Cox regression for multivariable studies. *Results.* The median age of the series was 53 years (range 20-73); 8% of the patients died during induction chemotherapy, 81% achieved complete remission, and 11% showed refractoriness to treatment. In the multivariate analysis, the presence of NPM1 or CEBPA mutations without FLT3-ITD was associated to increased CR rate (95% *vs.* 75%, P= 0.001). OS of the cohort at 4 years was 41±4,6%, DFS 44±4.6% and relapse probability (REL) 52±5%. Adverse prognostic factors for the OS in the multivariate analysis were age over 50 years (>50y *vs.* <=50y P<0.001, odd ratio [OR]: 2.5 CI95%: 1.6-3.9), and the absence of a favorable genotype (NPM1+,or CEBPA+/FLT3-ITD-)(P<0.001,OR:4, CI95%:2.2-7.5). Regarding DFS, the adverse prognostic factors were age over 50 years (p:0.023, OR: 1.7, CI95%:1.1-2.8), a white blood cell count (WBC) over $100\times10^9$/L (>=100 *vs.* <100, P:0.050, OR:1.7, CI95%:1-3) and the absence of a favorable genotype (P:0.003, OR:2.3, CI95%1.3-4). For REL, the independent adverse factors were, older age (>50y) (P:0.036, OR:1.7, CI95%:1-2.9), the absence of a favorable genotype (P:0.003, OR:2.6, CI95%:1.3-4.8), and the over-expression of BAALC gene (P:0.011, OR:2.6 CI95%:1.2-5.1). *Conclusions.* In AML with intermediate cytogenetic risk, the over-expression of BAALC was an adverse prognostic factor for relapse rate. Regarding DFS and OS, the well established prognostic factors such as age, leukocyte count and NPM1, CEBPA and FLT3 status were confirmed in this series. The results presented here, confirmed the need to adjust therapeutic decisions based in clinical and biological features.

## 0641

### ANTI-LEUKEMIC EFFECT OF SODIUM METAARSENITE (KML001) IN ACUTE MYLOGENOUS LEUKEMIA WITH BREAKING-DOWN THE RESISTANCE OF CYTOSINE ARABINOSIDE

Y Lee,[1] SS Yoon,[2] ES Kim,[2] K Kim[3]

*[1]Han Yang University Hospital, Seoul, South-Korea; [2]Cancer Research Institute Seoul National Unviersity, Seoul, South-Korea; [3]Department of Internal Medicine, Seoul National University College of Medicine, Seoul, South-Korea*

*Background.* Arsenic compounds have been used in traditional medicine for several centuries. Especially, arsenic trioxide ($As_2O_3$) has proven effective in the treatment of acute promyelocytic leukemia (AML M3 subtype). A drawback of arsenic trioxide is that it is administered intravenously, and not effective in the treatment of acute mylogenous leukemia (AML) except AML M3 subtype. Sodium metaarsenite ($NaAs_2O_3$ : code name KML001) is an orally bioavailable arsenic compound with potential anti-cancer activity. However, the effect of KML001 has not been well studied in AML. *Aims.* Firstly, to determine the anti-leukemic effect of KML001 in AML, and to compare the efficacy with arsenic trioxide, secondarily, to investigate the mechanism of anti-leukemic effect of KML001. *Methods.* Eleven AML cell lines were used in this study including Ara-C (cytosine arabinoside) resistant HL-60 (HL-60R) cells. AML blasts were isolated from 4 AML patients (2 M1 and 2 M2 subtypes) after obtaining informed consents. Cellular inhibition was measured by MTT assay. Expression of molecules was done by western blot. Analysis of cell cycle was used by flow cytometry. Transcriptional expression of catalytic subunit of telomerase, hTERT, was done by real-time PCR. *Results.* KML001 inhibited the cellular proliferation in all AML cell lines and primary AML blasts as well as HL-60R cells in a dose-dependent manner with $IC_{50}$ of $5\times10^{-8}$M. While KML001 effectively inhibited cellular proliferation of HL-60 cells ( $IC_{50}$; $5\times10^{-8}$M) as well as HL-60R cells ( $IC_{50}$; $1\times10^{-8}$M), and its anti-leukemic effect was almost same as Ara-C ($IC_{50}$; $5\times10^{-8}$M), Ara-C did not inhibit cellular proliferation in HL-60R as expected. Furthermore, arsenic trioxide was not effective in primary AML blasts and AML cell lines including HL-60 R cells. KML001 ($1\times10^{-7}$M) was induced G1 cell cycle arrest which was associated with decreased expression of cyclin D1, cyclin E1, CDK1 (cdc2p34), CDK4, and CDK6. While KML001 increased the p21 and p27 levels, and enhanced their bindings with CDK4 in HL-60 cells, the expression of p21 and p27 bound CDK2 was observed in HL-60R cells. Apoptotic molecules of Bcl-2, proform of caspase-3 and caspase-9 were decreased, in contrast, expression of PARP was increased in HL-60 and HL-60R cells treated with KML001. Real-time PCR with RNA extracted from KML001-treated HL-60 and HL-60R cells showed a significant reduction of catalytic subunit of telomerase, hTERT, at 12 hr. When treated KML001, DNA damage molecule (γ-H2AX) in HL-60 and HL-60R cells was increased. In addition, KML001 inhibited the activation of STAT1, 3, 5, NF-κB (p65 and p50 subunits), pAKT and PI3K in a time-dependent manner. On the other hand, activated PTEN was up-regulated.Summary/*Conclusions.* KML001, sodium metaarsenite, demonstrated anti-leukemic effect via various mechanisms including cell cycle arrest, induction of apoptosis, and inhibition of JAK/STAT and PI3K pathways. Especially, KML001 might target telomerase with DNA damage. Furthermore, it is probable that KML001 may overcome the resistance of chemotherapeutic agents. Collectively, KML001 may be a candidate agent for the treatment of *de novo*, refractory and relapsed AML.

