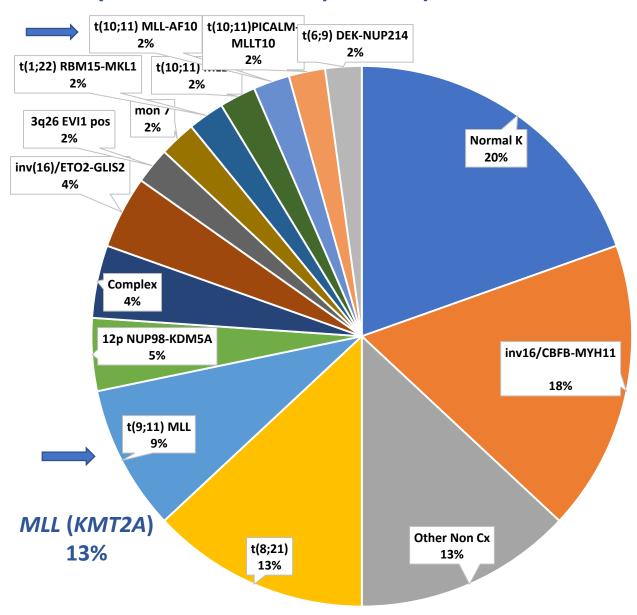
Myechild01

UK-France clinical trial
in Children with Acute Myeloid Leukemia
French Cytogenetic Data
on September 9th 2019
and
New cytogenetic stratification

Wendy CUCCUINI, MD, PhD (hôpitaux Saint-Louis & Robert Debré, Paris) wendy.cuccuini@aphp.fr

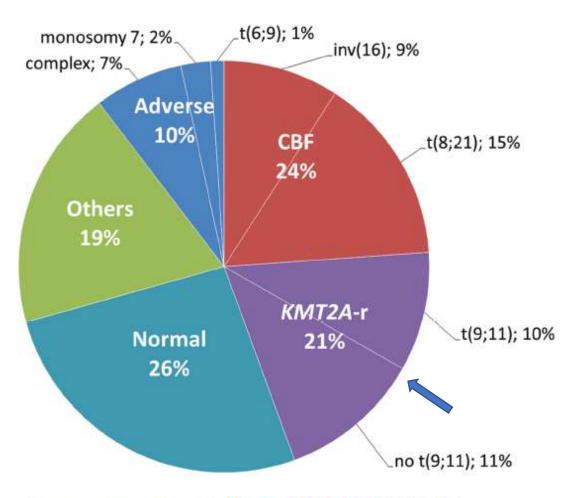
Marina LAFAGE ,MD, PhD (hôpital Timone Enfants, Marseille) marina.lafage@ap-hm.fr

Myechild01 46 French pts on Sept 9th 2019



ELAM02 n= 385 pts

Total cohort (0-18y)



Marceau-Renaut et al. HemaSphere (2018) 2:1

APPENDIX 1 - RISK GROUP STRATIFICATION

Cytogenetic and molecular abnormalities

Good Risk cytogenetic and molecular abnormalities

- t(8;21)(q22;q22)/RUNX1-RUNX1T1
- inv(16)(p13q22)/t(16;16)(p13;q22)/CBFB-MYH11
- Mutation of NPM1 without FLT3-ITD
- Double mutation of CEPBA without FLT3-ITD

Intermediate Risk Cytogenetic abnormalities

- t(9;11)(p21;q23)/MLL-MLLT3
- t(11;19)(q23;p13.3)/MLL-MLLT1
- All other MLL rearrangements not classified as high risk
 - All other abnormalities which are neither good or poor risk

Poor risk cytogenetic and molecular abnormalities

- inv(3)(q21q26)/t(3;3)(q21;q26)/abn(3q26)
- -5/del(5q)
- -7
- t(6,9)(p23;q34)/DEK-NUP214
- t(9;22)(q34;q11)/BCR-ABL1
- 12p abnormalities
- t(6,11)(q27;q23)/MLL-MLLT4
- t(4:11)(q21;q23)/MLL-AFF1
- t(10;11)(p11~14;q23)/MLL-MLLT10
- t(5;11)(q35;p15.5)/NUP98-NSD1
- t(7:12)(q36;p13)/MNX1-ETV6
- inv(16)(p13.3q24.3)/CBFA2T3-GLIS2
- FLT3-ITD without NPM1 or CBF

t(10;11)(p11~14;q23) non MLL-MLLT10 ?

