A multicenter, randomized study of decitabine as epigenetic priming with induction chemotherapy in children with AML

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ABSTRACT

Background: Decitabine is a deoxycytidine nucleoside derivative inhibitor of DNA-methyltransferases, which has been studied extensively and is approved for myelodysplastic syndrome in adults but with less focus in children. Accordingly, we conducted a phase 1 multicenter, randomized, open-label study to evaluate decitabine pre-treatment before standard induction therapy in children with newly diagnosed AML to assess safety and tolerability and explore a number of biologic endpoints.

Results: Twenty-four patients were fully assessable for all study objectives per protocol (10 in Arm A, 14 in Arm B). All patients experienced neutropenia and thrombocytopenia. The most common grade 3 and 4 non-hematologic adverse events observed were gastrointestinal toxicities and hypophosphatemia. Plasma decitabine PK were similar to previously reported adult data. Overall CR/CRi was similar for the two arms. MRD negativity at end-induction was 85% in Arm A versus 67% in Arm B patients. DNA methylation measured in peripheral blood over the course of treatment tracked with blast clearance and matched marrow aspirates at day 0 and day 21. Unlike end-point marrow analyses, promoter methylation in blood identified an apparent reversal of response in the lone treatment failure, one week prior to the patient’s marrow aspirate confirming non-response. Decitabine-induced effects of end-induction marrows in Arm A were reflected by changes in DNA methylation and gene expression comparison with matched paired marrow diagnostic aspirates.

Conclusions: This first-in-pediatrics trial demonstrates that decitabine prior to standard combination chemotherapy is feasible and well tolerated in children with newly diagnosed AML. Pre-treatment with decitabine may represent a newer therapeutic option for pediatric AML, especially as it appears to induce important epigenetic
alterations. The novel biological correlates studied in this trial offer a clinically relevant
window into disease progression and remission. Additional studies are needed to
definitively assess whether decitabine can enhance durability responses in children with
AML. This trial was registered at www.clinicaltrials.gov as NCT01177540.

Keywords: AML, epigenetics, pediatrics, pharmacokinetics, pharmacodynamics,
promoter methylation, repeat element transcription

BACKGROUND

Attaining complete response/remission (CR) is currently considered the essential
first step in the effective treatment of acute myelogenous leukemia (AML). Historically,
the most widely used induction therapy included seven days of cytarabine plus three
days of anthracycline (known as “7+3”). With this approach, 75-80% of children with
AML achieve CR (1-3). Subsequently, the addition of a third agent such as etoposide to
7+3 (ADE) along with expanded supportive care measures, has led to higher remission
induction rates of approximately 85%. Of patients who do not attain remission,
approximately one-half have resistant leukemia and a substantial proportion will die from
complications of the disease or treatment. Thus, there is a need to develop new
treatment strategies to improve outcomes for these patients.

Pediatric tumors have been shown to have lower mutation burdens than adult
tumors and many of these mutations occur in the plethora of known epigenetic
complexes (4). In addition, significant aberrant DNA methylation is also observed in
pediatric cancers such as AML including in patients with the poorest risk sub-types (5).
These studies argue for the importance of identifying novel epigenetic therapies that
target both histone and/or DNA methylation modifications. Specifically, reversal of
promoter DNA hypermethylation and associated gene silencing is an attractive
therapeutic approach in adult cancers. The DNA methylation inhibitors decitabine and
azacitidine are efficacious for hematological neoplasms at lower, less toxic, doses (6).
Experimentally, high doses induce rapid DNA damage and cytotoxicity, which do not
explain the prolonged response observed in adult patients (6). Studies have consistently
shown that transient low doses of DNA demethylating agents exert durable anti-tumor
effects on hematological and epithelial tumor cells (6). Moreover, studies have
demonstrated that DNA hypomethylating agents can sensitize resistant cancer cells to
cytotoxic agents in vitro and in vivo (7-15) and can enhance chemosensitivity of human
leukemia cells to cytarabine (16). Therefore, pretreatment with a DNA hypomethylating
agent may increase the efficacy of pediatric AML induction therapy (17). However, to
date there are no studies to demonstrate the safety, tolerability, or any signal of efficacy
of decitabine in combination with conventional multi-agent chemotherapy for AML in
children. We report here the first phase 1 clinical evaluation of decitabine in children
with newly diagnosed AML as a feasibility study to determine the safety, tolerability, and
preliminary efficacy when used as epigenetic pretreatment before induction
chemotherapy. In addition to assessing toxicity and morphologic remission, this study
examined decitabine pharmacokinetics and minimal residual disease (MRD) impact. We
also performed global DNA methylation and RNA-seq analyses to examine how
decitabine priming impacted the methylome and gene expression in end-induction
marrows when compared with matched diagnostic marrow baseline controls. We
believe that this feasibility study was essential prior to longer-term studies assessing
whether epigenetic-directed therapy in pediatric AML can lead to enhanced response
rates or more durable responses.
PATIENTS, MATERIALS, AND METHODS

Patient eligibility

Eligible patients were 1 to 16 years of age (inclusive), had histologically confirmed de novo AML with >20% bone marrow blasts and adequate cardiac function (defined as ejection fraction >50% or shortening fraction >26%). Patients with acute promyelocytic leukemia (FAB M3 subtype), symptomatic CNS involvement, white blood cell count over 100,000/μl, significant renal or hepatic disease, any prior chemotherapy or radiation therapy for AML, known HIV infection, history of CML, congenital syndromes known to predispose to AML (for example, Down syndrome, Fanconi anemia, Kostmann syndrome, or Diamond-Blackfan anemia) were excluded.

The study protocol was approved by the institutional review boards at participating sites and was conducted in accordance with the Declaration of Helsinki, Good Clinical Practice, and all local and federal regulatory guidelines. A parent or legal guardian provided written informed consent, with patient assent as appropriate according to institutional requirements.

