior line of

• For gilteritinib combination only: documented *FLT3* mutation (internal tandem duplication [ITD] or tyrosine kinase domain mutation) in BM or peripheral blood following completion of immediate prior therapy, as measured by the established threshold of the chosen assay (polymerase chain reaction [PCR], next-generation sequencing [NGS],

Diagnosis of promyelocytic leukemia or blast chronic myeloid leukemia

Mean corrected QT interval by Fredericia's formula (QTcF) >480 ms on triplicate 12-lead ECGs performed within

Clinical signs/symptoms of leukostasis or WBC >25×10⁹/L.

• Has received prior stem cell transplant and has not adequately recovered

Has received radiation, chemotherapy, immunotherapy, or any other anticancer therapy including investigational therapy <14 days or within 5 drug half-lives (whichever is shorter) prior to the first dose of study intervention

• KOMET-008 will determine the safety, tolerability, and preliminary clinical activity of ziftomenib in combination with gilteritinib, FLAG-IDA, and LDAC SOC regimens for the treatment of NPM1-m and KMT2A-r R/R AML.