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## The 65th ASH Annual Meeting Abstracts

## **ORAL ABSTRACTS**

## 616.ACUTE MYELOID LEUKEMIAS: INVESTIGATIONAL THERAPIES, EXCLUDING TRANSPLANTATION AND **CELLULAR IMMUNOTHERAPIES**

## A First-in-Human Phase 1 Study of the Menin-KMT2A (MLL1) Inhibitor JNJ-75276617 in Adult Patients with Relapsed/Refractory Acute Leukemia Harboring KMT2A or NPM1 Alterations

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**Background:** Relapsed/refractory (R/R)acute leukemia withalterations in *KMT2A* (also called *MLL1*; 9-15% of adult AML, 10% of ALL) or *NPM1* (30% of adult AML) are often associated with poor outcomes. Pre-clinical studies demonstrated the relevance of the menin-KMT2A protein-protein interaction in sustaining leukemic cells with *KMT2A* and *NPM1* alterations (Kuhn 2016). JNJ-75276617 is a potent and selective inhibitor of the interaction between the scaffolding protein menin and the methyltransferase KMT2A with preclinical activity in *KMT2A*-rearranged or *NPM1*-mutated leukemic cell lines and primary leukemia patient samples *in vitro* and *in vivo* (Kwon 2022). We report initial data investigating JNJ-75276617 in adult participants (pts) with R/R acute leukemia harboring *KMT2A* alterations (rearrangements, amplifications, or partial tandem duplications) or *NPM1* mutations.

**Methods:** 75276617ALE1001 (NCT04811560) is an ongoing Phase 1, multicenter, open-label, dose-finding study. Pts in dose escalation receive JNJ-75276617 orally on a 28-day cycle. As of 8 April 2023, multiple dose levels  $\geq$ 15 mg have been explored on either a daily or twice daily (BID) dosing schedule. AEs were graded by CTCAE v5.0. Responses were investigator-assessed per ELN2017. Preliminary safety, efficacy and PD data are reported herein, with a focused review of the efficacy in higher dose levels with  $\geq$ 3 pts dosed.

**Results:** Fifty-eight pts received JNJ-75276617. The median age was 63 (range: 19-83) years; 56 pts (97%) had R/R AML and 2 (3%) had R/R ALL. The median number of prior lines of treatment was 2 (range: 1-7), including 10 (17%) pts with a prior allogeneic stem cell transplant. A *KMT2A* or *NPM1* alteration was present in 33 (57%) and 25 (43%) pts, respectively.

Thirty (52%) pts experienced  $\geq$ 1 treatment-related AE (TRAE); most commonly differentiation syndrome (DS) (8 [14%]). Grade  $\geq$ 3 TRAEs were observed in 17 (29%) pts; those reported in  $\geq$ 2 pts were neutropenia (6 [10%]), anemia and thrombocytopenia (4 [7%] each), DS (3 [5%]), and ALT and AST increase (2 [3%] each). Dose limiting toxicities (DLTs) were observed in 5 (9%) pts, with DS (2 [3%]) as the only DLT reported in  $\geq$ 2 pts.

In 26 (63%) of the 41 pts with disease evaluation data, there was a reduction in bone marrow (BM) disease burden ( Figure 1). Of these, a  $\geq$ 50% decrease in BM blasts was observed in 16 (39%) pts. In the highest dose level with  $\geq$ 3 pts (90 mg BID; n=8), the ORR ( $\geq$ PR) was 50% (n=4), with all responders ongoing ( Figure 2). These responders (2 NPM1-, 2 KMT2A-altered) achieved CR (1 pt), CRh (1 pt), and CRi (2 pts). In a review of higher dose levels with  $\geq$ 3 pts ( $\geq$ 45 mg BID; n=20), the ORR was 40% (n=8), with 7 responders ongoing ( Figure 2). These responders (5 NPM1-, 3 KMT2A-altered) achieved CR (3 pts), CRh (1 pt), CRi (3 pts), and PR (1 pt); median (range) time to first response ( $\geq$ PR) 1.81 mos (1.0-3.3; n=8); time to CR, CRh, or CRi 1.77 mos (1.0-3.3; n=7); and time to CR 2.79 mos (1.8-2.9; n=3). Across all cohorts there were 12 responders, including 1 MRD negative CR. One responder discontinued treatment for allogeneic transplant; however, 8 responders continue on treatment, including 2 pts in cycle 9.