Study design

This multicenter, open-label study randomized patients to one of two arms: either five days of decitabine followed by standard induction chemotherapy with cytarabine, daunorubicin, and etoposide (Arm A=DADE), or standard induction chemotherapy with cytarabine, daunorubicin, and etoposide without decitabine (Arm B=ADE). The trial was listed under ClinicalTrials.gov identifier: NCT00943553. Twenty-five children age 1-16 years with newly diagnosed de novo AML were randomized to receive either Arm A or Arm B. Given the feasibility nature of the study, sample size was selected based on the likelihood of how many patients might be accrued in a reasonable time frame so that future studies could be planned. Patients were stratified by age group and then
randomized within each stratum in a 1:1 ratio by an Interactive Voice Response System via a random number generator. Three age strata were used: 1 to <2 years, 2-11 years, and 12-16 years, with efforts made to balance enrollment among the age groups.

All patients received one cycle of study treatment in the absence of clinically significant disease progression, unacceptable toxicity, or patient/guardian choice to discontinue participation. Patients were not pre-medicated prior to the first dose of decitabine; however, all other supportive care measures were allowed according to institutional standards. Following the completion of the study therapy, therapy continued at the treating physician’s discretion.

Treatment was administered to patients in hospital, and hospitalization through count recovery was mandated. The dose and schedule of decitabine used in this study was known to be safe and tolerable in adults and was known to induce adequate hypomethylation (18, 19), inhibit DNA methyltransferase, and induce tumor suppressor gene activation as early as 3-5 days following initiation. Treatment included: a) decitabine 20 mg/m² IV infusion for 1 hour daily for 5 days (Arm A) on Days 1-5; b) age-based dosing of intrathecal cytarabine (1 to <2 years: 30 mg; 2 to <3 years: 50 mg; >3 years: 70 mg) at the time of diagnostic lumbar puncture or on Day 1; c) cytarabine 100 mg/m²/dose (3.3 mg/kg/dose for BSA <0.6 m²) slow IV push over 15 minutes, every 12 hours for 10 days on Days 1-10 (Arm B) or Days 6 to 15 (Arm A); d) daunorubicin 50 mg/m² (1.67 mg/kg/dose for BSA <0.6 m²) IV over 6 hours for 3 days on Days 1, 3, 5 (Arm B) or Days 6, 8 and 10 (Arm A); and e) etoposide 100 mg/m²/dose (3.3 mg/kg/dose for BSA <0.6 m²) IV over 4 hours for 5 days on Days 1-5 (Arm B) or Days 6-10 (Arm A).

Toxicity was graded according to the National Cancer Institute Common Terminology Criteria for Adverse Events (CTCAE), version 4.0 (http://ctep.cancer.gov; National Cancer Institute, Bethesda, MD). Treatment-related toxicity was defined as
non-resolving grade 3 or grade 4 non-hematologic or hematologic toxicity or time to
platelet recovery to $\geq 100,000/\mu l$ and neutrophil recovery to $\geq 1,000/\mu l$ more than 55 days
from the last day of induction chemotherapy in the absence of leukemia. Events
considered by the investigator to be possibly, probably, or definitely related to decitabine
were considered treatment-related toxicity.

**Safety assessments**

Induction mortality was defined as death occurring within six weeks following
initial diagnosis of AML. An independent Data Safety and Monitoring Board assessed
the first 12 patients enrolled. This Board remained active for continuous analyses and
recommendations throughout the conduct of the study. Stopping rules were included in
the protocol to ensure appropriate safety of participants and that in the event of
unacceptable toxicity additional patients would not be placed at risk. All investigators
had access to the primary clinical trial data.

**On-study evaluations**

Required assessments included physical examinations and recording of adverse
events at screening/baseline, on day 5, and at the completion of study therapy.
Required hematology and serum chemistry assessments were performed on days 1, 2,
6, 7, 14, 15, and weekly thereafter. Bone marrow evaluations for morphology, MRD and
molecular analyses were performed at screening/baseline, 3-4 weeks following the
completion of induction chemotherapy regardless of peripheral blood count recovery,
and then as clinically indicated until count recovery. Any clinically appropriate
assessment or test was allowed at the treating physician’s discretion to maintain
standards of care.

**Efficacy assessments**

The primary efficacy variable was Complete Response (CR), defined by the
International Working Group 2003 criteria (20), requiring patients to have a morphologic
leukemia-free state and an absolute neutrophil count >1000/µL and platelets of 
>100,000/µL. Neither hemoglobin nor hematocrit was considered to have bearing on 
response although patients were required to be red blood cell transfusion independent to 
enroll. Secondary efficacy variables included Leukemia-Free Survival (LFS), Overall 
Survival (OS), methylation of DNA following decitabine therapy, times to platelet and 
neutrophil recovery, and level of minimal residual disease at the end of induction 
therapy. LFS and OS were assessed on patients every three months until disease 
progression, death, or loss to follow up. MRD analysis was performed at the post-
induction therapy assessment by multi-parameter flow immunophenotyping. Due to the 
small sample size, statistical analyses were primarily descriptive.

Pharmacokinetic evaluations

Serial blood samples (2 mL each) were drawn from all patients randomized to 
Arm A at pre-decitabine, 30, 60 (just prior to end of infusion), 65, 90, 120, and 180 
minutes after the start of decitabine infusion. A separate line was used to draw PK 
samples not in proximity (i.e., not the contralateral lumen of a double lumen line) to the 
decitabine infusion. Samples were collected in EDTA tubes containing 
tetrahydrouridine, a cytidine deaminase inhibitor, to prevent decitabine degradation, and 
were centrifuged at 4C within 30 minutes of collection. Plasma was harvested and 
stored frozen at -70 to -80C and shipped on dry ice for central analysis.

Pharmacokinetic parameters were calculated from plasma decitabine 
concentration-time data by non-compartmental methods using Phoenix WinNonlin 
version 6.2 (Pharsight Corporation, Mountain View, CA). The maximum plasma 
concentration (C_max) and the time at which C_max occurred (T_max) were determined by 
inspection of the individual data. AUC from time 0 until the last quantifiable 
concentration (AUC_{0-tau}) was determined by the linear up-log down trapezoidal rule. The
terminal phase elimination rate constant ($K_{el}$) was estimated from the slope of the concentration-time data during the log-linear terminal phase using least square regression analysis. The terminal phase elimination half-life ($t_{1/2}$) was calculated using the formula $0.693/K_{el}$. The AUC-time curve from 0 to infinity ($AUC_{0-infinity}$) was computed as $AUC_{0-t} + \frac{C_t}{K_{el}}$. Total body clearance ($CL_p$) was calculated by the formula $Dose/AUC_{0-infinity}$. The volume of distribution at steady state ($V_{dss}$) was calculated using the formula $CL_p \times MRT$. Area under the first moment curve ($AUMC$) was determined using the linear trapezoidal rule to calculate $AUMC_{0-tau}$ and extrapolated to infinity as $AUMC_{0-tau} + t \frac{C_t}{(K_{el})^2}$. The formula used to determine mean residence time (MRT) was $[AUMC/AUC_{0-infinity} - \tau/2]$, where $\tau$ is the duration of infusion.

