Table 1. Results of hemostatic tests of the patient with VWD type 3 and her parents.

Hemostatic assays	Father	Propositus	Mother
Closure time (Col/Epi) (sec)	120	>300	192
Closure time (Col/ADP) (sec)	84	>300	144
APTT (sec - ratio)	35-1.06	73.6-2.23	37-1.1
Prothrombin index (%)	91	93	95
Fibrinogen concentration (g/L)	3.2	3.6	2.7
FVIII:C (IU/ml)	0.79	0.01	0.87
VWF:RCo (IU/ml)	0.99	< 0.05	0.55
VWF:Ag (IU/ml)	0.90	< 0.01	0.47
Platelet count ×10 <sup>9</sup> /L	165	327	210
Blood group	0	0	0

lyzed with GeneScanv3.7 (Applied Biosystems).

We detected a homozygous 11pb deletion c.2574\_2584del (Figure 1) on exon 20 of the VWF gene in the proband DNA. To our knowledge, this mutation has never been previously described or referenced to sequence databases. This c.2574\_2584del results in a premature stop codon: p.Thr859ValfsX2. This frameshift mutation is clearly deleterious, leading to the truncation of the VWF protein or mRNA damage by nonsense mediated mRNA decay, which would explain the total plasma deficiency of VWF. The non-consanguineous parents of the patient were tested for the mutation by sequencing. We found a heterozygous 11pb deletion in the mother and, surprisingly, an absence of this mutation in the father. To test the hypothesis of uniparental disomy (UPD), 16 polymorphic genetic markers mapped to chromosome 12 were investigated. Every marker indicated a homozygosity of the entire chromosome 12 in the proband, consistent with maternal isodisomy.

To our knowledge, there has been no previous report of either paternal or maternal unidisomy involved in VWD. Interestingly, according to a recent review,<sup>11</sup> UPD of chromosome 12 has never been involved in a case of autosomal recessive disease.

This case highlights the need to perform extensive molecular analysis of the *VWF* gene in VWD type 3 patients in order to improve our knowledge of the molecular mechanisms and pathophysiology of the disease. Indeed, the discovery of a deletion indicates a high-risk factor for the occurrence of anti-VWF antibodies and may affect the therapeutic protocol for the patient. Moreover, identifying an association between UPD of chromosome 12 and VWD is important with regard to genetic counseling to inform parents about the negligible recurrence risk during a new pregnancy compared to the usual 25% risk related to an autosomal recessive transmission of type 3 VWD.

## Pierre Boisseau,<sup>1,5</sup> Mathilde Giraud,<sup>1,5</sup> Catherine Ternisien,<sup>2,5</sup> Agnès Veyradier,<sup>4,5</sup> Edith Fressinaud,<sup>4,5</sup> Armelle Lefrancois,<sup>1,5</sup> Stéphane Bezieau,<sup>1,3,5</sup> Marc Fouassier<sup>2,5</sup>

<sup>1</sup>CHU Nantes, Service de Génétique Médicale, Nantes, 44093; <sup>2</sup>CHU Nantes, Centre de Traitement des Hémophiles, Nantes, 44093; <sup>3</sup>Université de Nantes, Faculté de Médecine, Laboratoire Biométadys EA4273, 1 rue Gaston Veil, Nante; <sup>4</sup>Service d'hématologie biologique, Hôpital Antoine Béclère, Clamart; <sup>5</sup>Centre National de Référence de la Maladie de Willebrand, France. Correspondence: M. Fouassier, Centre de Traitement des Hémophiles, Centre Hospitalier Universitaire de Nantes, 9, Quai Moncousu, 44093 Nantes Cedex 1, France. Phone international 033240084049; fax: international 033240084026; E-mail: marc.fouassier@chu-nantes.fr;

Acknowledgments: we would like to thank Christine Thomas, Patricia Talarmain, and Olivier Pichon from the Service de Génétique Médicale for their technical assistance in carrying out this research.