Other poor risk categories

- Secondary leukaemia without good risk cytogenetics
- Induction failure after course 1: morphological failure confirmed by flow MRD in Good Risk /Standard Risk patients

MyeChild 01Protocol V2.0, 25-Jan-2018

Diagnosis and management of acute myeloid leukemia in children and adolescents: recommendations from an international expert panel

*Ursula Creutzig,1 *Marry M. van den Heuvel-Eibrink,2 Brenda Gibson,3 Michael N. Dworzak,4 Souichi Adachi,5 Eveline de Bont,6 Jochen Harbott,7 Henrik Hasle,8 Donna Johnston,9 Akitoshi Kinoshita,10 Thomas Lehrnbecher,11 Guy Leverger,12 Ester Mejstrikova,13 Soheil Meshinchi,14 Andrea Pession,15 Susana C. Raimondi,16 Lillian Sung,17 Jan Stary,18 Christian M. Zwaan,2 †Gertjan J. L. Kaspers,19 and †Dirk Reinhardt,1 on behalf of the AML Committee of the International BFM Study Group

Table 4. Genetically defined prognostic groups in pediatric AML

| Prognosis14,15,22,27 | Genetics |
|----------------------|--|
| Favorable | t(8;21)(q22;q22)/RUNX1-RUNX1T1 |
| | inv(16)(p13.1q22) or t(16;16)(p13.1;q22)/CBFB-MYH11 |
| | t(15;17)(q22;q21)/PML-RARA* |
| | Molecular (in CN-AML) |
| | NPM1-mutated AML |
| | CEBPA double mutation |
| | t(1;11)(q21;q23)/MLL-MLLT11(AF1Q) |
| | GATA1s† |
| Intermediate‡ | Cytogenetic abnormalities not classified as favorable or adverse§ |
| Adverse | -7, -5 or del(5q) |
| | inv(3)(q21q26.2) or |
| | t(3;3)(q21;q26.2)/RPN1-MECOM(EVI1-MDS1-EAP) |
| | t(6;9)(p23;q34)/DEK-NUP214 |
| | t(7;12)(q36;p13)/ETV6(TEL)-HLXB9(MNX1) |
| | t(4;11)(q21;q23)/MLL-MLLT2(AF4) |
| | t(6;11)(q27;q23)/MLL-MLLT4(AF6) |
| | t(5;11)(q35;p15.5)/NUP98-NSD1 |
| | t(10;11)(p12;q23)/MLL-MLLT10(AF10)¶ |
| | complex karyotype# |
| | WT1mut/FLT3-ITD** |
| | t(9;22)(q34;q11.2)†† |

Frequencies, response rates, and outcome measures should be reported by genetic group, and, if sufficient numbers are available, by specific subsets indicated. *t(15;17)/PML-RARA is treated separately from other AMLs.

†In particular in DS patients and infants with acute megakaryoblastic leukemia, analysis of GATA1s mutations should be included. Identification of GATA1s-associated leukemia in trisomy 21 mosaicism can prevent overtreatment.

‡Includes all AMLs with normal karyotype, except for those included in the favorable subgroup; most of these cases are associated with poor prognosis, but they should be reported separately as they may respond differently to treatment.

§For most abnormalities, adequate numbers have not been studied to draw firm conclusions on their prognostic significance.

Excluding recurrent genetic aberrations, as defined in the WHO 2008 classification.

¶Results in t(10;11)(p12;q23) are heterogeneous; therefore, intermediate prognosis may also be adequate.

#Three or more chromosome abnormalities in the absence of one of the WHO-designated recurring translocations or inversions.

**There are differences in the risk allocation of FLT3-ITD considering the allelic ratio. ††t(9;22) is rare, but it is included because its poor prognostic impact is known.

Case TNO195 (Caen): t(10;11)(p12;q23) MLL positive: no fusion transcript

- 7 month-old boy
- 24/04/2019: AML-M1, WBC 25x109/L
- Karyotype: 46,XY,t(10;11)(p11.2~12;q23)[13]/46,XY[9]
- FISH MLL positive:

.ish t(10;11)(D10Z1+,3'KMT2A+;5'KMT2A+)[16].nuc ish(KMT2Ax2)(5'KMT2A sep 3'KMT2Ax1)[160/200]

- RT-MLPA and Marshalek's lab: no fusion transcript
- NGS : normal (no mutation)

Question: Intermediate risk assignment at diagnosis?