**DNA methylation analysis**

Bone marrow and blood samples were obtained from all patients at baseline and at completion of induction therapy. In addition, blood samples were also collected on days 7 and 14. DNA was extracted from marrow or peripheral blood lymphocytes (buffy coat) using Qiagen’s AllPrep kit from samples enriched for leukemic blasts by standard Ficoll separation. Global DNA methylation was evaluated using the Infinium® Human Methylation450® BeadChip Array according to the manufacturer’s protocol (Illumina, San Diego, CA) and as previously described (21). A total of 18 paired patient samples with both diagnostic and remission bone marrows (9 pairs from Arm A and 9 pairs from Arm B, totaling 36 samples) were used for DNA methylation analyses. In addition, peripheral blood DNA from all time points was also analyzed. DNA Methylation levels for each CpG residue are presented as $\beta$ values, estimating the ratio of the methylated signal intensity over the sum of the methylated and unmethylated intensities at each locus. The average $\beta$ value reports a methylation signal ranging from 0 to 1 representing completely unmethylated to completely methylated values, respectively.
DNA methylation data were preprocessed using the Illumina Methylation Analyzer (IMA; doi: 10.1093/bioinformatics/bts013), including background and probe design corrections, quantile normalization and logit transformation. Loci with detection p-values >0.05 in 25% of samples, on sex chromosomes, or within 10 bp of putative SNPs were removed from analysis. Differential methylation analysis was performed by IMA. A paired Wilcoxon rank test was conducted to compare end-induction marrows with diagnostic marrows within each arm. Probes with \( p < 0.05 \) having group-wise differences in \( \beta \) values of at least 0.15 were considered statistically significant and differentially methylated. Differentially methylated loci were visualized on a heat map and separation of groups was assessed by hierarchical cluster analysis using Manhattan distance and Ward’s method. Unsupervised clustering was also performed on the top 0.1% most variable probes by standard deviation. The DNA methylation data discussed here were deposited in NCBI Gene Expression Omnibus Database and are accessible through GEO Series accession number GSE78963.

**RNA sequencing analysis**

Total RNA was isolated using Qiagen’s AllPrep kit and used to generate whole transcriptome libraries using Nugen’s Ovation RNA-Seq System v2 and KAPA Biosystems’ Library Preparation Kit with Illumina adapters. Equimolar libraries were pooled and used to generate clusters on Illumina HiSeq Paired End v3 flowcells on the Illumina cBot using Illumina’s TruSeq PE Cluster Kit v3. Clustered flowcells were sequenced by synthesis on the Illumina HiSeq 2000 using paired-end technology and Illumina’s TruSeq SBS Kit, extending to 83 bp for each of two reads and a 7bp index read. Approximately 75-100M reads per library were targeted for generation. Following sequencing, BCL files were converted to FASTQs using Illumina BCLConverter tool. FASTQ alignments were performed using Star to generate individual BAM files. Cufflinks/Cuffdiff and DEseq2 were used to identify differentially expressed transcripts.
Annotations were based on Gencode version 3 (ENSEMBL) build 37.1. The RNA-seq data discussed in this publication have been deposited in NCBI’s Gene Expression Omnibus, and are also accessible through the GEO series accession GSE78963.

**Analysis of repeat element transcription**

Kallisto (22) was used to quantify abundance of transcripts using ENSEMBL build 80 and human repeat exemplars from RepBase 20_07 (23). Transcripts were quantified in units of transcripts per million (TPM). The resulting estimates were imported using the Artemis package (24) and annotated for presentation using TxDbLite (25), the latter providing a “best fit” alignment of RepeatMasker and RepBase element-wise repeat phylogeny.

**Pathway analysis**

Gene lists of interest were uploaded into IPA (Ingenuity® Systems, Redwood City, CA) and the Core Analysis workflow was run with default parameters. Core Analysis provides an assessment of significantly altered pathways, molecular networks and biological processes represented in the samples’ gene list.

**RESULTS**

**Patients**

Twenty-five patients, aged 1-16 years (median 8.0 years) with WBC at diagnosis ranging from 1.19-58.09 x 10^3/μL were randomized between March and November 2011. Two patients did not receive the full induction regimen due to toxicity. As shown in Table 1, 24 were fully assessable for all study objectives per protocol (10 in Arm A, 14 in Arm B). Three patients had confirmed FLT3 internal tandem duplications, all with an allelic ratio of >0.5 and one had a FLT3 D835 point mutation. Two patients had NPM1 mutations and two patients had CEBPA mutations. No patients had mutations of TET2,
IDH1, IDH2, or C-CBL exons 8 or 9. One patient each had a KIT exon 8 (N822K) and 17 (D816H) mutation. Three patients had WT1 exon 7 mutations and one patient had a WT1 exon 9 mutation. On relative dose intensity analysis, patients received 99-100% of the intended doses of decitabine, daunorubicin, and etoposide and 84% of the intended doses of cytarabine.

