

Mapping epigenetic regulator gene mutations in cytogenetically normal pediatric acute myeloid leukemia

Acute myeloid leukemia (AML) accounts for approximately 15-20% of all childhood leukemias, and despite dramatic improvements in treatment outcome, only approximately 70% of children with AML are cured.¹ AML results from collaborating genetic aberrations in at least 2 different classes; type-I aberrations, inducing uncontrolled cell proliferation and/or survival, and type-II aberrations inhibiting cell differentiation. However, certain aberrations found in AML do not completely fit into our current definition of type-I and type-II aberrations.² These aberrations concern epigenetic modifier genes involved in DNA methylation and histone modification, such as Ten-Eleven Translocation 2 (*TET2*), Isocitrate Dehydrogenase 1 (*IDH1*), *IDH2*, Enhancer of Zeste Homolog 2 (*EZH2*), DNA (cytosine-5)-Methyltransferase 3 Alpha (*DNMT3A*) and Additional Sex Combs Like-1 (*ASXL1*). Most of these genes are frequently mutated in adult AML patients with a prevalence varying between 12% to 35% per gene.³⁻⁷ Reports on prognostic implications of these mutations are ambiguous. It has, however, been shown that patients with *IDH* mutations have a hypermethylation phenotype. This implies that demethylating agents such as decitabine and azacitidine may be of use in the treatment of *IDH*-mutated AML. In addition, a favorable outcome in elderly AML patients with *DNMT3A* mutations after treatment with decitabine has been reported.^{7,8}

These epigenetic regulator genes were also studied in pediatric AML. Most of these studies focused on the relevance of mutations in a single gene and mutations were detected in 1-4% of the patients.⁹⁻¹⁵ Although no significant

statements can be made since study cohorts were quite heterogeneous, most mutations seemed to occur in cytogenetically normal (CN) AML, a subgroup that comprises 20-25% of all pediatric AML. This distribution corresponds to adult AML data in which most epigenetic regulator gene mutations were also identified in CN patients. So far, no larger study focusing on pediatric CN-AML is available and identifying these genetic aberrations may lead to improved risk stratification and a rationale for the use of demethylating agents in these patients. Therefore, we decided to study the mutation prevalence of epigenetic regulator genes *EZH2*, *IDH1/2*, *DNMT3A*, *ASXL1* and *TET2* in a well-documented, international cohort of 65 de novo pediatric CN-AML patients.

Patient material was obtained from the Dutch Childhood Oncology Group (DCOG), the AML-Berlin-Frankfurt-Münster Study group (AML-BFM), the Czech Pediatric Hematology Group, and the Saint-Louis Hospital in Paris, France. A minor selection of the discovered mutations had been included in previous reports, but not with a focus on CN-AML and never within one cohort.¹¹⁻¹³ Exon 4 of *IDH1/2*, exon 13 of *ASXL1*, the SET-domain of *EZH2* and the entire coding region of *TET2* were screened using Sanger sequencing of genomic DNA. The mutational status of *DNMT3A* was assessed by screening cDNA and aberrations were verified in genomic DNA. The prevalence of cytogenetic and molecular aberrations was assessed as previously described.¹⁴

In our study cohort, aberrations in the genes *IDH1* and *IDH2* occurred with a frequency of 10.8% (95%CI ± 7.5%) and mutations in *TET2* and *DNMT3A* were found with a frequency of 4.6% (95%CI ± 5.1%) each. While all aberrations in *IDH1* and *IDH2* were confined to codon 132 and 140, respectively, various mutation loci were observed in *TET2* and *DNMT3A*. All epigenetic regulator gene muta-

Table 1. Clinical and genetic characteristics of pediatric CN-AML cases carrying an epigenetic regulator gene mutation.

