

# Outcome of Azacitidine Therapy in Acute Myeloid Leukemia Is not Improved by Concurrent Vorinostat Therapy but Is Predicted by a Diagnostic Molecular Signature

Charles F. Craddock<sup>1</sup>, Aimee E. Houlton<sup>2</sup>, Lynn Swun Quek<sup>3</sup>, Paul Ferguson<sup>1</sup>, Emma Gbandi<sup>2</sup>, Corran Roberts<sup>4</sup>, Marlen Metzner<sup>3</sup>, Natalia Garcia-Martin<sup>3</sup>, Alison Kennedy<sup>3</sup>, Angela Hamblin<sup>3</sup>, Manoj Raghavan<sup>1</sup>, Sandeep Nagra<sup>1</sup>, Louise Dudley<sup>2</sup>, Keith Wheatley<sup>2</sup>, Mary Frances McMullin<sup>5</sup>, Srinivas P. Pillai<sup>6</sup>, Richard J. Kelly<sup>7</sup>, Shamyla Siddique<sup>2</sup>, Michael Dennis<sup>8</sup>, Jamie D. Cavenagh<sup>9</sup>, and Paresh Vyas<sup>3</sup>



## Abstract

**Purpose:** Azacitidine (AZA) is a novel therapeutic option in older patients with acute myeloid leukemia (AML), but its rational utilization is compromised by the fact that neither the determinants of clinical response nor its mechanism of action are defined. Co-administration of histone deacetylase inhibitors, such as vorinostat (VOR), is reported to improve the clinical activity of AZA, but this has not been prospectively studied in patients with AML.

**Experimental Design:** We compared outcomes in 259 adults with AML ( $n = 217$ ) and MDS ( $n = 42$ ) randomized to receive either AZA monotherapy ( $75 \text{ mg/m}^2 \times 7$  days every 28 days) or AZA combined with VOR 300 mg twice a day on days 3 to 9 orally. Next-generation sequencing was performed in 250 patients on 41 genes commonly mutated in AML. Serial immunophenotyping of progenitor cells was performed in 47 patients.

**Results:** Co-administration of VOR did not increase the overall response rate ( $P = 0.84$ ) or overall survival (OS;  $P = 0.32$ ). Specifically, no benefit was identified in either *de novo* or relapsed AML. Mutations in the genes *CDKN2A* ( $P = 0.0001$ ), *IDH1* ( $P = 0.004$ ), and *TP53* ( $P = 0.003$ ) were associated with reduced OS. Lymphoid multipotential progenitor populations were greatly expanded at diagnosis and although reduced in size in responding patients remained detectable throughout treatment.

**Conclusions:** This study demonstrates no benefit of concurrent administration of VOR with AZA but identifies a mutational signature predictive of outcome after AZA-based therapy. The correlation between heterozygous loss of function *CDKN2A* mutations and decreased OS implicates induction of cell-cycle arrest as a mechanism by which AZA exerts its clinical activity. *Clin Cancer Res*; 23(21): 6430–40. ©2017 AACR.

<sup>1</sup>Centre for Clinical Haematology, Queen Elizabeth Hospital, Birmingham, United Kingdom. <sup>2</sup>Cancer Research UK Clinical Trials Unit, University of Birmingham, Birmingham, United Kingdom. <sup>3</sup>MRC Molecular Haematology Unit and Centre for Haematology, Weatherall Institute of Molecular Medicine, University of Oxford and Oxford University Hospitals NHS Trust, Oxford, United Kingdom. <sup>4</sup>Centre for Statistics in Medicine, Oxford, United Kingdom. <sup>5</sup>Department of Haematology, Queen's University, Belfast, United Kingdom. <sup>6</sup>University Hospitals of North Midlands, Stoke on Trent, United Kingdom. <sup>7</sup>Leeds Teaching Hospitals NHS Trust, Leeds, United Kingdom. <sup>8</sup>The Christie NHS Foundation Trust, Manchester, United Kingdom. <sup>9</sup>Department of Haemato-Oncology, St Bartholomew's Hospital, Bart's Health NHS Trust, London, United Kingdom.

**Note:** Supplementary data for this article are available at Clinical Cancer Research Online (<http://clincancerres.aacrjournals.org/>).

**Corresponding Authors:** Charles Craddock, Centre for Clinical Haematology, Queen Elizabeth Hospital, Birmingham, B15 2TH, UK. Phone: 447887571579; E-mail: Charles.Craddock@uhb.nhs.uk; Paresh Vyas, MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, University of Oxford, Oxford OX3 9DU, UK. Phone: 441865222489; Fax: 01865222500; E-mail: paresh.vyas@imm.ox.ac.uk.

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## Introduction

The DNA methyltransferase (DNMT) inhibitors azacitidine (AZA) and decitabine (DEC) represent important advances in the management of patients with acute myeloid leukemia (AML) and high-risk myelodysplasia (MDS) ineligible for intensive chemotherapy (IC) (1). Recent randomized trials have demonstrated that AZA improves outcome in older adults with AML and high-risk MDS (2, 3). More recently, AZA has been shown to possess significant clinical activity in relapsed and refractory AML (4–6). However, the clinical utility of AZA in both newly diagnosed and advanced disease is limited by relatively low rates of complete remission (CR) and the fact that all patients relapse despite continuing therapy. There is consequently an urgent need to identify novel therapies with the potential to improve the outcome after AZA monotherapy. Co-administration of AZA with histone deacetylase (HDAC) inhibitors augments killing of leukemic cell lines *in vitro* (7) and single-arm trials have described increased clinical activity of AZA in combination with a number of HDAC inhibitors including sodium valproate and vorinostat (VOR; refs. 4, 8, 9).

### Translational Relevance

The clinical benefit of azacitidine (AZA) monotherapy in patients with acute myeloid leukemia (AML) is blunted by low response rates and the inevitability of disease progression. Combination therapy with histone deacetylase (HDAC) inhibitors has been proposed to improve outcome but has not been prospectively studied in AML. The demonstration in this randomized study that co-administration of AZA with the HDAC inhibitor vorinostat does not improve outcome in newly diagnosed or relapsed AML confirms the importance of identifying new therapeutic partners for AZA. In this context, the observation that mutations in the cell-cycle checkpoint activator *CDKN2A* correlate with adverse clinical outcome represents the first clinical validation of *in vitro* data implicating induction of cell cycle arrest as a mechanism of AZA's clinical activity informing the design of novel drug combinations. Furthermore, persistence of stem/progenitor populations throughout therapy identifies their role as a biomarker of response to AZA-based regimens.

Although recent randomized trials have reported no benefit of combined AZA and HDAC inhibitor therapy in patients with high-risk MDS, there have been no randomized trials in AML (10–12).