## 0642

### FLOW-CYTOMETRIC MULTIPLEX IMMUNOBEAD ASSAY FOR THE DETECTION OF CBFβ-MYH11 AND AML1-ETO FUSION PROTEINS IN ACUTE MYELOID LEUKEMIA

E Dekking,[1] V Velden,[1] N Boeckx,[2] E Sonneveld,[3] J Flores-Montero,[4] S Boettcher,[5] M Comans-Bitter,[1] J van Dongen[1]

*[1]ErasmusMC, Rotterdam, Netherlands; [2]Universitair ziekenhuis De Gasthuisberg, Leuven, Belgium; [3]Dutch Children Oncology Group, The Hague, Netherlands; [4]University of Salamanca, Salamanca, Spain; [5]University of Kiel, Kiel, Germany*

The prognostic classification of acute myeloid leukemias (AML) is generally based on the presence or absence of specific genetic aberrations-particularly fusion genes-that are detected by karyotyping, FISH or PCR. These techniques are laborious and demand specialized laboratories. Therefore fast and easy research-based cytometric bead array (CBA) assays (BD Biosciences) are being developed for detection of fusion proteins in cell lysates of leukemic cells that contain these well-defined fusion gene aberrations. Here we present data of a multiplex AML "core-factor"CBA which detects the AML1-ETO and CBFβ-MYH11 "core-factor"fusion proteins. AML patients harboring either of those fusion proteins comprise a biologically distinct and prognostically favorable subgroup of patients who often achieve long-lasting complete remissions. Therefore accurate identification of CBFβ-MYH11/ inv(16) and AML1-ETO/ t(8;21) positive cases is essential. Monoclonal antibodies were generated against the fusion proteins (both N- and C-terminus). Based on the recognized epitopes, the antibodies should recognize all variants of the CBFβ-MYH11 fusion proteins which result from translocations in the different breakpoint cluster regions. In the CBA, catcher antibodies were coupled to separate CBA beads and the detector antibodies with fluorochrome-labeling. A specific signal in the flow cytometer is only detectable when the relevant fusion protein is present in the analyzed sample. Since wild-type proteins are not recognized by the antibody couples, no signal should be obtained when samples are analyzed that do not contain the fusion protein. To limit the number of cells required for analysis, the two assays were combined into a multiplex so-called "AML core-factor"CBA. The multiplex assay appeared specific (cell lines that express other fusion proteins were not detected) and sensitive since it detects at least 10-15 % of fusion protein positive leukemic cells diluted in normal PB-MNCs or WBC's. The suitability of the multiplex AML core-factor CBA was tested in five EuroFlow laboratories: 63 myeloid and monocytic AML samples were analysed (blood and bone marrow).The presence or absence of CBFB-MYH11 or AML1-ETO transcripts in the specimens was determined by RQ-PCR analysis according to the EAC program. The performance of the CBA was assessed by parallel analysis of well-defined positive and negative control samples. The multiplex AML assay had full concordance with the RQ-PCR results (18/18 positive and 45/45 negative) with identification of all AML1-ETO (5/5) and CBFβ-MYH11 (13/13) positive patients. The multiplex AML core-factor CBA is suitable for accurate and simultaneous detection of CBFβ-MYH11 and AML1-ETO containing samples. The assay is specific and can be performed within 4-5 hours in a routine diagnostic setting, without the need of special equipment other than a flow cytometer. The novel CBA will enable fast and easy classification of AML patients that express CBFβ-MYH11 and AML1-ETO fusion proteins. These patients can be included at an early stage in the right treatment protocols, much faster than by use of current molecular techniques. The CBA can be run in parallel to routine immunophenotyping and is particularly attractive for clinical settings without direct access to molecular diagnostics.

## 0643

### GENE EXPRESSION ANALYSIS IN AML CELL LINE MV4-11 FOLLOWING TREATMENT WITH THE ANTI-CANCER APTAMER AS1411

S Sederovich,[1] A Ajami,[2] B Doran,[1] F McLaughlin,[1] D Jones[1]

*[1]Antisoma Research Limited, Welwyn Garden City, UK; [2]Antisoma Inc, Cambridge, MA, USA*

*Background.* AS1411 is a 26-base DNA aptamer which is shortly due to enter a phase IIb clinical trial in acute myeloid leukaemia (AML). In