

# Hypermethylation of the *FANCC* and *FANCL* promoter regions in sporadic acute leukaemia

C.J. Hess<sup>a,\*</sup>, N. Ameziane<sup>b,\*</sup>, G.J. Schuurhuis<sup>a</sup>, A. Errami<sup>c</sup>, F. Denkers<sup>a</sup>, G.J.L. Kaspers<sup>d,f</sup>, J. Cloos<sup>d</sup>, H. Joenje<sup>b</sup>, D. Reinhardt<sup>e</sup>, G.J. Ossenkoppele<sup>a</sup>, C.M. Zwaan<sup>f,g</sup> and Q. Waisfisz<sup>a,\*\*</sup>

<sup>a</sup> Department of Hematology, VU University Medical Center, Amsterdam, The Netherlands

<sup>b</sup> Department of Clinical and Human Genetics, VU University Medical Center, Amsterdam, The Netherlands

<sup>c</sup> MRC-Holland BV, Amsterdam, The Netherlands

<sup>d</sup> Pediatric Hematology/Oncology, VU University Medical Center, Amsterdam, The Netherlands

<sup>e</sup> AML-BFM Study Group, Hannover, Germany

<sup>f</sup> Dutch Childhood Oncology Group, Den Haag, The Netherlands

<sup>g</sup> Department of Pediatric Oncology, Erasmus Medical Center/Sophia Children's Hospital, Rotterdam, The Netherlands

**Abstract.** *Objective:* Inactivation of the FA-BRCA pathway results in chromosomal instability. Fanconi anaemia (FA) patients have an inherited defect in this pathway and are strongly predisposed to the development of acute myeloid leukaemia (AML). Studies in sporadic cancers have shown promoter methylation of the *FANCF* gene in a significant proportion of various solid tumours. However, only a single leukaemic case with methylation of one of the FA-BRCA genes has been described to date, i.e. methylation of *FANCF* in cell line CHR1-288. We investigated the presence of aberrant methylation in 11 FA-BRCA genes in sporadic cases of leukaemia.

*Methods:* We analyzed promoter methylation in 143 AML bone marrow samples and 97 acute lymphoblastic leukaemia (ALL) samples using methylation-specific multiplex ligation-dependent probe amplification (MS-MLPA). Samples with aberrant methylation were further analyzed by bisulphite sequencing and tested for mitomycin C sensitivity using Colony Forming Units assays.

*Results:* MS-MLPA showed promoter methylation of *FANCC* in one AML and three ALL samples, while *FANCL* was found methylated in one ALL sample. Bisulphite sequencing of promoter regions confirmed hypermethylation in all cases. In addition, samples with hypermethylation of either *FANCC* or *FANCL* appeared more sensitive towards mitomycin C in Colony Forming Units assays, compared to controls.

*Conclusion:* Hypermethylation of promoter regions from FA-BRCA genes does occur in sporadic leukaemia, albeit infrequently. Hypermethylation was found to result in hypersensitivity towards DNA cross-linking agents, a hallmark of the FA cellular phenotype, suggesting that these samples displayed chromosomal instability. This instability may have contributed to the occurrence of the leukaemia. In addition, this is the first report to describe hypermethylation of *FANCC* and *FANCL*. This warrants the investigation of multiple FA-BRCA genes in other malignancies.

**Keywords:** Sporadic acute leukaemia, Fanconi anaemia, methylation, MS-MLPA

## 1. Introduction

The FA-BRCA pathway is thought to be essential for specific DNA repair processes [1,2]. Cells, which are defective for one of the FA-BRCA genes, display genomic instability and are hypersensitive to DNA

cross-linking agents. This cellular phenotype is associated with increased cancer risk as observed in patients with Fanconi anaemia (FA) [OMIM#227650]. These patients are characterized by a diversity of clinical symptoms including an increased risk to develop malignancies in particular myelodysplastic syndrome and acute myeloid leukaemia (AML), but also solid tumours.

In the past years a number of papers have reported on the potential role of acquired disturbances in the FA-pathway in sporadic cancers [3,4]. Hypermethylation of the *FANCF* promoter has been described to oc-

\*These authors contributed equally to this work.