The development of pharmacological strategies to improve the outcome of AZA-based therapy in AML has been hampered by our limited understanding of its mechanism of action. Although *in vitro* and animal studies demonstrate that induction of cell-cycle arrest and upregulation of cell-cycle genes correlates with AZA's anti-leukemic activity, the mechanism by which it exerts a clinical antitumor effect remains a matter of conjecture (7). Furthermore, although disease progression appears inevitable in patients treated with AZA little is understood of the mechanism of disease resistance (13). Recent immunophenotypic characterization of the stem/progenitor cell compartments containing leukemic stem cells (LSCs) in AML have demonstrated their persistence in a proportion of patients consistent with the hypothesis that this cellular population represents a reservoir of resistant disease, although this proposition has not been prospectively examined in AZA-treated patients (4, 14).

We therefore examined whether co-administration of the HDAC inhibitor VOR increases response rates and OS in patients with AML and high-risk MDS treated with AZA and correlated these clinical endpoints with both diagnostic genotypes and serial stem/progenitor quantitation.

## Subjects and Methods

### Trial design

RAvVA was a multicenter, open-label, prospective, randomized phase II trial designed to assess the activity and safety of AZA monotherapy compared to combined AZA and VOR therapy in AML and high-risk MDS patients (ISRCTN68224706, EudraCT 2011-005207-32) which was reviewed by an independent research ethics committee and delivered by the Bloodwise Trials Acceleration Program (TAP) in accordance with recognized

ethical guidelines. All participants gave written informed consent in accordance with the Declaration of Helsinki.

### Patients

Patients with newly diagnosed, relapsed, or refractory AML as defined by the World Health Organization (WHO) Classification or high-risk MDS (IPSS INT-2 or high-risk) according to the International Prognostic Scoring System (IPSS) deemed ineligible for IC on the grounds of age or comorbidities were eligible for inclusion in this trial (15). A high presentation white count was not an exclusion to trial entry and patients were permitted to receive hydroxycarbamide after AZA administration for the first cycle of therapy. All patients required adequate renal and hepatic function and an Eastern Cooperative Oncology Group (ECOG) performance status  $\leq 2$  as a condition of trial entry. Patients with acute promyelocytic leukemia, a prior allogeneic stem cell transplant or prior treatment with AZA or other DNMT inhibitors were ineligible.

### Treatment regimens

Patients were randomized on a 1:1 basis using a minimization algorithm with three variables: disease category (AML vs. MDS), stage of disease (newly diagnosed vs. relapsed/refractory) and age ( $<70$  vs.  $70+$ ). Patients in the control arm received AZA ( $75 \text{ mg/m}^2$ ) by subcutaneous (SC) injection on a five-two-two schedule, commencing on day one of 28-day cycles for up to six cycles. In the combination arm, patients received the same schedule of AZA in conjunction with additional VOR (300 mg twice a day) orally for seven consecutive days commencing on day three of each cycle. All study participants achieving a CR, CR with incomplete blood count recovery (CRi), marrow CR (mCR), or partial response (PR) within the first six cycles of treatment, were permitted to continue study treatment until loss of response. Nonresponding patients discontinued trial therapy. Bone marrow (BM) samples for morphology and immunophenotypic assessment were collected after cycles three and six and every 3 months thereafter. Compliance to treatment was defined as the number of patients who received treatment as planned according to the trial protocol.

### Efficacy endpoints

Two primary endpoints were defined: overall response rate (ORR) and overall survival (OS). ORR was defined as acquisition of CR, CRi, mCR, or PR within six cycles of treatment utilizing modified Cheson or IWG criteria (16, 17). For each patient, the response after the third and sixth cycle of trial treatment was reviewed and the better of the two was considered the "best response" and used here. OS was defined as the time from date of randomization to the date of death from any cause. Secondary outcome measures included CR/CRi/mCR rate within six cycles of trial therapy, duration of response defined as time from response to relapse, dose intensity defined as the total dose prescribed to each patient as a proportion of the protocol dose and NCI CTCAE v4 defined grade  $\geq 3$  adverse event or SAE. Induction death was defined as death prior to the first response assessment.

### Next-generation sequencing and bioinformatic analysis

BM aspirates were collected at diagnosis in consenting patients. Mutational analysis using next-generation sequencing (NGS) was performed on 250 diagnostic BM samples. Genomic DNA was

subjected to multiple x PCR on the Fluidigm Access Array. The panel consists of 904 amplicons across 41 genes frequently mutated in AML and myeloid malignancies, covering areas with high frequency of AML gene mutations (hotspots), or whole exons if no hotspots were previously reported in COSMIC (Supplementary Tables S1 and S2). Sequencing was performed on an Illumina MiSeq with 300 bp paired-end reads, yielding an average read depth of 912 reads per amplicon. Fluorescent capillary electrophoresis was performed in addition to NGS for the detection of FLT3 internal tandem duplications (ITD), because the rate of detection of ITDs is ~60% using NGS alone (18). Details of NGS methodology is provided within Supplementary Information (Supplementary Tables S1–S3).

### Bioinformatic analysis

Sequencing quality was assessed using FASTQC (Samtools) and aligned using a Burroughs-Wheeler Aligner algorithm in Stampy. A Phred score of 30 was set as a minimum quality threshold for variant calling. We used two variant callers: VARSCAN and Pindel, using the following parameters: minimum coverage 100 reads; minimum variant frequency 0.05; minimum read depth of variant 5; *P* value 0.05. As germline DNA was not available, we implemented criteria to optimize calling of disease-associated mutations and to exclude likely germline SNPs or technical artifacts.

Inclusion criteria for variant calling and filtering were as follows: (i) mutations in protein coding regions or conserved splice sites; and (ii) previous documentation as a somatic mutation in hematopoietic samples in COSMIC with a minimum variant allele frequency (VAF) of 0.05; or (iii) novel truncating variants (nonsense, deleterious missense/indels, variants affecting splicing) with a minimum VAF of 0.05; or (iv) novel single nucleotide variants with a minimum variant frequency of 0.1, if they cluster within three codons of a previously documented somatic variant reported in COSMIC or in the large AML dataset of Papaemmanuil NEJM 2016 (19); (v) SNVs with a VAF > 0.1, which did not meet the exclusion criteria below.

Exclusion criteria for variants were the following: (i) variants predicted to result in a silent amino acid change; (ii) known polymorphisms present in human variation databases at a population frequency of >0.0014 (0.14% reflecting the population incidence of myeloid disease); (iii) 1-bp indels present adjacent to regions of four homopolymer bases at <0.2 variant frequency; (iv) variants that occur in >3 samples of our cohort at a VAF of 0.05 to 0.1 that are not previously documented in COSMIC, which likely constitute PCR or sequencing artifacts in genomic regions prone to error. All putative variants were further validated by visualization using the Integrated Genome Viewer.