Gene	Patient	Mutation ¹	Protein change ²	Age (yrs)	Sex	WBC count (x10 ⁹ /uL)	Other mutations	Survival status	Months of follow up
<i>IDH1</i>	1	c.395G>A	p.R132H	3.6	M	14.1	<i>NUP98-NSD1</i> ; <i>K-RAS</i>	Death after relapse	23
<i>IDH1</i>	2	c.395G>A	p.R132H	14.3	F	44.8	<i>FLT3-ITD</i> ; <i>MLL-PTD</i>	Alive	50
<i>IDH1</i>	3	c.395G>A	p.R132H	15.1	M	9.6		Alive	104
<i>IDH1</i>	4	c.394C>T	p.R132C	12.6	F	3.0		Death after relapse	46
<i>IDH1</i>	5	c.395G>A	p.R132H	13.0	M	226.0	<i>NUP98-NSD1</i> ; <i>FLT3-ITD</i>	Alive	32
<i>IDH2</i>	6	c.419G>A	p.R140Q	7.5	M	120.4	<i>MLL-PTD</i> ; <i>FLT3-ITD</i>	Alive	71
<i>IDH2</i>	7	c.419G>A	p.R140Q	6.0	M	N/A	<i>NPM1</i> ; <i>FLT3-ITD</i>	Alive	40
<i>DNMT3A</i>	8	c.2146G>T	p.V716F	15.3	M	30.8	<i>NPM1</i> ; <i>N-RAS</i>	Alive	65
<i>DNMT3A</i>	9	c.2644C>T	p.R882C	8.4	M	25.0	<i>WT1</i> ; <i>FLT3-ITD</i>	Alive	52
<i>DNMT3A</i>	10	c.1450C>T	p.R484W	15.7	F	9.5	<i>CEBPA</i> dm	Alive	6
<i>TET2</i>	11	c.3803+2_3ins T	Unknown	11.1	F	163.0	<i>NPM1</i> ; <i>FLT3-ITD</i>	Alive	51
<i>TET2</i>	12	c.3646C>T c.4210C>T	p.R1216* p.R1404*	6.9	F	25.1	<i>N-RAS</i>	Alive	50
<i>TET2</i>	13	c.1599G>A	p.M533I	14.3	M	2.2		Alive	34

yrs: years; F: female; M: male; N/A: not available; WBC: white blood cell count; dm: double mutant. ¹The nucleotide sequence variations are designated according to the recommendations of the Human Genome Variation Society (HGVS, <http://www.hgvs.org/mutnomen/>). Numbering of nucleotides is done by using the first base of the translated part of the gene as nucleotide 1. Transcripts used as a reference are: NM_005896.2 for *IDH1*, NM_002168.2 for *IDH2*, NM_175629.2 for *DNMT3A* and NM_001127208.2 for *TET2* (National Center for Biotechnology Information). ²The protein changes are theoretically deduced and designated according to the recommendations of the HGVS.