\*\* Corresponding author: Quinten Waisfisz, PhD, Department of Hematology, BR248, VU University Medical Center, De Boelelaan 1117, 1081 HV Amsterdam, The Netherlands. Tel.: +31 02 4447409; Fax: +31 20 4442601; E-mail: q.waisfisz@vumc.nl.

cur in various tumour types such as those of the ovaries [5], cervix [6], lungs and oral cavity [7]. Also in AML the occurrence of inherited and somatic abnormalities in the FA-BRCA genes has been studied [8–11]. Only in a small proportion of cases data was provided showing that these abnormalities were indeed associated with functional inactivation of the FA-BRCA pathway. In an adult AML sample functional abnormality was suggested but in this case the molecular mechanism remained unidentified [10]. *FANCF* was found hypermethylated in the leukaemic CHR288 cell line resulting in hypersensitivity towards DNA cross-linking agents [9]. However, 36 additional AML patient samples appeared to be negative for *FANCF* hypermethylation suggesting that this is not a common event in leukaemia. This was recently substantiated by Meyers et al., who found no evidence for hypermethylation of either the *FANCF* or *FANCB* gene in a total of 33 AML and 48 acute lymphoblastic leukaemia (ALL) samples [12].

Here we report results from a study exploring aberrant methylation of 11 FA-BRCA genes (*FANCA*, *FANCB*, *FANCC*, *FANCD1/BRCA2*, *FANCD2*, *FANCE*, *FANCF*, *FANCG*, *FANCI/BRIP1*, *FANCL* and *FANCM*) in sporadic acute leukaemia, using the recently described Methylation Specific (MS)-MLPA [13] technique.

## 2. Materials and methods

### 2.1. Sample characteristics

Samples were obtained from the cell banks of the VU medical center, the AML-BFM Study Group and the DCOG. Snap frozen cell pellets of bone marrow samples obtained from newly diagnosed adult AML patients ( $n = 119$ , median blast cell percentage was 66%, range 4–97%) together with 15 adult ALL (B-cell precursor (BCP)-ALL;  $n = 10$ , T-cell ALL;  $n = 5$ , median blast cell percentage of adult ALL samples was 85%, range 10–99%) samples were randomly selected. Additionally, 20 paediatric AML samples with a complex karyotype, defined as 2 or more random aberrations, or loss of chromosome 5 or 7, or the long arms of these chromosomes, were studied, as well as 4 biphenotypic leukaemic samples. For the analysis of 82 newly diagnosed paediatric ALL patients (BCP-ALL;  $n = 67$ , T-cell ALL;  $n = 15$ , median blast cell percentage of paediatric ALL samples was 94%, range 16–100%) cytospin slides were selected at random. All specimens were collected with informed consent ac-

ording to institutional guidelines and in accordance with the Helsinki Declaration of 1975. Control CD34+ cells were derived from healthy volunteers.

### 2.2. DNA isolation and treatment

Genomic DNA from cell pellets was isolated using QIAamp<sup>®</sup> DNA Blood Minikit (Qiagen, Valencia, CA, USA) according to the manufacturer's recommendations. DNA from cytospin slides was isolated using phenol, chloroform and isoamylalcohol (PCI; 25:24:1).

Methylated DNA was obtained by treating control genomic DNA with SssI CpG methyltransferase (M.SssI, New England Biolabs) according to the manufacturer's recommendations.

### 2.3. MS-MLPA

MS-MLPA reagents were kindly provided by MRC-Holland, Amsterdam, The Netherlands ([www.mlpa.com](http://www.mlpa.com)). Target DNA was diluted in TE buffer (10 mM Tris-HCl, pH 8.5, 1 mM EDTA) to a concentration of 100 ng/ $\mu$ l in a total volume of 5  $\mu$ l and denatured for 10 min at 98°C. MS-MLPA was performed as previously described [13]. Probes were designed such that these were targeted to the CpG islands within the promoter regions of 11 FA-BRCA genes and contained a recognition site for the methylation-sensitive restriction enzyme *HhaI*. The probe mix contained single probes directed to *FANCA*, *FANCD2*, *FANCG*, two probes directed to different sites of *FANCB*, *FANCC*, *FANCD1/BRCA2*, *FANCE*, *FANCI/BRIP1*, *FANCL* and *FANCM* and three probes directed to different sites of *FANCF*. In addition to the 11 FA-BRCA genes, probes were included for *BRCA1*, *ATM*, *MLH1*, *XPA*, *WRN*, *BLM* and *NBS1*. For quantification of the levels of methylation seven control probes lacking *HhaI* sites were also included. Probe sequences are shown in Table 1.