### Stem/progenitor immunophenotypic quantitation

BM aspirate samples were collected for sequential quantification of leukemic stem/progenitor populations pretreatment, during treatment, and at relapse. Mononuclear cells (MNCs) were isolated by Ficoll density gradient and viably frozen using 10% DMSO and stored in liquid nitrogen. Frozen MNCs from BM samples were thawed on the day of analysis, washed with Iscove's modified Dulbecco's medium (IMDM; Thermo Fisher Scientific), supplemented with 10% FBS (Sigma) and 1 mg/mL bovine pancreatic DNase I (Sigma). Cells were stained for FACS analysis

as detailed below. FACS analysis was carried out on either BD LSR Fortessa or a BD FACSAria Fusion (Becton Dickinson).

Antibodies used in the lineage (Lin) depletion cocktail were: anti-CD2, anti-CD3, anti-CD4, anti-CD8a, anti-CD10, anti-CD19, anti-CD20, and anti-CD235a. Antibodies used to analyze different subpopulations were: anti-CD34, anti-CD38, anti-CD90, anti-CD45RA, anti-CD123, anti-CD117, and 7AAD were used as a live/dead stain. Details of each antibody/streptavidin are listed in Supplementary Table S4. We did not deplete CD11b, CD14, CD7, CD56 expressing cells as these markers may be expressed by CD34<sup>+</sup> and CD34<sup>−</sup>CD117<sup>+</sup> LSC populations. We assessed LSC populations pretreatment, during treatment, and in a subset of patients, at relapse. Patients were selected for longitudinal LSC assessment based on availability of appropriate viably-banked samples and documented clinical outcome. The size of the stem/progenitor subpopulations of each sample was determined as a percentage of live Lin<sup>−</sup> MNCs, and expressed as a fold change of the upper limit values of normal control BM (Supplementary Table S5). An example of the gating strategy is demonstrated in Supplementary Fig. S1.

### Statistical analysis

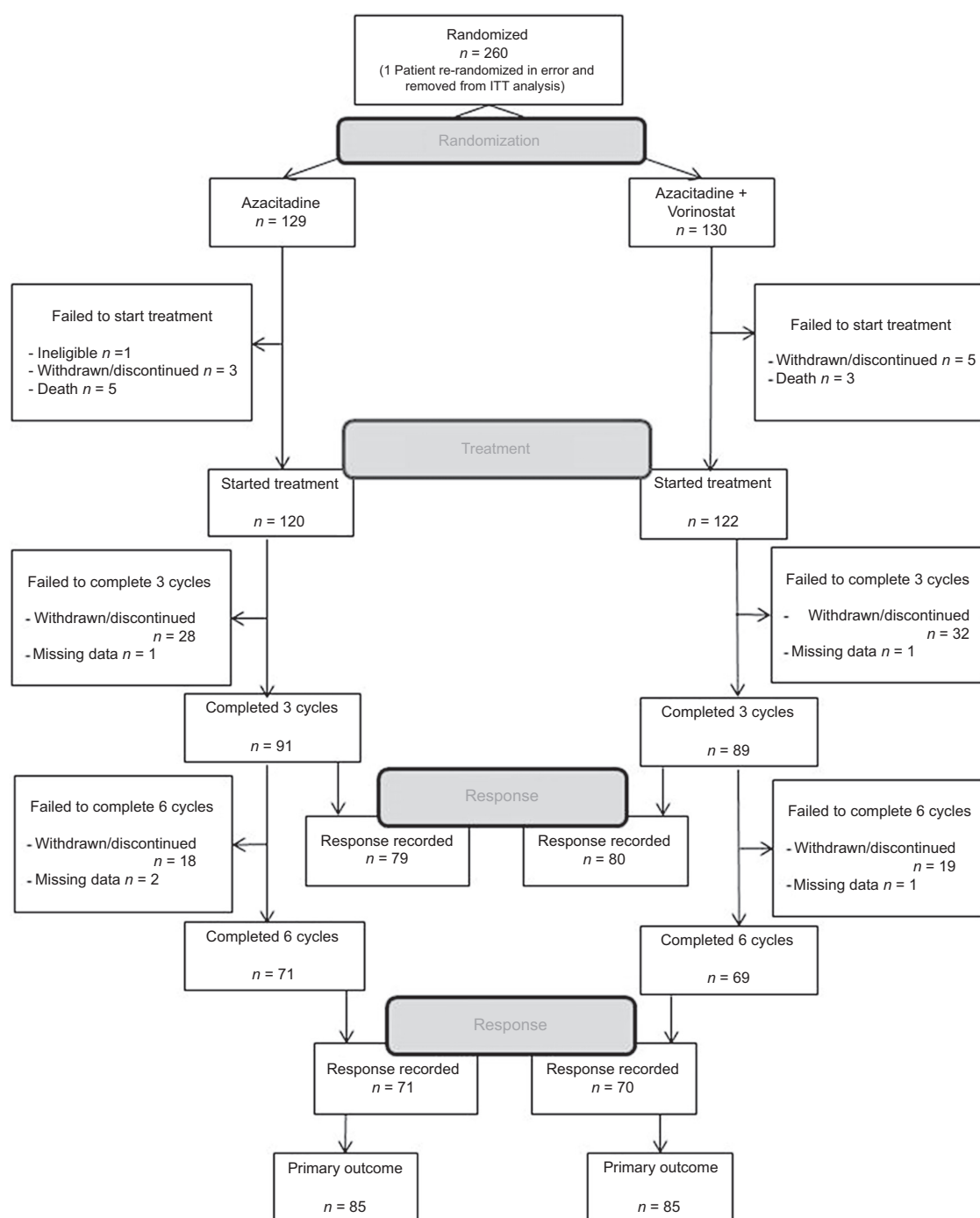
The sample size was calculated on conventional phase III criteria but with a relaxed alpha and was originally powered to recruit 160 patients (ORR:  $P_0 = 15\%$ , detectable difference = 15%, two-sided  $\alpha$  and  $\beta = 0.15$  and 0.2, respectively, OS control rate at 1 year = 15%, detectable difference of 15%, two-sided  $\alpha$  and  $\beta = 0.1$  and 0.2, respectively). At 2 years based on the advice of the Data Monitoring Committee, the sample size was updated to 260 (ORR:  $P_0 = 0.2$ , detectable difference = 0.15, two-sided  $\alpha = 0.1$ ,  $\beta = 0.15$ , OS:  $P_0 = 0.15$ , detectable difference = 0.15, two-sided  $\alpha = 0.1$ ,  $\beta < 10\%$ ). Given the increased sample size, the final trial had sufficient power to investigate a trend of activity for both ORR and OS in a predetermined subgroup analysis of the newly diagnosed and advanced disease groups (detectable difference in ORR and OS = 20% and 20%, respectively, two-sided  $\alpha = 0.2$ ,  $\beta = 0.2$ ).