Key words: von Willebrand, type 3, uniparental disomy, chromosome 12.

Citation: Boisseau P, Giraud M, Ternisien C, Veyradier A, Fressinaud E, Lefrancois A, Bezieau S, and Fouassier M. An unexpected transmission of von Willebrand disease type 3: the first case of maternal uniparental disomy 12. Haematologica 2011;96(10):1567-1568. doi:10.3324/haematol.2010.036897

The information provided by the authors about contributions from persons listed as authors and in acknowledgments is available with the full text of this paper at www.haematologica.org.

Financial and other disclosures provided by the authors using the ICMJE (www.icmje.org) Uniform Format for Disclosure of Competing Interests are also available at www.haematologica.org.

## References

- Sadler JE. A revised classification of von Willebrand disease. For the Subcommittee on von Willebrand factor of the Scientific and Standardization Committee of the International Society on Thrombosis and Haemostasis. Thromb Haemost. 1994;71(4):520-5.
- Sadler JE, Budde U, Eikenboom JC, Favaloro EJ, Hill FG, Holmberg L, et al. Working Party on von Willebrand Disease Classification. Update on the pathophysiology and classification of von Willebrand disease: a report of the Subcommittee on von Willebrand Factor. J Thromb Haemost. 2006;4(10):2103-4.
- Mancuso DJ, Tuley EA, Westfield LA, Worrall NK, Shelton-Inloes BB, Sorace JM, et al. Structure of the gene for human von Willebrand factor. J Biol Chem. 1989;264(33):19514-7.
- Weiss HJ, Ball AP, Mannucci PM. Incidence of severe von Willebrand's disease. N Engl J Med. 1982;307(2):127.
- Castaman G, Rodeghiero F, Tosetto A, Cappelletti A, Baudo F, Eikenboom JC, et al. Hemorrhagic symptoms and bleeding risk in obligatory carriers of type 3 von Willebrand disease: an international, multicenter study. J Thromb Haemost. 2006;4(10):2164-9.
- Peake IR, Bowen D, Bignell P, Liddell MB, Sadler JE, Standen G, et al. Family studies and prenatal diagnosis in severe von Willebrand disease by polymerase chain reaction amplification of a variable number tandem repeat region of the von Willebrand factor gene. Blood. 1990;76(3):555-61.
- van Amstel HK and Reitsma PH. Tetranucleotide repeat polymorphism in the vWF gene. Nucleic Acids Res. 1990;18(16):4957.
- Cumming AM, Armstrong JG, Pendry K, Burn AM, Wensley RT. Polymerase chain reaction amplification of two polymorphic simple repeat sequences within the von Willebrand factor gene: application to family studies in von Willebrand disease. Hum Genet. 1992;89(2):194-8.
- Casaña P, Martinez F, Aznar JA, Lorenzo JI, Jorquera JI. Practical application of three polymorphic microsatellites in intron 40 of the human von Willebrand factor gene. Haemostasis. 1995;25(6):264-71.
- Zhang ZP, Deng LP, Blombäck M, Anvret M. Dinucleotide repeat polymorphism in the promoter region of the human von Willebrand factor gene (vWF gene). Hum Mol Genet. 1992;1(9): 780.
- Engel E. A fascination with chromosome rescue in uniparental disomy: Mendelian recessive outlaws and imprinting copyrights infringements. Eur J Hum Genet. 2006;14(11):1158-9.

Minimal residual disease-directed preemptive treatment with azacitidine in patients with NPM1-mutant acute myeloid leukemia and molecular relapse

Therapeutic options are often limited in patients with acute myeloid leukemia (AML) who relapse after inten-

sive chemotherapy or allogeneic hematopoietic stem cell transplantation (HSCT); only a few will achieve longlasting remissions with salvage chemotherapy or a 2<sup>nd</sup> HSCT. Furthermore, relapse treatment with intensive chemotherapy is often associated with significant morbidity and mortality. Therefore, the prevention of hematologic relapse (HR) remains the main goal in the care of patients with AML.