Table 1. Patient Characteristics (by arm and overall)

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Patients</th>
<th>...in Arm A</th>
<th>...in Arm B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Consented</td>
<td>25 (100%)</td>
<td>11 (44%)</td>
<td>14 (56%)</td>
</tr>
<tr>
<td>Randomized and treated</td>
<td>25 (100%)</td>
<td>11 (44%)</td>
<td>14 (56%)</td>
</tr>
<tr>
<td>Evaluable for all study endpoints</td>
<td>24 (96%)</td>
<td>10 (40%)</td>
<td>14 (56%)</td>
</tr>
<tr>
<td>Sex:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>12 (48%)</td>
<td>7 (58%)</td>
<td>5 (42%)</td>
</tr>
<tr>
<td>Female</td>
<td>13 (52%)</td>
<td>4 (31%)</td>
<td>9 (69%)</td>
</tr>
<tr>
<td>Age, years</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Median (range)</td>
<td>8.0 (1-16)</td>
<td>8 (2-16)</td>
<td>7.5 (1-16)</td>
</tr>
<tr>
<td>Race:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>20 (80%)</td>
<td>8 (32%)</td>
<td>12 (48%)</td>
</tr>
<tr>
<td>African-American</td>
<td>1 (4%)</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Asian</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
<td>1 (4%)</td>
</tr>
<tr>
<td>American Indian or Alaska native</td>
<td>1 (4%)</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Other</td>
<td>2 (8%)</td>
<td>1 (4%)</td>
<td>1 (4%)</td>
</tr>
<tr>
<td>Ethnicity, Hispanic</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ethnicity, not Hispanic or Latino</td>
<td>6 (24.0)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cytogenetic Risk Groups:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Favorable</td>
<td>4 (8%)</td>
<td>1 (4%)</td>
<td>3 (12%)</td>
</tr>
<tr>
<td>Intermediate</td>
<td>17 (68%)</td>
<td>6 (24%)</td>
<td>11 (44%)</td>
</tr>
<tr>
<td>Unfavorable</td>
<td>4 (16%)</td>
<td>4 (16%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Cytogenetics:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Normal</td>
<td>7 (28%)</td>
<td>3 (12%)</td>
<td>4 (16%)</td>
</tr>
<tr>
<td>t(8;21)</td>
<td>4 (16%)</td>
<td>1 (4%)</td>
<td>3 (12%)</td>
</tr>
<tr>
<td>11q23</td>
<td>9 (36%)</td>
<td>5 (20%)</td>
<td>4 (16%)</td>
</tr>
<tr>
<td>Other</td>
<td>5 (20%)</td>
<td>2 (8%)</td>
<td>3 (12%)</td>
</tr>
</tbody>
</table>
Toxicity

Treatment-emergent AEs are summarized in Table 2. The most common grade 3 and grade 4 AEs were hematologic, including WBC decreased, anemia, platelet count and neutrophil count decreased. Colitis (n=2), anorexia (n=3), hypophosphatemia (n=2), and hypokalemia (n=3) were also noted. One patient in Arm A experienced colonic perforation on Day 6 due to leukemic infiltration of the bowel wall that led to study discontinuation. Two patients in Arm A died 6 months after completion of induction therapy; one of necrotic bowel and *Pseudomonas* sepsis, and one of multisystem organ failure. The latter patient died 5 months after study treatment as a complication of stem cell transplantation. Neither death was attributed to decitabine nor to the chemotherapy regimen received during study participation.

<table>
<thead>
<tr>
<th>Location:</th>
<th>Decitabine + Chemotherapy</th>
<th>Chemotherapy only</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alberta (Canada)</td>
<td>1 (4%)</td>
<td>1 (4%)</td>
</tr>
<tr>
<td>Children's Hospital Central California</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Denver</td>
<td>8 (32%)</td>
<td>5 (20%)</td>
</tr>
<tr>
<td>Emory</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Johns Hopkins</td>
<td>5 (20%)</td>
<td>5 (20%)</td>
</tr>
<tr>
<td>John Hunter Hospital (Australia)</td>
<td>2 (8%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Mayo Clinic</td>
<td>1 (4%)</td>
<td>1 (4%)</td>
</tr>
<tr>
<td>Nationwide Children's Hospital</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Phoenix Children's Hospital</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Primary Children's Hospital</td>
<td>1 (4%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Royal Children's Hospital (Australia)</td>
<td>3 (12%)</td>
<td>1 (4%)</td>
</tr>
</tbody>
</table>

Table 2. Grade 3 and Grade 4 treatment-emergent adverse events (TEAEs) reported in treated patients fully assessable for all study endpoints, as assessed by the Common Terminology Criteria for Adverse Events, version 4.0.
<table>
<thead>
<tr>
<th>Any Grade 3 or Grade 4 TEAEs</th>
<th>7 (87.5)</th>
<th>7 (87.5)</th>
<th>7 (77.8)</th>
<th>7 (77.8)</th>
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</thead>
<tbody>
<tr>
<td><strong>Blood and lymphatic system</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>disorders</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Anemia</td>
<td>6 (75.0)</td>
<td>2 (25.0)</td>
<td>4 (44.4)</td>
<td>1 (11.1)</td>
</tr>
<tr>
<td>Febrile neutropenia</td>
<td>1 (12.5)</td>
<td>0</td>
<td>4 (44.4)</td>
<td>0</td>
</tr>
<tr>
<td>Other: Neutropenia</td>
<td>1 (12.3)</td>
<td>3 (37.5)</td>
<td>1 (11.1)</td>
<td>1 (11.1)</td>
</tr>
<tr>
<td>Other: Thrombocytopenia</td>
<td>4 (50.0)</td>
<td>4 (50.0)</td>
<td>0</td>
<td>2 (22.2)</td>
</tr>
<tr>
<td><strong>Gastrointestinal disorders</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Colitis</td>
<td>2 (25.0)</td>
<td>0</td>
<td>2 (25.0)</td>
<td>0</td>
</tr>
<tr>
<td><strong>Investigations</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Neutrophil count decreased</td>
<td>0</td>
<td>0</td>
<td>1 (11.1)</td>
<td>3 (33.3)</td>
</tr>
<tr>
<td>Platelet count decreased</td>
<td>0</td>
<td>1 (12.5)</td>
<td>2 (22.2)</td>
<td>3 (33.3)</td>
</tr>
<tr>
<td>White blood cell count decreased</td>
<td>6 (75.0)</td>
<td>6 (75.0)</td>
<td>3 (33.3)</td>
<td>5 (55.6)</td>
</tr>
<tr>
<td><strong>Metabolism and nutrition</strong></td>
<td></td>
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<tr>
<td>disorders</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Decreased appetite</td>
<td>3 (37.5)</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Hypokalemia</td>
<td>3 (37.5)</td>
<td>0</td>
<td>1 (11.1)</td>
<td>0</td>
</tr>
<tr>
<td>Hypophosphatemia</td>
<td>2 (25.0)</td>
<td>0</td>
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<td>0</td>
</tr>
</tbody>
</table>

**Pharmacokinetics**

Plasma concentrations of decitabine were quantifiable in all patients up to the last time point of 180 minutes. Post-infusion, plasma concentrations declined in a bi-exponential manner (Figure 1). Selected PK parameters of decitabine in subjects overall are shown in Table 3. The overall mean (standard deviation) PK parameters for the decitabine-treated patients were: $C_{\text{max}}$, 294(104) ng/mL; AUC$_{0-\infty}$, 214(72.4) ng•h/mL; CL, 128(92.3) L/h; $V_{\text{ss}}$, 45.5(41.1) L; $t_{1/2}$, 0.453(0.0804) h; $t_{\text{max}}$, 0.831h(0.253). Estimated
PK values for a 70-kg adult male receiving a 1 hour decitabine 20 mg/m² infusion are shown for reference. The mean exposure to decitabine, as measured by Cₘₐₓ and AUC was similar in patients aged 12-16 years compared with those aged 2-11 years as shown, and similar to those in adults. However, inter-patient variability in this study was high.