Standard statistical methods were used for all analysis in the trial: Fisher exact or chi-squared tests for categorical endpoints (e.g., response), Kaplan–Meier curves and log rank tests for time-to-event endpoints (e.g., survival), cumulative incidence curves and Cox models for time to event endpoints with competing risks (e.g., time to first response). To investigate clinical factors predicting outcome after AZA-based therapy, we performed logistic and Cox multivariable analysis on all trial patients for ORR and OS including treatment arm as a covariable. Subgroup analysis is presented using forest plots with test for interaction displayed. *P* values of 0.1 were considered significant for both primary outcomes and a *P* value of 0.05 was considered significant throughout the rest of the analysis. No multiple testing adjustments have been carried out as the analysis conducted was exploratory and hypothesis generating.

## Results

### Baseline characteristics of patients

Between November 2012 and September 2015, 260 patients were recruited from 19 UK centers as outlined in the CONSORT diagram (Fig. 1). One patient was randomized for a second time in error and removed from the analysis. Baseline patient characteristics are listed in Table 1. Two hundred and seventeen patients had a diagnosis of AML at the time of randomization, and 42 had a



**Figure 1.**  
CONSORT diagram. Schematic representation of patient disposition in the trial.

diagnosis of MDS. Of the 217 patients with AML, 111 were newly diagnosed, 73 had relapsed disease, and 33 were refractory to at least one prior line of therapy.

#### Treatment administration and toxicities

Patients received a median of six cycles (IQR: 2, 8) of treatment in both arms of the trial. Average compliance to AZA across all

cycles of treatment was 73% in the AZA arm and 71% in the combination arm. There was no difference in dose intensity across treatment arms with a median intensity of 100% of the dose delivered in the first six cycles of treatment. A total of 106 patients in the AZA arm experienced one or more toxicity compared to 110 patients in the combination arm and there was no difference between treatment arms ( $P = 0.87$ ). Adverse events (grades 3

**Table 1.** Demographics of study population

	Whole population (n = 259) No. (%)	Azacitidine alone (n = 129) No. (%)	Azacitidine + Vorinostat (n = 130) No. (%)
Age, years			
<70 years old	96 (37)	48 (37)	48 (37)
≥70 years old	163 (63)	81 (63)	82 (63)
Gender			
Male	156 (60)	75 (58)	81 (62)
Female	103 (40)	54 (42)	49 (38)
AML disease stage			
Newly diagnosed	111 (43)	57 (44)	54 (42)
Relapsed	73 (28)	34 (26)	39 (30)
Refractory	33 (13)	17 (13)	16 (12)
MDS disease stage			
Newly diagnosed	36 (14)	16 (12)	20 (15)
Relapsed	5 (2)	4 (3)	1 (1)
Refractory	1 (0)	1 (1)	0 (0)
ECOG performance status			
0	84 (32)	52 (40)	32 (25)
1	133 (51)	63 (49)	70 (54)
2	26 (10)	9 (7)	17 (13)
Missing	16 (6)	5 (4)	11 (8)
Cytogenetic group			
Favorable risk	13 (5)	2 (2)	11 (8)
Intermediate risk	109 (42)	58 (45)	51 (39)
Poor risk	54 (21)	26 (20)	28 (22)
Risk not known/not done	73 (28)	38 (29)	35 (27)
Missing	10 (4)	5 (4)	5 (4)
BM morphology, % blasts			
Mean	46.2	48	44.4
SD	28.4	27.7	29.1
Hemoglobin, g/L			
Mean	131.1	120.9	141.1
SD	184.9	167.5	200.9
Platelets, 10 <sup>9</sup> /L			
Mean	85.4	78.1	92.7
SD	131.2	79.2	167.7
WCC, 10 <sup>9</sup> /L			
Mean	14.1	15.6	12.6
SD	24.6	29	19.4
Neutrophils, 10 <sup>9</sup> /L			
Mean	3.1	3	3.2
SD	9.2	8.4	9.9

and 4) experienced by 5% or more of patients are listed in Supplementary Table S6.

### Response and survival

There was no difference in either ORR [41% vs. 42%; OR, 1.05 (95% CI, 0.64–1.72);  $P = 0.84$ ] or CR/CRi/mCR rate [22% and 26%; OR, 0.82 (95% CI, 0.46–1.45);  $P = 0.49$ ] between the control and combination therapy arms. Time to first response and duration of response at 1 year was similar in the AZA and combination arm (6.2 months vs. 5.7 months and 67% vs. 58%, respectively; Supplementary Fig. S2). In predetermined subgroup analysis, patients with relapsed/refractory disease demonstrated an increased CR in the AZA/VOR arm ( $P = 0.02$ ), although this did not translate to an improvement in OS.