### 2.4. Sodium bisulphite sequencing

One  $\mu$ g of genomic DNA was converted by sodium bisulphite using the EZ DNA Methylation Gold kit<sup>™</sup> (ZYMO Research Corporation, Orange, CA) to confirm the aberrant methylation status. Bisulphite-treated genomic DNA was amplified by PCR using primers *FANCC-F* 5'-TTTTATATTTTGAATAGAATATGGAAGAAG-3' and *FANCC-R* 5'-CAATACATTCTAAAACCTAACTAAC-3' for *FANCC*, or *FANCL-F*

Table 1  
FA-BRCA probe mix

Size (bp)	Gene	Chr pos	Probe 1	Probe 2
130	*FLJ22301	01q44	GGTGAACCTGGCCACAGCTCAC	CTGGAACAGCCACAATGTCTGCCCTTAGAGAAGAACCATG
136	FANCF	11p15	GCGAAAGGAAGCGGAGACGTTTCAT	GACTGGCATCATCTCGCAGTGGTTCGGAAATCTCGGTACATG
142	BRCA1	17q21	CCCTTGGTTTCCGTGGCAACGGA	AAAGCGCGGGAATTACAGATAAAATTAACCTGCGACT
148	BRCA2	13q12.3	CGGGTTAGTGGTGGTGGTGGTGGT	GGGACGAGCGCGTCTTCCGCAGTCCCAGTCCAGCGTGGCATG
154	*MLH1	03p22.1	GGAGGGAGGCCTGAAGTTGATTAGATCCA	AGACAATGGCACCGGATCAGGGTAAGTAAAACCTCAAAGTAG
160	ATM	11q23	GCGGAGACCGCGTGATACTGGAT	<u>GCGC</u> ATGGGCATACCGTGTCTGCGGCTGCTTGCCATG
166	MLH1	03p22.1	CGTTGAGCATCTAGACGTTTCCCTGGCTCT	TCTGGCGCCAAAATGTGCTTCTGTTGGCAGGGGTTATTC
175	*BRCA2	13q12.3	CAGCTGGCTTCAACTCCAATAATATTC	AGAGCAAGGGCTGACTCTGCCGCTGTACCAATCTCTGTAAAAGAAT
184	FANCB	Xp22.31	CCAGACCCAGGCGTCCGCAAT	GGATTGGGCGGTGCGGCGCGCTTCTGTCCGCCTCATG
211	FANCB	Xp22.31	CCGGACCCGGAAGCCGCTCT	GAGGCCCGGGACCGA <u>GCGC</u> CGTGTGCAGGCATG
220	FANCE	06p21.3	CGCGTCCGGTGTGCCATGCC	GGGGCACGGGTGCC <u>GCGC</u> CGCCCTACTCTGGT
229	*RELA	11q13	GCTTGTAGGAAAGACTGCCG	GGATGGCTTCTATGAGGCTGAGCTCTGCCCG
238	FANCF	11p15	CTGCTCTCTCT <u>GCGC</u> CTGCTGGA	GAACCGGGCCCTCGGGGATGCAGCTCGTTACCACCTGGCATG
247	FANCF	11p15	GTCGCCGTCTCAAGGTGAAAGCGGAA	GTAGGGCCTT <u>GCGC</u> ACCTCATGGAATCCCTTCTGCAGCACCTCATG
256	FANCM	14q21.3	CTGCCGAGACTCAT <u>GCGC</u> ATTAT	TAAGCGTTACTCTAAATATGGTCCCGGTGCGGTTCCGGCATG
265	XPA	09q22.3	GGCAGGCCACCCGAGCCCT	TAACT <u>GCGC</u> AGCGCTCTCACTCAGAAAGCCGCTGGGTGCATG
274	FANCA	16q24.3	CAGGGAGCCGCCCGGGGCT	GTAG <u>GCGC</u> CAAGGCCATGTCGACTCGTGGG