Patients who are at an increased risk of HR can be identified by monitoring minimal residual disease (MRD) using leukemia specific molecular markers. Among many aberrations recently identified, mutations of the *NPM1* gene, coding for the nucleophosmin protein, are the most frequent genetic alterations in AML with normal karyotype (NK), which allows a polymerase chain reaction (PCR)-based quantification of MRD.<sup>1</sup> In contrast to other molecular aberrations, *NPM1* mutations appear to be stable during the disease course, because they are considered to be a primary pathogenetic lesion in AML.<sup>2</sup> The detection of increasing *NPM1*-defined MRD is predictive of impending hematologic relapse<sup>3.5</sup> and can thus guide early preemptive interventions.

Generally, the optimal therapeutic approach for the treatment of MRD should be associated with a reliable efficacy and also be well tolerated. The DNA-methylation inhibitor 5-azacitidine (AZA) seems to be a promising drug for this treatment indication. Indeed, it is active in patients with AML and advanced myelodysplastic syndrome (MDS),<sup>6</sup> has a low rate of extramedullary toxicity and can be administered on an outpatient basis.

We report for the first time a notable number of patients (n=10) with NK-AML and NPM1 mutation (NPM1+) who underwent preemptive treatment with

Table 1. Patient and treatment characteristics.

	Median (range)	
Age in years	49 (33-68)	
	N. (%)	
Sex		
Male	5 (50)	
Female	5 (50)	
AML subtype according to the French–American–British (FAB) classification FAB M1 1		
FAB M2	1 4	
FAB M4	1	
FAB M5	2	
Unclassified	2	
Karyotype		
normal	10 (100)	
Molecular markers NPM1 +/FLT3 ITD+ NPM1 +/FLT3 ITD-	3 (30) 7 (70)	
Remission status prior to molecular relapse		
1 <sup>st</sup> CR	7 (70)	
2 <sup>nd</sup> CR	3 (30)	
Pretreatment Conventional chemotherapy (Induction/consolidation) autologous HSCT Allogeneic HSCT	5 (50) 2 (20) 3 (30)	
Time from last therapy to MRD		
Persistent MRD after last therapy	3 (30)	
MRD recurrence after $\leq 6$ months	3 (30)	
≥6 months	4 (40)	

AZA to avoid HR (Table 1). All patients were in 1<sup>st</sup> or 2<sup>nd</sup> complete remission (CR) after intensive pretreatment with conventional chemotherapy, autologous or allogeneic HSC but displayed molecularly detectable MRD consistent with imminent relapse. One of these patients was discussed as a case report in 2010, however only with a short follow up; this has now been extended.<sup>7</sup>

According to our institutional MRD guidelines, screening was routinely performed during the disease course by using sequential real-time PCR specific for NPM1 mutants A, B, and D in bone marrow and peripheral blood samples as described in recent studies.<sup>47</sup> In cases of molecular relapse or persistent MRD defined as an increase or a persistence of NPM1/ABL ratio of more than 1% in the bone marrow after the last therapy, preemptive treatment with AZA was initiated at a dose of 75 mg/m²/day s.c. on days 1-7 every 28 days. Two patients received dose-modified therapy (100 mg/day, days 1-5). Molecular response was defined as a minimum of 1-log MRD reduction compared to the baseline MRD value before treatment initiation.