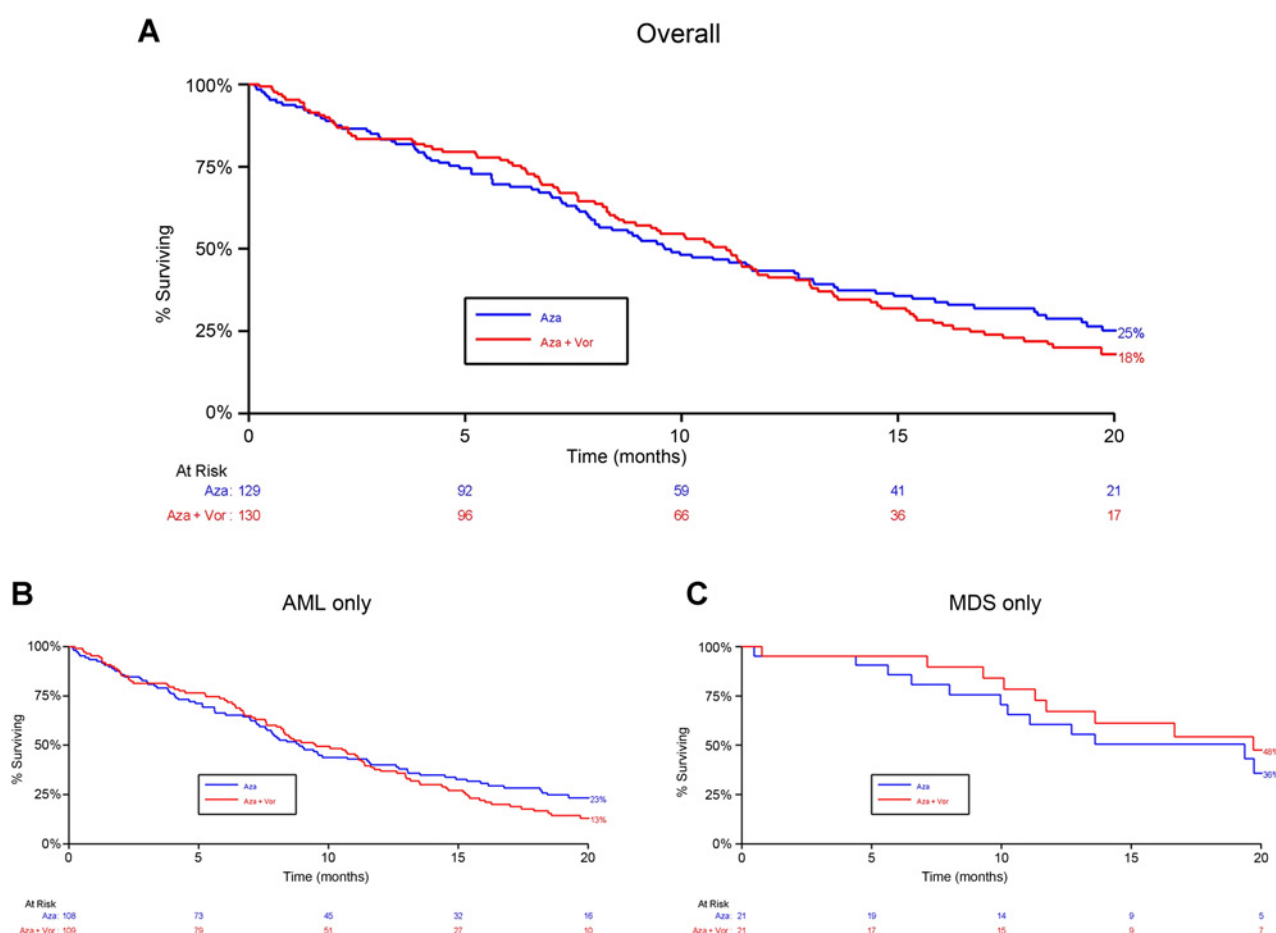
No difference was observed in OS between patients treated with AZA monotherapy (median OS = 9.6 months; 95% CI, 7.9–12.7) and patients in the AZA/VOR arm (median OS = 11.0 months; 95% CI, 8.5–12.0; HR, 1.15; 95% CI, 0.87–1.51;  $P = 0.32$ ). Specifically, there was no difference in OS between treatment arms in patients with newly diagnosed or relapsed/refractory AML (Fig. 2 and Supplementary Fig. S3).

### Clinical and molecular factors predicting outcome after AZA-based therapy

We next wished to identify clinical factors predictive of response to AZA-based therapy in the trial cohort. Multivariable logistic regression demonstrated higher ORR rates in newly diagnosed disease versus refractory/relapsed disease ( $P = 0.038$ ). Neither diagnosis (AML vs. MDS,  $P = 0.22$ ) nor presentation karyotype (favorable vs. intermediate vs. poor,  $P = 0.76$ ) predicted ORR in the same model. Cox regression analysis demonstrated increased OS in patients with MDS as opposed to AML ( $P = 0.012$ ), a low ECOG score ( $P = 0.09$ ), and a presentation WBC  $<10 \times 10^9/l$  ( $P = 0.019$ ). Presentation karyotype did not correlate with OS.

The impact of diagnostic mutational status on clinical response and OS was then studied using the results of NGS performed on 250 patients at trial entry (Fig. 3A). The mean mutation number per patient was 3.4 (Fig. 3B). Mutations in *RUNX1* were most frequent (73 patients, 29%). Mutations in *DNMT3A* (59 patients 23%), *IDH2* (57 patients, 23%), and *TET2* (56 patients, 22%) were also common (Fig. 3A). The observed mutational frequency was broadly consistent with that previously reported in older, but



**Figure 2.**

Overall survival of trial patients. **A**, Survival in all study patients. **B**, Survival in patients with AML. **C**, Survival in patients with MDS.

not younger, AML and MDS patients (19–21) (Fig. 3C). In univariate analysis there was a lower complete response (CR, CRi, mCR) rate in patients with an *IDH2* mutation ( $P = 0.029$ ) and *STAG2* mutation ( $P = 0.002$ ) but an increased CR rate in patients with an *NPM1* mutation ( $P = 0.038$ ; Table 2). When considered in a multivariable analysis and adjusted for all clinical variables, the presence of *STAG2* and *IDH2* mutations was not shown to have a significant association with acquisition of CR (Table 2). However, *NPM1* mutation remained of prognostic significance ( $P = 0.012$ ).

Mutations in *CDKN2A* ( $P = 0.0001$ ), *IDH1* ( $P = 0.004$ ), *TP53* ( $P = 0.003$ ), *NPM1* ( $P = 0.037$ ), and *FLT3-ITD* ( $P = 0.04$ ) were associated with reduced OS in univariate analysis. In multivariate analysis adjusted for all clinical variables, mutations in *CDKN2A*, *IDH1*, and *TP53* were associated with decreased OS (Table 2). No mutations were associated with improved OS. Mutations in *ASXL1* ( $P = 0.035$ ) and *ETV6* ( $P = 0.033$ ) were associated with a reduced duration of response. No mutations were associated with improved duration of response.

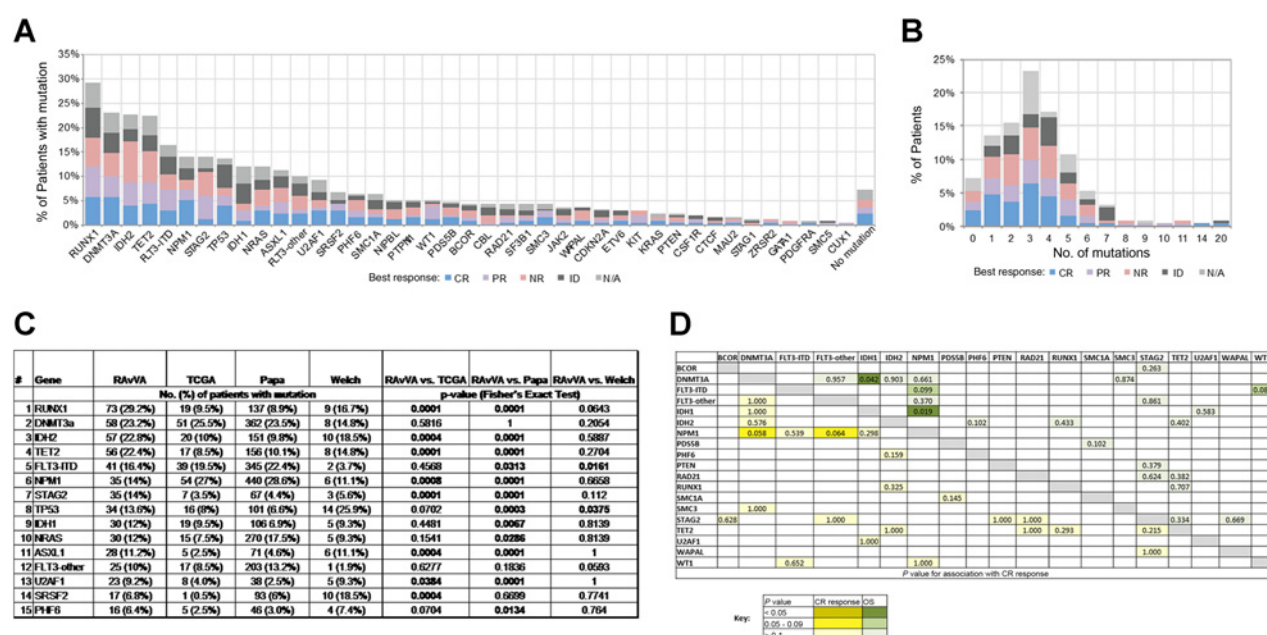
Among other frequently co-occurring mutations, we observed significant co-occurrence of *NPM1* mutations with *DNMT3A*, *FLT3-ITD*, *FLT3-other*, and *IDH1* as well as *DNMT3A* with *FLT3-other*, *IDH1*, and *IDH2* ( $P < 0.05$  for all compar-