Table 3. Mean Pharmacokinetic Parameters of Decitabine on Day 5 of Treatment—Overall and by Age Group, Pharmacokinetic Analysis Population

<table>
<thead>
<tr>
<th>Pharmacokinetic Parameter</th>
<th>Age Group (y)</th>
<th>Arm A Total (N=11)</th>
<th>Comparator 70-kg Adult Maleᵃ</th>
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<tr>
<td></td>
<td>2 - 11 (N=7)</td>
<td>12 - 16 (N=4)</td>
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<tr>
<td>Cₘₐₓ (ng/mL)</td>
<td>286 (131)</td>
<td>307 (36·9)</td>
<td>294 (104)</td>
</tr>
<tr>
<td>tₘₐₓ (h)</td>
<td>0·803 (0·272)</td>
<td>0·88 (0·243)</td>
<td>0·831 (0·253)</td>
</tr>
<tr>
<td>t½ (h)</td>
<td>0·458 (0·0777)</td>
<td>0·446 (0·0967)</td>
<td>0·453 (0·0804)</td>
</tr>
<tr>
<td>AUC₀-ₜ (ng•h/mL)</td>
<td>211 (90·0)</td>
<td>218 (35·1)</td>
<td>214 (72·4)</td>
</tr>
<tr>
<td>AUC₀-∞ (ng•h/mL)</td>
<td>212 (90·0)</td>
<td>219 (35·7)</td>
<td>215 (72·5)</td>
</tr>
<tr>
<td>CL (L/h)</td>
<td>110 (113)</td>
<td>161 (23·9)</td>
<td>128 (92·3)</td>
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<tr>
<td>Vdₚₛ (L)</td>
<td>40·7 (52·0)</td>
<td>54·1 (9·67)</td>
<td>45·5 (41·1)</td>
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</table>

AUC = area under the concentration-time curve; CL = total body clearance; Cₘₐₓ = maximum concentration; NR = not reported; t½ = half-life; tₘₐₓ = time to Cₘₐₓ; Vdₚₛ = volume of distribution at steady-state concentrations.

ᵃ: Data based on population pharmacokinetic analysis
ᵇ: cumulative AUC value over entire 5-day dosing period. Single-day AUC value = 116 ng•h/mL.

All values presented as mean ± SD. standard deviation cannot be calculated where n=2

Anti-leukemic response

Morphologic CRs and CRs with incomplete count recovery (CRi) rates were similar in both treatment arms: 100% CR/CRi in Arm A (decitabine) and 92% CR/CRi in Arm B (control). The patient who discontinued study participation on day 6 after receiving all decitabine doses and only one dose of cytarabine remained in a complete
remission for two months without any further leukemia-directed treatment. She eventually resumed standard therapy two months later and remains in CR 56+ months later. MRD by multi-parameter flow cytometry showed that 85% of patients in Arm A were MRD negative at day 30 of induction compared to 67% in Arm B. In a follow-up of patients as of August 2015, 8 of 14 (57%) in Arm B and 5 of 10 (50%) of evaluable patients in Arm A relapsed following additional treatment.

**Biological marker analysis**

Quantitative DNA methylation analyses revealed global changes in methylation following decitabine priming. Diagnostic and end-induction marrows were analyzed in 9 patients in each Arm (Figure S1). Paired differential methylation analysis of end-induction marrows to patient matched screening marrows revealed 6990 differentially methylated CpG loci (DML) encompassing 2518 genes in Arm A compared to only 1090 DML (539 genes) in Arm B (Tables S1A-B). Only DML in Arm A (n=4597) survived false discovery p-value correction. Of all DML in Arm A, 4134 were hypomethylated and 2856 were hypermethylated. In Arm B, 785 DML were hypomethylated and 305 were hypermethylated. There were 795 DML (438 genes) common to both arms. Although about 80% of genes altered by DNA methylation in Arm B were common to Arm A, there were significantly more probes altered for a given gene in Arm A. Moreover, 78% of hypomethylated probes in Arm B were common with Arm A, compared with 56% of hypermethylated probes common between treatment arms. The median delta-beta values for Arms A and B were -0.27 and -0.28, respectively, indicating modest overall hypomethylation induced by either treatment regimen at the specified delta-beta cut-off. Forty-one percent of DML were hypermethylated after decitabine therapy compared with 28% after chemotherapy only. Regional and functional CpG distribution of DML after therapy in both treatment arms was also examined. Functional distribution relates CpG position to transcription start sites (TSS) −200 to −1500 bp, 5’ untranslated region (UTR),
and exon 1 for coding genes as well as gene bodies. In both treatment arms, gene body
hypermethylation was the most frequent change, followed by gene body
hypomethylation and TSS 200 hypomethylation (Figure S2). Regional distribution of
DML was assessed based on proximity to the closest CpG island. In addition to CpG
islands, shores are 0-2 kb from CpG islands, shelves are 2-4 kb away, and open sea
regions are isolated loci without a designation. CpG island hypomethylation occurred in
greater than 68% of DML in both groups. Hypermethylation occurred most prominently
in open sea regions and to a greater degree in Arm A patients compared with those in
Arm B receiving chemotherapy alone (Figure S3).