Patients started treatment of MRD with AZA at a median NPM1/ABL ratio of 194% (range 3-7129%) in the bone marrow. The median time from last therapy to molecular relapse was seven months. At this time point all patients were still in CR with a median neutrophil and platelet count of 3.1×10<sup>9</sup>/L and 137×10<sup>9</sup>/L, respectively. A median of 5 cycles were given (range 2-12 cycles) and were usually well tolerated. The most frequent side effect was myelosuppression with reversible neutropenia and thrombocytopenia grades 3/4 in 80% and 40% of patients, respectively. Although similar results were reported in the AZA001 study,<sup>6</sup> these patients had a manifest active disease, whereas in our study they were treated for MRD, being otherwise not impaired by the imminent disease recurrence. Therefore, patients undergoing AZA treatment for MRD should be monitored closely to avoid a reduction in their quality of life due to cytopenia associated complications. Nevertheless, in future trials the dose of AZA might be further reduced possibly without loosing its efficiency, as recently described by Lima et al.8

After a median follow-up time of 10 months (range 2-

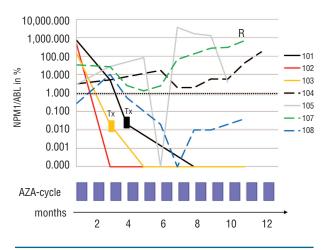


Figure 1. MRD course of 7 patients with molecular response to single agent azacitidine. Tx: date of allogeneic HSCT; R: hematologic relapse. MRD monitoring in bone marrow samples is represented by the continuous lines; dashed lines reflect MRD monitoring from peripheral blood samples. 12 months) from initiation of AZA treatment only 3 patients developed a hematologic relapse. A molecular response with an at least 1-log decrease in the MRD level was observed in 7 of the 10 (70%) patients. Five of them responded within 3 cycles, another 2 patients responded after cycle 4 and 5. However, some patients had only a temporary response consistent with the opinion that AZA treatment might only have delayed the time to hematologic relapse in some patients (Figure 1). A stable course of MRD was documented in one patient and early progressive increase of the NPM1+ clone despite AZA treatment was observed in 2 patients.

Interestingly, the 2 patients with the highest NPM1+ values (>1000%) before initiation of AZA treatment ultimately relapsed after 4 and 6 cycles, respectively. This might reflect the existence of a threshold above which a patient is not likely to obtain long-term benefit from preemptive AZA application.

Among the 7 responders there were 3 patients suffering from molecular relapse after previous allogeneic SCT. One of these showed complete clearance of NPM1+ after 4 cycles. We, therefore, speculate that AZA, besides its direct effects on leukemic cells, might also influence the donor immune system and reconstitute the graft-*versus*-leukemia (GvL) effect as suggested recently.<sup>9</sup>

Taken together, the results of the present analysis are promising, especially when considering the published data describing the natural disease course in NPM1+ AML, with disease progression to full clinical relapse within a median of eight weeks after detection of MRD.<sup>4,5,10</sup> In contrast to these data, we found 7 of 10 patients to be still in complete hematologic remission after a median follow-up time of ten months, suggesting a potential efficacy of AZA in NPM1-defined treatment of MRD. Especially elderly patients and those with a history of serious treatment-related toxicities may benefit from this well tolerated treatment approach. Furthermore, for patients with no available matched donor at the time of molecular relapse, this strategy might be preferable to bridge to subsequent allogeneic HSCT.

Further investigations are necessary to define the patient population who could benefit most from this treatment approach. Since our study included only a relatively small number of patients, prospective clinical trials addressing the impact of MRD-directed therapy with AZA in NPM1 mutant AML are warranted.

Katja Sockel,<sup>1</sup> Martin Wermke,<sup>1</sup> Jörgen Radke,<sup>1</sup> Alexander Kiani,<sup>2</sup> Markus Schaich,<sup>1</sup> Martin Bornhäuser,<sup>1</sup> Gerhard Ehninger,<sup>1</sup> Christian Thiede<sup>1</sup> and Uwe Platzbecker<sup>1</sup>