isons). Patients with mutations in both *DNMT3A* and *IDH1* had reduced OS (median OS = 9.8 months; 95% CI, 1.5–11.6 months) compared to patients without both mutations (median OS = 10.7; 95% CI, 8.9–12). Patients with both *NPM1* and *IDH1* mutations had reduced OS (median OS = 3.8 months; 95% CI, 1.6–NE) compared to patients without both mutations (median OS = 10.7; 95% CI, 9.0–11.8). No significantly co-occurring mutations were found to be predictors of acquisition of CR (Fig. 3D).

#### Impact of AZA-based therapy on the LSC population

An expanded  $CD34^+$  progenitor population was observed in 42/45 studied patients at diagnosis, whereas a  $CD34^-$  expanded precursor population was observed in 3/45 (Fig. 4A). The majority of expanded populations were lymphoid-primed multipotential progenitors (LMPP: Lin- $CD34^+CD38^-CD90^-CD45RA^+$ ), which have been previously characterized as an LSC population with functional leukemia-propagating activity in serial xeno-transplant assays (14), and as a novel biomarker of AML disease response and relapse (4). Quantitatively, the immunophenotypic LMPP population is usually very small in normal BM ( $<2$  in  $10^5$  cells; Vyas *et al.*, data under review). Therefore, expansion of the LMPP

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**Figure 3.**

Mutation profile of study population and correlation with clinical response. **A**, Frequency of mutations (as % of patients) in patients at trial entry. Patients are further divided according to best response achieved. **B**, Frequency of number of mutations detected per patient pretreatment. **C**, Comparison of mutations detected in RAVVA cohort compared with recently published AML cohorts [Papa: Papaemmanuil *et al.* (19); TCGA(20); Welch *et al.* (21)]. **D**, Correlation of combinations of detected mutations with CR and OS: only genes where there were at least five patients with two mutations are included in this analysis. Unadjusted *P* values from a Fisher exact test are shown. The top right half of the table (values in shades of green) show mutation combinations significantly associated with decreased OS. The bottom left half of the table (with values in shades of yellow) shows absence of significant mutation combinations predictive of CR. Key: CR (includes CR, CRI), PR, NR (no response including stable disease and progressive disease), ID (induction death), NA (response data not available).

population can be a sensitive measure of residual disease at CR in patients with AML. For these reasons, we focused on quantitation LMPP by immunophenotyping to measure the impact of therapy on putative LSC populations at best response and relapse.

In seven patients with resistant disease, there was no reduction in LMPP numbers measured as a fold change (Fig. 4B). Of interest, there was no significant reduction of LMPP numbers in eight patients achieving a PR, where the average BM blast percentage was reduced by 50%. In contrast, in 22 patients with CR/CRI/mCR, there was a significant reduction in LMPP numbers with AZA-based therapy. However, even here, LMPP numbers failed to normalize in 16/22 (Fig. 4B). In seven patients with expanded LMPP numbers, who achieved a CR, sequential monitoring demonstrated expansion progenitor populations prior to disease relapse (Fig. 4C).

## Discussion

Co-administration of the HDAC inhibitor VOR did not improve response or survival in patients with AML or MDS treated with AZA. This observation is consistent with previous randomized studies in high-risk MDS but is the first demonstration that HDAC inhibitors have no impact on clinical outcomes in patients with newly diagnosed or relapsed AML-treated with AZA (10–12). Why might our study have failed to replicate earlier single arm studies of strikingly increased clinical activity of combined AZA and HDAC inhibitor treatment

(8, 9, 22)? Clinical and molecular characterization demonstrates comparability between study arms and confirms that the trial population was broadly representative of older patients with high-risk AML and MDS. Alternatively, the clinical activity of the experimental study arm might have been blunted because VOR associated drug toxicity resulted in under-dosing of AZA. Detailed pharmacovigilance studies excluded this possibility and indeed AZA dose intensity was similar in both treatment arms. Consideration should however be given to the possibility that co-administration of HDAC inhibitors might inhibit cellular uptake of aza-nucleosides and exploration of alternative dosing schedules may be worth exploring.

The search for novel drug partners with the potential to improve the clinical activity of AZA has been hampered by the fact that its mechanism of clinical activity remains unknown. Cell line and animal data have identified upregulation of epigenetically silenced genes and consequent restoration of cell-cycle checkpoints as an important potential mechanism of action and indeed previous *in vitro* studies have correlated the antitumor activity of both AZA and DEC with their ability to effect changes in cell-cycle gene expression and induce G<sub>2</sub> phase arrest (7, 23, 24). Consequently, the observation that heterozygous predicted loss of function mutations in *CDKN2A*, a cell-cycle checkpoint activator, are correlated with decreased survival in AZA-treated patients is supportive of the hypothesis that induction of cell-cycle arrest is a potentially important mechanism of action of this agent. In our study the *CDKN2A* mutations were nonsense in two patients and in the other seven were either nonsynonymous SNVs that had