Unsupervised clustering analysis of DML for both treatment arms demonstrated
strong separation of screening and end-induction marrows except for one sample pair in
Arm A and three sample pairs in Arm B (Figure 2, top panels). In two of these cases,
pre- and post-treatment samples co-clustered with its matching sample. One case in
Arm A and Arm B clustered with diagnostic marrows, suggesting the marrow was
possibly unaffected by therapy and indeed the sample in Arm A (1006_1004) was from a
patient with stable disease. Overall, these data indicate that decitabine therapy has a
homogenizing effect on the recovering end-induction marrow in AML. This was evident
when compared with Arm B samples, where DNA methylation was more heterogeneous
after standard chemotherapy treatment.

To further assess the changes in recovering marrows in both arms, we
performed an unsupervised clustering analysis of the top 0.1% most variable CpG
probes (~430 probes) in the post-processed data. These data confirmed that the end-
induction recovering marrows were distinctive from screening marrows and more
homogenized in the decitabine-treated arm compared with those in the control arm
(Figure 2, lower panels). To ensure that samples were not molecularly different at
screening between the arms, we performed the above analyses comparing screening
marrs in Arm A with Arm B and observed only 492 DML. Of these, 291 were common
to the Arm A DML list, while 3 DML were common to both Arm A and B comparisons and
0 DML were common to Arm B DML (Figure 3). These intrinsically different loci were
excluded from downstream gene-level analysis. Among the genes most prevalently
hypomethylated in Arm A were FOXG1, VSTM2A, WT1, ZNF135, ZIC1, and ZIC4,
(Figure 4), which may potentially be used to measure decitabine activity. In addition,
time-dependent promoter hypomethylation of these genes also occurred in peripheral
blood lymphocytes (Figure 5), confirming their significance as potential biomarkers of
decitabine response. Most notably, recovery of promoter methylation in peripheral blood
was seen in a patient with stable disease and whose recovering marrow co-clustered
with diagnostic marrow, hinting at signs of preliminary efficacy. The data point to the
potential utility of these genes as biomarkers of minimal residual disease in patients
treated with decitabine.

Table 4 shows DNA methylation changes in several key biological pathways
potentially important to response to decitabine and chemotherapy. The top canonical
pathways in IPA for Arm A DML included gene alterations affecting mostly neuronal
signaling such as neuropathic pain signaling and glutamate receptor signaling (Table 4).
In Arm B, the top IPA canonical pathways included DML affecting embryonic stem cell
signaling and Rho GTPase signaling (Table 4).

Table 4. Ingenuity Pathway Analysis of Differentially Methylated Genes.

<table>
<thead>
<tr>
<th>Arm A Top Canonical Pathways</th>
<th>p-value</th>
<th>Overlap n (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neuropathic Pain Signaling in Doral Horn Neurons</td>
<td>7.5e-12</td>
<td>35/100 (35.0%)</td>
</tr>
<tr>
<td>Glutamate Receptor Signaling</td>
<td>2.45e-11</td>
<td>25/57 (43.9%)</td>
</tr>
<tr>
<td>Amyotrophic Lateral Sclerosis Signaling</td>
<td>2.05e-09</td>
<td>31/98 (31.6%)</td>
</tr>
<tr>
<td>Synaptic Long Term Potentiation</td>
<td>1.00e-06</td>
<td>30/119 (25.2%)</td>
</tr>
<tr>
<td>Hepatic Fibrosis/Hepatic Stellate Cell Activation</td>
<td>1.01e-06</td>
<td>40/183 (21.9%)</td>
</tr>
</tbody>
</table>
Differentially methylated genes for Arm A (decitabine + chemotherapy; n=2518) and Arm B (chemotherapy alone; n=539) were entered into the core pathway analysis option. Top 5 canonical pathways are shown along with a significant p-value and the number of genes in each list belonging to the pathway.

This study is unique in comparing the epigenetic and RNA expression consequences of induction chemotherapy following pre-treatment with decitabine vs chemotherapy alone in end-induction recovering bone marrow. This comparison revealed 104 differentially expressed genes in Arm A (Table S2A) and 74 genes in Arm B (Table S2B). There are 5 genes common to both treatment arms. Twelve genes that were differentially expressed in Arm A had DNA methylation changes affecting 72 DML (Table S3A). Among these were 57 probes impacting PCDGHGB2, the potential calcium-dependent cell-adhesion protein; the gene was hypomethylated but downregulated. In Arm B there were only 23 DML (Table S3B) corresponding to eight differentially expressed genes. Only SIX3 overlapped between both arms at a single DML. Additionally, we saw no evidence of sustained repeat element reactivation in recovering week three marrows with or without decitabine pre-treatment (Figure 6).

**DISCUSSION**

This first-in-pediatric randomized trial of epigenetic priming in children with newly diagnosed AML demonstrated safety and tolerability and establishes the feasibility required to develop future trials for assessing durability of response. We did not assess durable responses in this study because its main purpose was to first assess safety and
tolerability of decitabine in children. The results trended towards non-inferiority of morphologic, immunophenotypic, and MRD response, although the small sample size limited statistical analyses. There was also evidence of decitabine-induced effects in end-induction bone marrow aspirates compared with those obtained at diagnosis. Children treated with decitabine as a single agent for five days prior to conventional cytotoxic therapy did not have rapid progression of their leukemic burden during the pre-phase, further supporting the feasibility and safety of this approach. Based on these results, a dose of 20 mg/m² daily for 5 days prior to standard conventional chemotherapy could be considered for testing for durable responses.

Most non-hematologic AEs reported in this study were mild to moderate in severity (grade 1 or 2), reversible, and easily managed. In general, the safety profile of decitabine in children with AML was consistent with that seen in adults. No previously unreported decitabine toxicities were observed. Drug-related hematologic toxicity, anorexia, and asymptomatic grade 3 hypokalemia and hypophosphatemia were slightly more common in decitabine treated patients.

This trial was not powered to detect a difference in response between the two arms and treatment with decitabine prior to standard induction therapy resulted in a similar morphological response compared to standard induction therapy. Of note, there were more high-risk cytogenetic patients in the decitabine arm (4 versus 0), which may indicate a benefit for decitabine priming prior to treatment in these patients. Patients in this study were generally representative of children with de novo childhood AML in age, gender, and biologic features, however there were slightly more patients with WT1 and CEBPA mutations than previously reported. In addition, the impact on MRD suggests that decitabine may induce a higher percentage of MRD negative remissions; however, again the numbers in this study are too small to calculate statistics in a meaningful way. There was a non-significant trend toward a longer time to recover neutrophil and platelet...
counts in the decitabine-treated patients (data on file), and no AEs or SAEs were noted
as a result of delays in count recovery. These results suggest that exposure to
decitabine may have important implications for sensitizing potentially resistant leukemic
clones to cytotoxic chemotherapy, resulting in deeper remissions predictive of more
favorable outcomes. Larger randomized studies are needed to confirm these findings.