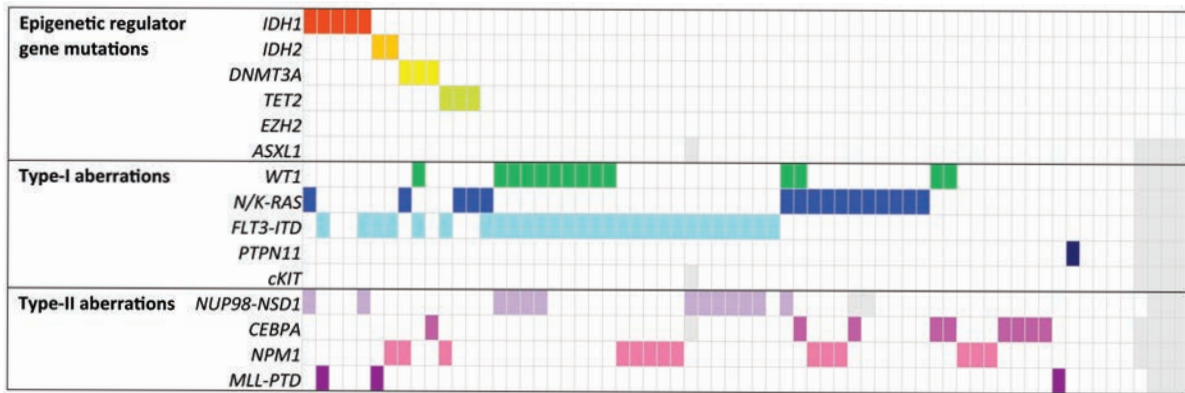


Figure 1. Distribution of somatic mutations in 65 pediatric CN-AML patients. Patients are represented vertically (patient number 1 to number 65 from left to right, 1 column per patient) and molecular aberrations horizontally. Each mutated patient is represented by a colored rectangle, a wild-type patient by a white rectangle and when data are not available due to lack of patient material, the rectangle is gray. *CEBPA* is considered mutated in case of a double mutation only.

tions appeared to be mutually exclusive (Figure 1) and no mutations were identified in *EZH2* or *ASXL1*. The number of patients with a mutation was too small to allow for survival analysis. The specifics of the identified aberrations and the main clinical and genetic features of the patients carrying an epigenetic regulator gene mutation are summarized in Table 1. The epigenetic regulator gene mutations co-occurred with well-known type-I/II aberrations (Figure 1). Out of 13 patients with 10 epigenetic regulator gene mutation also carried a *FLT3-ITD* ($n=6$) or *RAS* mutation ($n=4$), and 6 of 13 patients were found to have a *CEBPA* double mutation ($n=1$), *NPM1* mutation ($n=3$), or *NUP98-NSD1* translocation ($n=2$). Overall, epigenetic regulator gene mutations were shown to co-exist with both a type-I and type-II driver aberration in 7 of 13 patients.

In this study of a substantial pediatric CN-AML cohort, we have identified recurrent somatic mutations in the epigenetic regulator genes *IDH1*, *IDH2*, *DNMT3A* and *TET2* in 13 of 65 cases (20%). *IDH1/2* mutations occurred significantly more often in pediatric CN-AML than in previously reported pediatric AML cohorts with patients carrying various cytogenetic aberrations ($P=0.025$).¹² Although the aberration frequency of epigenetic regulator gene mutations is relatively high for a pediatric AML cohort, the prevalence is still evidently lower in pediatric CN-AML than in adult CN-AML. In addition, within adult AML, *IDH2*, *ASXL1* and *TET2* mutations are significantly more prevalent in elderly patients, suggesting an increasing prevalence of these mutations as a function of age.^{3,4,6} A recent study from Welch *et al.* identified *DNMT3A*, *IDH1/2*, *TET2*, *ASXL1* and *NPM1* mutations as possible major initiating or driver mutations in CN-AML, rather than co-operating events acquired at a later stage of clonal evolution.¹⁵ However, we found epigenetic regulator gene mutations in only 20% of our pediatric CN-AML cohort, and in addition, these mutations often co-occurred with other type-I/II aberrations thought to have leukemia driving capabilities, such as *NUP98-NSD1* and *NPM1*. This suggests that there might be other, as yet unidentified driver mutations in pediatric AML, reflecting potential differences in pathophysiology between childhood and adult AML. Future clonal evolution studies of pediatric CN-AML might lead to a better

understanding of the initiating and co-operating events in this disease.

Mutations in *ASXL1* and *EZH2* were absent in our pediatric CN-AML cohort. This corresponds to literature reports that *ASXL1* and *EZH2* mutations in childhood AML are very rare. *EZH2* mutations seem to be highly uncommon in pediatric as well as in adult AML, in contrast to the high prevalence observed in other myeloid malignancies such as adult myelodysplastic syndrome.⁵

In summary, we identified epigenetic regulator gene mutations to be mutually exclusive and recurrent, but infrequent in pediatric CN-AML. *IDH1/2* aberrations were more frequent in pediatric CN-AML than in published series of other cytogenetic AML subgroups. The frequency of epigenetic regulator gene mutations is lower in pediatric than in adult CN-AML which underlines the difference in pathophysiology between the two. While there is currently insufficient solid rationale for routine screening of epigenetic regulator gene mutations in newly diagnosed pediatric CN-AML patients, new agents are emerging that may make screening more therapeutically appealing.

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