Myechild01 / CONECT-AML meeting

Novel prognostic subgroups in childhood 11q23/MLL-rearranged acute myeloid leukemia: results of an international retrospective study

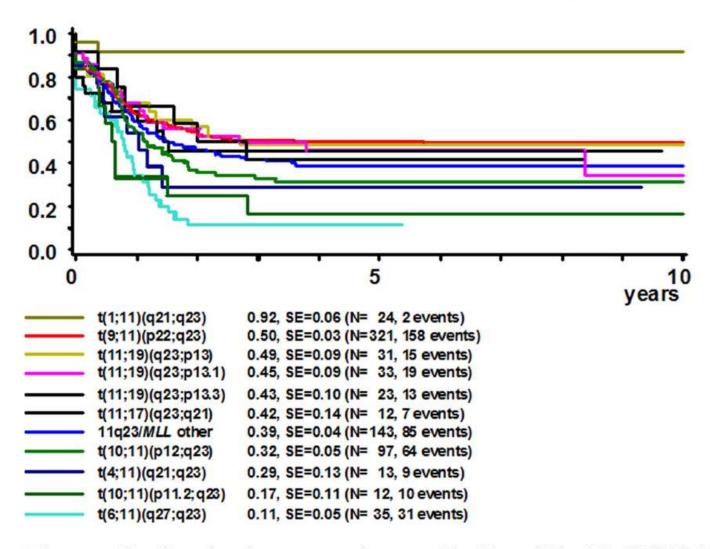


Figure 2. Survival curves for patients with 11q23/MLLrearranged pediatric AML grouped on the basis of different translocation partners. (A) Event-free survival curves.

Novel prognostic subgroups in childhood 11q23/MLL-rearranged acute myeloid leukemia: results of an international retrospective study

Brian V. Balgobind,¹ *Susana C. Raimondi,^{2,3} *Jochen Harbott,⁴ Martin Zimmermann,⁵ Todd A. Alonzo,³ Anne Auvrignon,⁶ H. Berna Beverloo,^{7,8} Myron Chang,⁹ Ursula Creutzig,¹⁰ Michael N. Dworzak,¹¹ Erik Forestier,¹² Brenda Gibson,¹³ Henrik Hasle,¹⁴ Christine J. Harrison,¹⁵ Nyla A. Heerema,^{3,16} Gertjan J. L. Kaspers,¹⁷⁻¹⁹ Anna Leszl,²⁰ Nathalia Litvinko,²¹ Luca Lo Nigro,²² Akira Morimoto,^{23,24} Christine Perot,⁶ Rob Pieters,¹ Dirk Reinhardt,⁵ Jeffrey E. Rubnitz,² Franklin O. Smith,^{3,25} Jan Stary,²⁶ Irina Stasevich,²¹ Sabine Strehl,¹¹ Takashi Taga,^{23,27} Daisuke Tomizawa,^{23,28} David Webb,^{18,29} Zuzana Zemanova,³⁰ †C. Michel Zwaan,^{1,17} and †Marry M. van den Heuvel-Eibrink^{1,17}

Patients with a t(1;11)(q21;q23) showed independent favorable outcome with overall survival at 5 years of $100\% \pm 0\%$, and an event-free survival of $92\% \pm 5\%$. Several rearrangements were identified as predictors of poor clinical outcome, including t(6;11)(q27;q23), t(10;11)(p11.2;q23), t(4;11)(q21;q23), and t(10;11)(p12;q23).