<sup>1</sup>Medizinische Klinik und Poliklinik I, Universitätsklinikum "Carl Gustav Carus" Dresden; <sup>2</sup>Klinikum Bayreuth, Germany. Correspondence: Uwe Platzbecker, Universitätsklinikum Carl-Gustav-Carus, Medizinische Klinik I, Fetscherstraße 74, 01307 Dresden, Germany; Phone: international +49.351.4582583; Fax: international +49.351.4584373; E-mail: uwe.platzbecker@uniklinikum-dresden.de Key words: AML, nucleophosmin, NPM1, MRD, azacitidine. Citation: Sockel K, Wermke M, Radke J, Kiani A, Schaich M, Bornhäuser M, Ehninger G, Thiede C, and Platzbecker U. Minimal residual disease-directed preemptive treatment with azacitidine in patients with NPM1-mutant acute myeloid leukemia and molecular relapse. Haematologica 2011; 96(10):1568-1570. doi:10.3324/haematol.2011.044388

The information provided by the authors about contributions from persons listed as authors and in acknowledgments is available with the full text of this paper at www.haematologica.org.

Financial and other disclosures provided by the authors using the ICMJE (www.icmje.org) Uniform Format for Disclosure of Competing Interests are also available at www.haematologica.org.

## References

- Gorello P, Cazzaniga G, Alberti F, Dell'Oro MG, Gottardi E, Specchia G, et al. Quantitative assessment of minimal residual disease in acute myeloid leukemia carrying nucleophosmin (NPM1) gene mutations. Leukemia. 2006;20(6):1103-8.
- Grimwade D, Vyas P, Freeman S. Assessment of minimal residual disease in acute myeloid leukemia. Curr Opin Oncol. 2010;22(6): 656-63.
- Bacher U, Badbaran A, Fehse B, Zabelina T, Zander AR, Kröger N. Quantitative monitoring of NPM1 mutations provides a valid minimal residual disease parameter following allogeneic stem cell transplantation. Exp Hematol. 2009;37(1):135-42.
- 4. Shayegi N, Bornhäuser M, Schaich M, Schetelig J, Kramer M, Platzbecker U, et al. Quantitative monitoring of mutated NPM1 enables early detection of impending relapse in patients with acute myeloid leukemia following conventional chemotherapy and allogeneic stem cell transplantation. Bone marrow transplantation (EBMT Annual Meeting Abstracts). 2011. abstract 1158.
- Schnittger S, Kern W, Tschulik C, Weiss T, Dicker F, Falini B, et al. Minimal residual disease levels assessed by NPM1 mutation-specific RQ-PCR provide important prognostic information in AML. Blood. 2009;114(11):2220-31.
- Fenaux P, Mufti GJ, Hellstrom-Lindberg E, Santini V, Finelli C, Giagounidis A, et al. Efficacy of azacitidine compared with that of conventional care regimens in the treatment of higher-risk myelodysplastic syndromes: a randomised, open-label, phase III study. Lancet Oncol. 2009;10(3):223-32.
- Wermke M, Thiede C, Kiani A, Ehninger G, Bornhäuser M and Platzbecker U. Successful treatment of molecular relapse in NPM1positive AML using 5-azacytidine. Leukemia. 2010;24(1):236-7.
- de Lima M, Giralt S, Thall PF, de Padua Silva L, Jones RB, Komanduri K, et al. Maintenance therapy with low-dose azacitidine after allogeneic hematopoietic stem cell transplantation for recurrent acute myelogenous leukemia or myelodysplastic syndrome: a dose and schedule finding study. Cancer. 2010;116(23):5420-31.
- Goodyear O, Agathanggelou A, Novitzky-Basso I, Siddique S, McSkeane T, Ryan G, et al. Induction of a CD8+ T-cell response to the MAGE cancer testis antigen by combined treatment with azacitidine and sodium valproate in patients with acute myeloid leukemia and myelodysplasia. Blood. 2010;116(11):1908-18.
- Hokland P, Ommen HB. Towards individualized follow-up in adult acute myeloid leukemia in remission. Blood. 2011;117(9): 2577-84.