Alterations in DNA methylation and RNA expression patterns in end-induction
bone marrow between the two groups of patients suggest important consequences of
exposure to decitabine pretreatment on hematopoietic recovery after exposure to
intensive chemotherapy, where decitabine appears to have a homogenizing effect on
end-induction marrows that may ultimately be important in priming for chemotherapy
sensitization. Our data suggest that while chemotherapy alone may have an effect on
DNA methylation, the effect is clearly augmented by the addition of decitabine via
epigenetic changes that may impact both leukemic, normal hematopoietic progenitors,
as well as bone-marrow stromal cells. Furthermore, the data suggest that decitabine
therapy can be used to measure MRD/or patient response to therapy by assessing DNA
methylation status of specific promoter regions non-invasively in blood. The pathway
analysis conducted to compare differentially methylated loci in the decitabine treated
arm to the chemotherapy only arm revealed a number of pathways implicated to
neuronal signaling but the results were quite distinct from the ADE only arm. While the
implications of neuronal signaling are not currently clear, we postulate it must be related
to the bone marrow niche post-treatment since no dorsal root ganglia or other neuronal
tissue exist in the marrow. Presumably this could be due to ion channel currents that
play an important role in bone-marrow derived mesenchymal stem cells and
hematopoietic progenitors (26). Our observations further suggest that monitoring
changes in normal progenitors may be important in understanding the short and longer-


The toxicity and PK results observed in the patients in this study suggest that decitabine can be safely combined with standard doses and schedules of anticancer agents in children with newly diagnosed AML. Furthermore, our data suggest that this regimen alters DNA methylation and RNA expression compared to ADE chemotherapy alone, and patients treated with decitabine could have minimal residual disease measured by assessing DNA methylation status of specific promoter regions. Preclinical studies have shown additive or synergistic activity when decitabine is combined with a variety of other anticancer therapies (27-30) and results from trials such as this provide further evidence of feasibility, safety and possible strategies for larger randomized trials in patients with newly diagnosed or recurrent/refractory leukemia as well as in the minimal disease state during post-remission follow-up. No excess or unexpected toxicities were seen. The most common drug-related grade 3 or grade 4 AEs were hematologic and PK/PD were as expected. Complete remission rates were similar. Patients treated with decitabine prior to conventional chemotherapy had distinct changes in DNA methylation and...
transcriptional regulation. Repeat element transcription may be of interest for further mechanistic study. In conclusion, epigenetic therapy with decitabine is safe for use in children and the clinical findings together with molecular correlative studies suggest that there may be early signs of enhanced efficacy. However, further studies are needed to definitively determine the long-term patient outcomes of decitabine priming in children with AML.

LIST OF ABBREVIATIONS:

ADE = cytarabine/daunorubicin/etoposide chemotherapy regimen
AML = acute myelogenous leukemia
AUC = area under the curve
BSA = body surface area
C max = maximum plasma concentration
CML = chronic myelogenous leukemia
CNS = central nervous system
CR = complete remission
CR = complete remission with incomplete count recovery
DADE = decitabine plus daunorubicin/cytarabine/etoposide chemotherapy regimen
DML = differentially methylated loci
DNA = deoxyribonucleic acid
FAB = French-American-British classification
HIV = human immunodeficiency virus
LFS = leukemia-free survival
MRD = minimal residual disease
OS = overall survival
PD = pharmacodynamics
PK = pharmacokinetics
RNA = ribonucleic acid
Tmax = time to maximum plasma concentration

DECLARATIONS

Ethics Approval and Consent to Participate:
The study protocol was approved by each institutional review boards at every participating site and was conducted in accordance with the Declaration of Helsinki, Good Clinical Practice, and all local and federal regulatory guidelines. A parent or legal guardian provided written informed consent, with patient assent as appropriate according to institutional requirements.

Consent for Publication: Not applicable

Availability of Data and Materials:
The datasets generated and analyzed in this study are included in this article and are available from the corresponding author on reasonable request. In addition, the DNA methylation and RNA-seq data discussed in this publication have been deposited in NCBI’s Gene Expression Omnibus, and are accessible through the GEO series accession number GSE78963.

Competing Interests:
Mark Jones and Peter Tarassoff are former employees of Eisai Pharmaceuticals. Robert Arceci was a consultant for Pfizer. Partial support from Eisai was obtained for
correlative laboratory studies (R.J.A., S.M.). There are no other potential conflicts of interest to declare.

**Funding and Support:**

This work was partially supported by Eisai Pharmaceuticals, Inc. In addition, the studies were partially supported by the Ron Matricaria Institute of Molecular Medicine at Phoenix Children’s Hospital (R.J.A.), the University of Arizona (R.J.A.), and TGen, Inc (R.J.A., B.S.). During part of the study period, R.J.A. was supported by the King Fahd Chair in Pediatric Oncology at Johns Hopkins University. Additional support was from The McCormick Tribune Foundation (L.G.), Alex’s Lemonade Stand (L.G.), the Morgan Adams Foundation (L.G. and M.E.M.), the St. Baldrick’s Foundation (R.J.A.), The Lund Foundation (R.J.A.), and the Najafi Fund (R.J.A.). M.E.M. was partially supported by the National Institutes of Health K12 CA086913-08. J.E.F. is partially supported by the Arkansas Biosciences Institute. L.G. is partially supported by the Clark Family and Ergen Chairs in Pediatric Cancer Therapeutics at Children’s Hospital Colorado.