t(9;11)(p22;q23) MLL-AF9/t(11;19)(q23;p13)MLL-ENL/ELL/t(1;11)(q21;q23)MLL-AF1Q Données ELAM02

```
MLL positifs
                                                    (n=95)
                                 t(9;11) 43%
                                                     (n=39) dont 70% isolée
                                 t(11;19) 16%
                                                      (n=12)
                                 t(1;11) 5%
                                                     (n=5)
                                 « MLL autres » 43%
                                                      (n=39)
Event Free Survival
                                             - t(1;11) n=5, 5 yr-EFS 49% ± 15%
                                                Others MLL n=39, 5 yr-EFS 60% ± 22%
    40-
                                            - t(11;19) n=12, 5 yr-EFS 51% ± 8%
    20-
                                              - t(1;11) n=5, 5 yr-OS 80% ± 18%
% Overall Survival

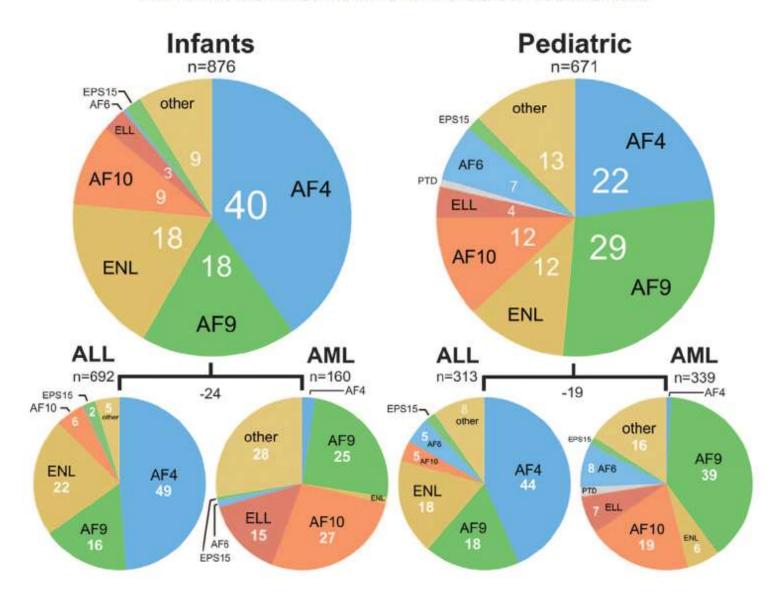
→ t(9;11) n=39, 5 yr-OS 76% ± 7%

                                              Others MLL n=39, 5 yr-OS 70% ± 8%
   60-
                                              - t(11;19) n=12, 5 yr-OS 56% ± 15%
   40-
   20-
```

Time (year)

Christine RAGU, PhD - Ingénieur de Recherche Clinique Hôpital Armand Trousseau - Hôpitaux universitaires Paris Est, AP-HP Service d'Hématologie et d'Oncologie Pédiatrique

MLL recombinome in acute leukemia



MLL recombinome in acute leukemia

| ins(10;11)(p12;q23) | 10p12 | NEBL | Cóser et al. (2010) | AML |
|------------------------|---------|-------------|-----------------------|-----------------------------|
| ins(10;11)(p12;q23q13) | 10p12 | MLLT10/AF10 | Chaplin et al. (1995) | AML, t-AML, ALL, T-ALL, BAL |
| t(10;11)(p11.2;q23) | 10p11.2 | ABI1 | Taki et al. (1998) | AML |

MLL recombinome in acute leukemia

No partner gene fused to 5'-MLL gene 16 t(1;11)(p13.1;q23) 1p13.1 PMF t(6;11)(q27;q23) Not published yet AML 6q27 16 t(9;11)(p13.3;q23) t-ALL 9p13.3 16 t(11;11)(q23;q23.3) 11q23.3 ALL, AML 16 t(11;11)(q23;q24.3) 11q24.3 AML 16

21q22

t(11;21)(q23;q22)

t-ALL

APPENDIX 1 - RISK GROUP STRATIFICATION

Cytogenetic and molecular abnormalities

Good Risk cytogenetic and molecular abnormalities

- t(8;21)(q22;q22)/RUNX1-RUNX1T1
- inv(16)(p13q22)/t(16;16)(p13;q22)/CBFB-MYH11
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- All other abnormalities which are neither good or poor risk

Poor risk cytogenetic and molecular abnormalities

- inv(3)(q21q26)/t(3;3)(q21;q26)/abn(3q26)
- -5/del(5q)
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- t(5;11)(q35;p15.5)/NUP98-NSD1
- t(7;12)(q36;p13)/MNX1-ETV6
- inv(16)(p13.3q24.3)/CBFA2T3-GLIS2
- FLT3-ITD without NPM1 or CBF