Preliminary PD data from unfractionated BM and/or PBMCs in paired samples among responders (n=12) show biologic activity as indicated by reduction in expression (mean fold change from baseline calculated as [on-tx-baseline]/baseline [range]) of menin-KMT2A target genes ( MEIS1 -0.42 [-1.0-9.0]; HOXA9 -0.03 [-1.0-21.7]; FLT3 18.6 [-1.0-425]) and induction of genes associated with differentiation ( ITGAM 55.0 [-0.93-1467]; MNDA 5.9 [-1.0-83.5]). Compared to baseline, the percentage of KMT2A-altered cells or NPM1 variant allele frequency (VAF) was reduced in responders, with a decrease in KMT2A-altered cells by break-apart FISH probe from 59.2% at baseline to 8.1% post-treatment and in NPM1 VAF using a myeloid gene NGS panel from 13.1% at baseline to 2.8% post-treatment.

**Conclusions:** Dose escalation in 75276617ALE1001 is ongoing with the RP2D(s) yet to be determined. Pts in dose expansion will receive JNJ-75276617 at the identified RP2D(s). Preliminary results of this FIH Phase 1 study demonstrate that JNJ-75276617 monotherapy has an acceptable safety profile, encouraging antileukemic activity, and emerging biologic activity consistent with the proposed mechanism of action in pts with R/R acute leukemia harboring KMT2A or NPM1 alterations.

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■ KMT2A ■ NPM1 ■ Not Reported 80 70 60 50 Best Relative Change from Baseline (%) 40 30 20 10 0 -10 -20 -30 -40 -50 -60 -70 -80 -90

Figure 1. Best Percent Change from Baseline in Bone Marrow Blasts With JNJ-75276617 Monotherapy in R/R Acute Leukemia

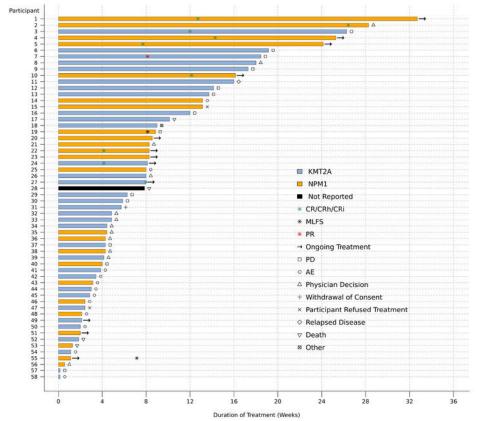
Note: Bars are only presented for participants where a measurable change from baseline is found in the data (n=41; 23 KMT2A-altered, 17 NPM1-altered, 1 Not Reported).

Note: Each bar represents a unique study participant.

Note: One participant did not have NPMI or KMTZA mutation reported as of data-cut.

Note: Five participants had best relative change from baseline of >100%.

Figure 2. Preliminary Clinical Activity of JNJ-75276617 Monotherapy in R/R Acute Leukemia



Key: CR=Complete Response; CRh=CR with Partial Hematologic Recovery; CRi=CR with Incomplete Hematologic Recovery; MLFS=Morphologic Leukemia-Free State; PR=Partial Remission; PD=Progressive Disease; AE=Adverse Event
Note: Participant 2 was sent for transplant after discontinuing treatment.
Note: Participant 2 did not have NPM1 or KM72A mutation reported as of data-cut.
Note: Participant 55 had incomplete duration of treatment information entered at time of data-cut.

Figure 1

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