**Table 2.** Univariate and multivariate analysis of predictors of CR and OS in the study population

		Overall response			
		Univariate analysis		Multivariable analysis <sup>a</sup>	
Covariate		OR (95% CI)	P <sup>b</sup>	OR (95% CI)	P
Clinical variables					
Disease status			(<0.001)		
	Refractory (vs. relapsed)	0.2 (0.1, 0.9)	0.03	Not estimable	
	Newly diagnosed (vs. relapsed)	2.1 (1.0, 4.6)	0.051	3.6 (1.1, 11.7)	0.037
Baseline WBC	≥10 (vs. <10)	0.7 (0.3, 1.5)	0.39	0.5 (0.2, 1.8)	0.292
Cytogenetic risk					
			(0.416)		
	Intermediate (vs. poor)	0.6 (0.3, 1.3)	0.204	0.6 (0.2, 2.0)	0.424
	Favorable (vs. poor)	1.0 (0.2, 4.9)	0.951	0.8 (0.1, 5.6)	0.843
Age	≥70 (vs. <70)	1.3 (0.7, 2.5)	0.447	1.3 (0.4, 3.8)	0.674
ECOG P.S.					
			(0.98)		
	1 (vs. 0)	1.0 (0.5, 1.9)	0.92	1.6 (0.6, 4.4)	0.395
	2 (vs. 0)	1.1 (0.4, 3.2)	0.902	1.0 (0.2, 5.8)	0.981
Mutations					
STAG2 mutation	Present (vs. absent)	0.2 (0.1, 0.6)	0.002	0.3 (0.1, 1.4)	0.117
IDH2 mutation	Present (vs. absent)	0.4 (0.2, 0.9)	0.029	0.4 (0.1, 1.3)	0.139
NPM1 mutation	Present (vs. absent)	2.5 (1.0, 6.2)	0.038	8.6 (1.6, 45.8)	0.012

		Overall survival				
		Median OS	Univariate analysis		Multivariable analysis <sup>c</sup>	
Covariate		(95% CI), months	HR (95% CI)	P <sup>d</sup>	HR (95% CI)	P
Clinical variables						
Diagnosis	MDS	19.4 (11.3, 22.7)	1		1	
	AML	9.1 (8.0, 11.1)	2.0 (1.3, 3.0)	0.0008	2.3 (1.3, 4.3)	0.007
Baseline WBC	<10	11.5 (9.8, 13.6)	1		1	
	≥10	8.8 (6.7, 10.5)	1.5 (1.1, 2.0)	0.0116	2.2 (1.4, 3.5)	0.001
Disease Status				(0.0132)		
	Relapsed	7.6 (6.4, 10.5)	1		1	
	Refractory	9.8 (8.3, 13.2)	0.8 (0.5, 1.2)	0.218	1.0 (0.5, 1.8)	0.976
	Newly diagnosed	11.7 (10.1, 14.9)	0.6 (0.5, 0.9)	0.005	0.5 (0.3, 0.8)	0.003
ECOG P.S.				(0.0235)		
	0	12.7 (9.6, 19.4)	1		1	
	1	10.1 (8.0, 11.5)	1.6 (1.1, 2.1)	0.009	1.6 (1.0, 2.6)	0.035
	2	9.5 (7.8, 15.4)	1.5 (0.9, 2.4)	0.0968	1.6 (0.9, 2.9)	0.131
Age	<70	9.3 (7.6, 11.6)	1		1	
	≥70	11.1 (9.0, 13.5)	0.8 (0.6, 1.1)	0.1706	1.6 (0.9, 1.8)	0.448
Cytogenetic risk				(0.8589)		
	Poor	9.5 (7.1, 11.1)	1		1	
	Intermediate	11.4 (8.1, 15.3)	0.9 (0.6, 1.3)	0.6367	1.2 (0.7, 1.9)	0.549
	Favorable	12.0 (1.7, N/E)	0.8 (0.4, 1.8)	0.6392	1.1 (0.5, 2.8)	0.802
Mutations						
CDKN2A mutation	Absent	11.0 (9.3, 12.6)	1		1	
	Present	4.5 (0.2, 7.8)	3.9 (1.9, 8.0)	0.0001	10.0 (3.3, 30.3)	<0.001
TP53 mutation	Absent	11.3 (9.4, 13.0)	1		1	
	Present	7.6 (2.4, 9.6)	1.8 (1.2, 2.6)	0.003	4.7 (2.5, 9.0)	<0.001
IDH1 mutation	Absent	11.1 (9.4, 12.7)	1		1	
	Present	5.6 (2.8, 9.8)	1.9 (1.2, 2.9)	0.004	3.6 (1.7, 7.6)	0.001
NPM1 mutation	Absent	11.1 (9.1, 12.6)	1		1	
	Present	8.1 (5.6, 10.7)	1.5 (1.0, 2.2)	0.037	0.6 (0.4, 1.1)	0.122
FLT3ITD mutation	Absent	11.1 (9.0, 12.7)	1		1	
	Present	8.8 (6.1, 11.6)	1.5 (1.0, 2.1)	0.04	1.0 (0.6, 1.8)	1

Abbreviations: ECOG P.S., Eastern Cooperative Oncology Group Performance Status; N/E, not estimable values in brackets refer to *P* value of the overall test for the specified variable; WBC, white blood cell.

<sup>a</sup>Logistic regression model adjusted for all variables in the table.

<sup>b</sup>Given by the Chi-square or Fisher exact test, corresponding to pairwise comparisons or the overall comparison as indicated between parentheses.

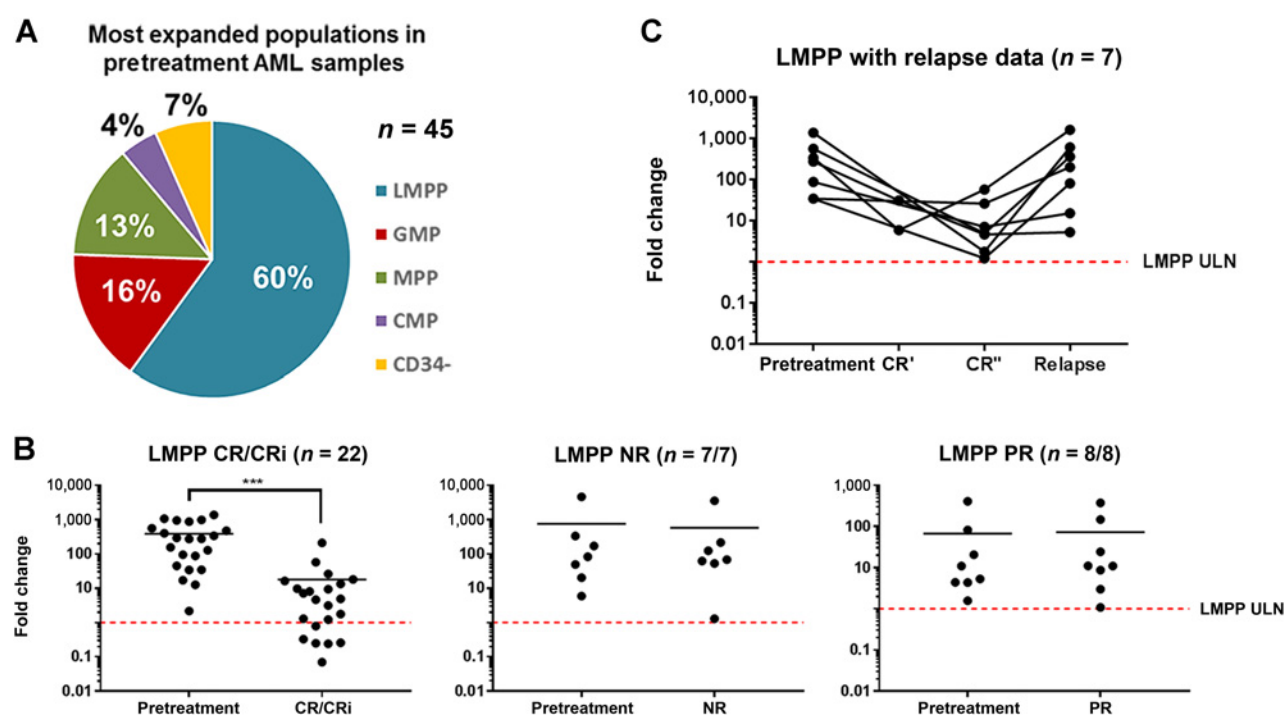
<sup>c</sup>Cox proportional hazards model adjusted for all variables in the table.