And other t(10;11)(p11~14) with MLL rearrangement

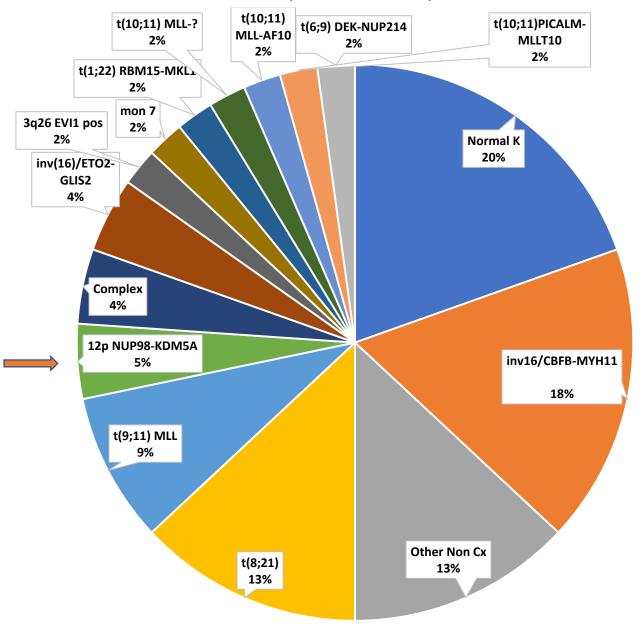
(sept 2019)

Other poor risk categories

- Secondary leukaemia without good risk cytogenetics
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MyeChild 01Protocol V2.0, 25-Jan-2018

46 French patients on Sept 9th 2019

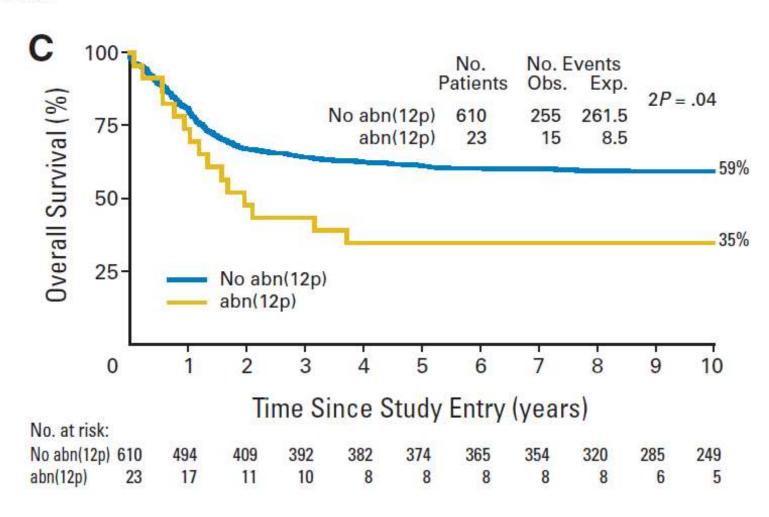


Myechild01

Cytogenetics of Childhood Acute Myeloid Leukemia: United Kingdom Medical Research Council Treatment Trials AML 10 and 12

JOURNAL OF CLINICAL ONCOLOGY

Christine J. Harrison, Robert K. Hills, Anthony V. Moorman, David J. Grimwade, Ian Hann, David K.H. Webb, Keith Wheatley, Siebold S.N. de Graaf, Eva van den Berg, Alan K. Burnett, and Brenda E.S. Gibson



AMKL

Leucémie Aiguë Mégacaryoblastique (AMKL) 4~15% des nouveaux diagnostics LAM pédiatrique.

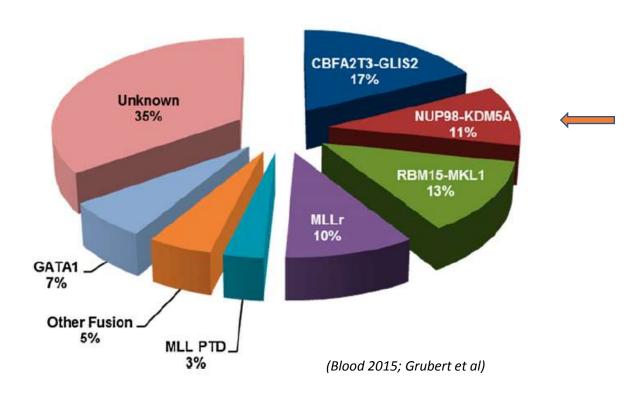
AMKL chez les enfants atteints du **syndrome de Down (DS)** (+21c) sont caractérisée par une mutation **de GATA1** qui coopère avec la trisomie 21, suivie de l'acquisition d'autres mutations somatiques.

Non-DS-AMKL se caractérise par une chimère oncogénique, comprenant des gènes connus pour jouer un rôle dans l'hématopoïèse normale.

CBFA2T3-GLIS2, fusion la plus fréquente identifiée à ce jour dans ce sous-ensemble de patients => mauvais pronostic.