**Authorship Contributions:**

L.G. and R.J.A. designed and wrote the study concept and scientific hypotheses, derived the full protocol, provided study oversight during the conduct of the study, enrolled patients on the study, reviewed data and toxicity of patients, and interpreted the data. R.J.A. performed many of the scientific experiments and contributed to a draft of the manuscript. L.G. performed the literature search, wrote the first, all drafts and the final manuscript, helped prepare and reviewed the Figures and Tables, and collated and incorporated comments from all co-authors. B.S. conducted experiments and provided oversight of the scientific experiments not completed by R.J.A., prepared and reviewed the Figures and Tables, and contributed substantially to the data analysis and writing.
and editing of the manuscript. T.T. helped analyze and review the experiments and
Figures and Tables, and assisted substantially in the writing and reviewing of the final
manuscript. J.E.F., D.W., C.L., G.C.G., W.S.L., J.C., D.L., and S.M. contributed to the
scientific experiments and data analyses including Figure preparation and review. J.E.F.
and T.T. also contributed to writing the Methods sections, reviewing, and editing the
manuscript. S.M. contributed to the data analysis and commentary. F.A., M.E.M., C.A.,
P.B., T.C., L.M., A.N., J.P., J. B. enrolled patients on the clinical trial and reviewed and
commented on the manuscript prior to submission. M.J., L.C., S.S., and P.T. reviewed
the study and manuscript. M.J. representing the Eisai Inc., provided study enrollment
materials, oversight and analysis within the context of the protocol operations and data
analysis. Eisai, Inc., is the manufacturer of decitabine and the company providing partial
support for the conduct of this trial.

Acknowledgements:

Dr. Francoise Mechinaud (Royal Children’s Hospital, Australia) and Dr. Wendy Tcheng
(Children’s Hospital of Central California) also treated patients on this trial. Dr. Peter
Tarrasoff had oversight and analysis of the protocol operations on behalf of Eisai, Inc.,
the manufacturer of decitabine and the company providing partial support for the
conduct of this trial.

Lori Cuyugan and Shobana Sekar (Translational Genomics Research Institute, Phoenix,
AZ) for the generation and analysis of RNA-seq data.

Dedication:
The authors of this paper would like to recognize the fundamental contributions that Dr.
Robert Arceci made not only in the conception, design, and conduct of this study and the
associated biology work incorporated within, but to the field of pediatric oncology as a whole. During the laboratory correlate analysis and preparation of this manuscript, Dr. Arceci’s life was tragically cut short in a fatal traffic accident. His collaborators on this study wish to acknowledge his myriad contributions to this work and the field, and remain dedicated to pursuing the highest degree of scientific collaboration and integrity in his honor.

REFERENCES


Figure 1. Mean decitabine blood concentration-time profile measured in whole blood by age group.

Figure 2. Hierarchical clustering of differentially methylated loci (DML) in Arm A (decitabine + chemotherapy) and Arm B (chemotherapy alone). Top Panel: unsupervised clustering analysis of 6990 DML in Arm A and 1090 DML in Arm B revealed separation of end of induction recovering marrows at week 3 from screening marrows (X0BM). Lower Panel: Unsupervised hierarchical clustering of the top 0.1% most variable loci (SD) also separated screening marrows (X0BM) from end of induction recovery marrows at week 3. In both analyses, Arm A shows better separation of the two time points than in Arm B, indicating that
decitabine therapy appears to homogenize marrows to a larger degree than in chemotherapy alone.

**Figure 3.** Overlap of differentially methylated loci between arms and time points in Arm A (DADE), Arm B (ADE), and screening vs. recovery marrow aspirates. Screening marrows for samples in Arm A and Arm B are also compared and demonstrate little intrinsic bias between groups.

**Figure 4.** Integrated Genomic Viewer snapshot of differentially methylated genes affected by hypomethylation in response to decitabine therapy. Vertical heatmaps represent significantly differentially methylated (p value <0.05) probes in the 6 genes illustrated. Each row on the heatmap represent a unique sample. Many more probes were differentially methylated in Arm A (decitabine + chemotherapy) compared with Arm B (chemotherapy alone) for the probes shown. Hypomethylation (green) in response to decitabine (Arm A) is evident in end of induction recovery marrows (wk 3) compared with diagnostic marrows (screen). Array avg \( \beta \) values are represented in the heatmap. Scale ranges from 0-1, where 0 is unmethylated (green) and 1 is fully methylated (red). Tracks shown: gene, CpG 450K probe, and CpG island.

**Figure 5.** Time-course collection of peripheral blood samples in Arm A reveal consistent decreases in promoter methylation at relevant transcription start sites over treatment in all responders, as well as a reversal of this decrease in the sole non-responsive patient (1006-1004). A distinct uptick in the patient’s promoter
methylation from day 14 to 21 is noted, which corresponded clinically to the
patient’s disease progression.

Figure 6. Unsupervised hierarchical clustering of repeat element expression in
screening and week 3 bone marrows, with (Arm A) or without (Arm B) decitabine
priming, in transcripts per million (TPM). No clear separation by trial arm is
visible, and a maximum of 4 transcripts per million is observed, suggesting that
mobilization of repeats by demethylating agents does not persist beyond the
course of treatment and is not significantly different between the treatment arms.

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Schema of sample analysis workflow.

Figure S2. Distribution of differentially methylated loci (DML) according to functional
CpG contextual distribution in Arms A (decitabine + chemotherapy) and B
(chemotherapy alone). Pie charts demonstrate the frequency by which hyper or
hypomethylated loci are distributed according to their functional position.

Figure S3. Distribution of differentially methylated loci (DML) according to CpG Island
contextual distribution in Arms A (decitabine + chemotherapy) and B (chemotherapy
alone). Pie charts demonstrate the frequency by which hyper or hypomethylated loci are
distributed according to their proximity of CpG islands.
Figure 2.

**ARM A**

DML

**ARM B**

S

**Color Key**

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<tr>
<th>Value</th>
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**Legend**

- XOBM
- wk3BM
Figure 3.

Arm A screening marrow vs
Arm B screening marrow

Arm A screening marrow vs.
3 week recovery marrow

198
291
5904

3
792

0

295

Arm B screening marrow vs.
3 week recovery marrow
Figure 5.

Promoter methylation over the course of DADE induction (Arm A)

<table>
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<td>VSTM2A</td>
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<td>1003–1008</td>
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<tr>
<td>ZNF135</td>
<td>1006–1001</td>
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<tr>
<td>ZIC1</td>
<td>1006–1002</td>
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<td>ZIC4 (TSS1)</td>
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<table>
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</tbody>
</table>

Methylation at TSS, in blood

Days since beginning treatment
Figure 6.