<sup>d</sup>Given by the log-rank test, corresponding to pairwise comparisons, or the overall comparison as indicated between parentheses.

previously been reported (six patients) or within two codons of a previously reported mutation (one patient). *CDKN2A* encodes P14, P16, and ARF. P14 and P16 inhibit the cyclin-dependent kinase CDK4, which regulates the G<sub>1</sub> cell-cycle checkpoint. ARF sequesters the E3 ubiquitin-protein ligase MDM2, a protein responsible for the degradation of p53. Thus, if loss of *CDKN2A* abrogates the clinical activity of AZA it raises the possibility that

AZA induces G<sub>1</sub> cell-cycle arrest and requires at least some p53 function for its antileukemic activity. We acknowledge that the findings of this study are based on a small sample size and that it is important to replicate this clinical association of *CDKN2A* mutations with poor clinical response to AZA in larger studies. If confirmed, our data highlight further study of P14, P16, and ARF function as a potentially fruitful line of investigation in



**Figure 4.**

Flow cytometric measurement of LSC populations. **A**, Quantitation of expanded CD34<sup>+</sup> progenitor or CD34<sup>-</sup> precursor LSC populations in AML patients pretreatment. **B**, Quantitation of LMPP-like LSC pretreatment and at CR expressed as fold change of upper limit of LMPP frequency in normal BM (upper limit of normal, ULN, dotted line, assessed in 12 normal donors). **C**, Longitudinal quantitation of LMPP-like LSC in patients pretreatment, at CR (multiple time points in two patients: CR' and CR'') and at relapse.

understanding and potentially improving the outcomes of AZA-based therapy.

The identification of both clinical and molecular predictors of outcome with AZA therapy is important if this agent is to be optimally deployed. Improved survival was observed in patients with newly diagnosed disease, a low presentation white count and ECOG score. Importantly, and in contrast to patients treated with myelosuppressive chemotherapy, we observed no impact on survival of an adverse risk karyotype after AZA-based therapy (25). Our data also demonstrate that NGS improves risk stratification because mutations in *CDKN2A*, *IDH1*, and *TP53* were independently associated with decreased survival in AZA-treated patients. We did not identify any impact of mutations in *TET2* or *DNMT3A* on outcome, in contrast to previous smaller retrospective studies (26–29). Although *TP53* mutations have previously been shown to be associated with decreased survival in patients treated with intensive chemotherapy (30), it has recently been reported that the presence of a *TP53* mutation was associated with a higher response rate in patients treated with DEC (21). In contrast, our data demonstrating no impact of *TP53* on response rate to AZA but decreased OS in mutated patients implies that these two DNMT inhibitors may have distinct mechanism of action.

The development of strategies to overcome the inevitability of disease relapse in patients with AML treated with AZA is essential if outcomes are to improve. It is postulated that disease recurrence in patients with AML treated with either myelosuppressive chemotherapy or DNMT inhibitors occurs as a result of expansion of chemo-resistant LSC. However, correlative data in large cohorts of patients treated with either modality of therapy has been lacking.

Thus, the demonstration in this study of LSC persistence in AZA-treated patients who achieve a CR is consistent with the hypothesis that this recently identified cellular population may serve as a reservoir of resistant disease in AZA-treated patients. These data contrast with observations in patients treated with conventional chemotherapy where durable clearance of LSC appears to correlate with long-term remission and highlight the potential importance of quantitation of this cellular population as a biomarker of response in future studies of novel AZA-based combinations (4, 31, 32).

#### Disclosure of Potential Conflicts of Interest

C. Craddock reports receiving other commercial research support and speakers bureau honoraria from Celgene. L.S. Quek reports receiving commercial research grants and speakers bureau honoraria from Celgene. M. Raghavan reports receiving speakers bureau honoraria from Celgene. M. McMullin reports receiving speakers bureau honoraria from Celgene and Novartis. P. Vyas reports receiving commercial research grants from Celgene, and speakers bureau honoraria from Celgene and Jazz. No potential conflicts of interest were disclosed by the other authors.

#### Authors' Contributions

**Conception and design:** C.F. Craddock, E. Gbandi, M. Raghavan, K. Wheatley, S. Siddique, J.D. Cavenagh, P. Vyas

**Development of methodology:** L.S. Quek, M. Dennis, P. Vyas

**Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.):** C.F. Craddock, L.S. Quek, P. Ferguson, M. Metzner, N. Garcia-Martin, A. Kennedy, A. Hamblin, M. Raghavan, S. Nagra, M.F. McMullin, R.J. Kelly, M. Dennis, J.D. Cavenagh, P. Vyas

**Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis):** A.E. Houlton, L.S. Quek, E. Gbandi, C. Roberts, M. Metzner, N. Garcia-Martin, A. Kennedy, K. Wheatley, P. Vyas

**Writing, review, and/or revision of the manuscript:** C.F. Craddock, A.E. Houston, L.S. Quek, E. Gbandi, C. Roberts, M. Metzner, N. Garcia-Martin, L. Dudley, K. Wheatley, M.F. McMullin, R.J. Kelly, M. Dennis, J.D. Cavenagh, P. Vyas  
**Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases):** L. Dudley, S. Siddique, P. Vyas  
**Study supervision:** C.F. Craddock, M. Dennis, P. Vyas  
**Other (recruited patients and collected patient data):** S.P. Pillai

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# Clinical Cancer Research

## Outcome of Azacitidine Therapy in Acute Myeloid Leukemia Is not Improved by Concurrent Vorinostat Therapy but Is Predicted by a Diagnostic Molecular Signature

Charles F. Craddock, Aimee E. Houlton, Lynn Swun Quek, et al.

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