« hauts risques » MyeChild 01



Diagnosis and management of acute myeloid leukemia in children and adolescents: recommendations from an international expert panel

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| Table 4. Genetically | y defined p | rognostic | groups in | pediatric AML |
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| | Molecular (in CN-AML) | | |
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| | t(1;11)(q21;q23)/MLL-MLLT11(AF1Q) | | |
| | GATA1s† | | |
| Intermediate‡ | Cytogenetic abnormalities not classified as favorable or adverse§ | | |
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| | t(7;12)(q36;p13)/ETV6(TEL)-HLXB9(MNX1) | | |
| | t(4;11)(q21;q23)/MLL-MLLT2(AF4) | | |
| | t(6;11)(q27;q23)/MLL-MLLT4(AF6) | | |
| | t(5;11)(q35;p15.5)/NUP98-NSD1 | | |
| | t(10;11)(p12;q23)/MLL-MLLT10(AF10)¶ | | |
| | complex karyotype# | | |
| | WT1mut/FLT3-ITD** | | |
| | t(9;22)(q34;q11.2)†† | | |

Frequencies, response rates, and outcome measures should be reported by genetic group, and, if sufficient numbers are available, by specific subsets indicated.
*t(15;17)/PML-RARA is treated separately from other AMLs.

†In particular in DS patients and infants with acute megakaryoblastic leukemia, analysis of GATA1s mutations should be included. Identification of GATA1s-associated leukemia in trisomy 21 mosaicism can prevent overtreatment.

‡Includes all AMLs with normal karyotype, except for those included in the favorable subgroup; most of these cases are associated with poor prognosis, but they should be reported separately as they may respond differently to treatment.

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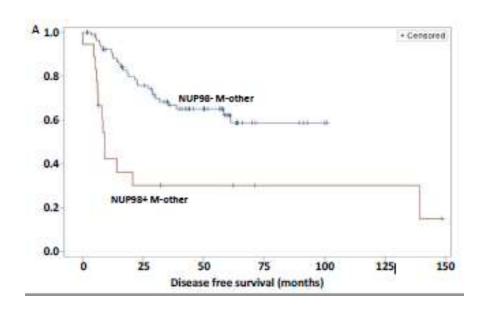
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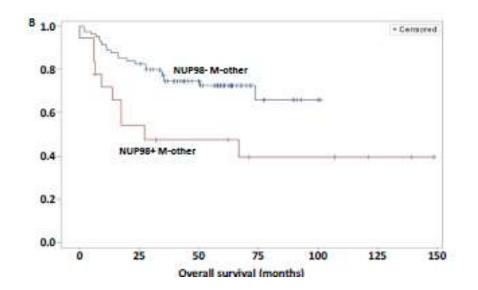
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**There are differences in the risk allocation of FLT3-ITD considering the allelic ratio. ††t(9;22) is rare, but it is included because its poor prognostic impact is known.

NUP98 is rearranged in 3.8% of pediatric AML forming a clinical and molecular homogenous group with a poor prognosis Struski S et al, GFCH, Leukemia 2016





La survie sans maladie à 5 ans est de 30% par rapport à 62% dans les NUP98 négatifs (p <0,001), semblable à d'autres publications (Holllink Ih et al, Blood 2011 et Shiba N et la, Genes Chrom Cancer , 2013)

La survie globale à 5 ans (OS) à 48% significativement plus faible par rapport au groupe témoin à 72% (p <0,001), légèrement mieux que l'OS à 4 ans rapporté par d'autres publications (20% ou 33) (Holllink Ih et al, Blood 2011 et Shiba N et al, Gene Chrom Cancer, 2013)

Après la phase induction :

13/22 patients (72%) sont refractaires,2 patients ont reçu que de la chimiothérapie (rechute à 6 mois et décédés), les autres 11 enfants ont été greffés, donc biais de greffe, les enfants greffés survivent par rapport à ceux traités par la chimiothérapie.

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- t(7;12)(q36;p13)/MNX1-ETV6
- inv(16)(p13.3q24.3)/CBFA2T3-GLIS2
- FLT3-ITD without NPM1 or CBF

Including t(11;12)(p15;p13) / NUP98- KDM5A (JARID1A)

And other NUP98

(sept 2019)

Other poor risk categories

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- Induction failure after course 1: morphological failure confirmed by flow MRD in Good Risk /Standard Risk patients

MyeChild 01Protocol V2.0, 25-Jan-2018

MyeChild 01

Acknowledgments:

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Cytologists (GFHC)

Molecular biologists (GBMHM)

Emmanuelle DELABESSE Audrey GUILMATRE Maxime FERREBEUF

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