283	*FANCD2	03p25.3	GGTGTGGCCAAGTGGGGATAAAGA	GAAGAGCAACATCTAATGACCAGTCCATGCTCTGCTCCATG
292	FANCC	09q22.3	CGCCGGGGCTTCC <u>GCGC</u> GAAA	CCGGAAACACTGGAGCAGTACCGACTCCGCTCGCCTAGAA
301	BRCA2	13q12.3	CGGGAGAAGCGTGAAGGACAGATTTGTG	ACCG <u>GCGC</u> GGTTTTTGTGCAGCTTACTCCGGCCAAAAAAGA
310	BRIP1	17q23.2	CTAAGAAGACGGCTTCCGCTCAAAGGA	GGTAAGGATAGGCTCCCTCCTCAGGTTTTCTGCCCATG
319	WRN	08p12	CTTGACTCGGCAGCGGGGAAT	AAAGTTTGCTGATTGGTGTCTAGCTGGATGCCTGGGCATG
328	FANCC	09q22.3	TGACACGTGT <u>GCGC</u> CGCGCGGCT	CCACTGCCGGGCGACCGGGGAAAATCCAAAAAACTCA
337	*ATM	11q23	CAGAGTCAGAGCACTTTTTCCGATGC	TGTTTGATAAAAAATCAGAAACAATGCTTGTGTTGTGGACTACATG
346	BLM	15q26.1	GGCGGGTTCGCCGTACAG <u>GCGC</u>	CGGGAGGGACGCGTATCTCAAAGCCCAATCAGAGTC
355	FANCL	02p14	GCGTCCGAGCGCCAGCGGACT	<u>GCGC</u> ATGTGCAGGACCCAGCAGGTCTAGAGCTTTTCTGTGCATG
364	FANCM	14q21.3	CTGCTGGCAAAG <u>GCGC</u> CTTTGG	AGCTGCCAGGGCTCTGAGGTCGCTCAGTCCGGAGCTCATG
373	FANCD2	03p25.3	CGGTGATGGGCGAGCTTCTTCA	CCGGG <u>GCGC</u> AGTTGCTTCTCTCTGACGTCGCCTC
382	NBS1	08q21	CAACCACCAGGTGGCGGGCAA	<u>GCGC</u> CAAGTCGCACTCCCGCTCATCCAAGGCAGCCCATG
391	*NF1	17q11.2	CTCCCTACCCTGGCCACTGTAACA	GTGGACGAACCTGCCACGGATCCGCAAGCCAAGTGCAGAAGCATG
400	FANCL	02p14	CCATGGCGGTGACGGAAGCGAGCCTGT	T <u>GCGC</u> CAGTGCCCTGCTTCTGCCCCAGAACCCTGCGCATG
409	FANCE	06p21.3	CACCGCCGCTCAGGGAC <u>GCGC</u>	<u>GCT</u> GGAGTCTCCGTTCCCTCAGCCTCTGAGCT
418	WRN	08p12	GCAGCGAGGGCTCCACGCAT	<u>GCGC</u> ACCGCGCGCTGGGCGGGGCTGGATCATG
427	XPA	09q22.3	CCCGGATGACAAGAGAGCAGGTAGTT	AGGCGGTACTCCGTGTCC <u>GCGC</u> ATACCCAGACTCCGCCATG
436	BRIP1	17q23.2	CTCGACTCCA <u>GCGC</u> CAATA	GCCCAGCGAGCTCGACCAATCACCCGCCAAGGCCCATG
445	*TNFRSF7	12p13	GAAAGTCTGTGGAGCCTGCA	GAGCCTTGCTGTACAGTGCCTCCAGGGAGG
454	FANCG	09p13	GCGGTAAGTGGAGACGAGGG <u>GCGC</u>	TCCGTAATCGTCCATCTTCTCTGCTCACTGTGAGC
463	MLH1	03p22.1	CTGCTGAGGTGATCT <u>GCGC</u> CAGA	GCGGAGGAGGTGCTT <u>GCGC</u> CTTCTCAGGCTCTCTCTCATG
472	NBS1	08q21	CATGCCGACCGAGGCGCGT	ATCC <u>GCGC</u> TCGTCTAGCAGCCCCGGTTACGCGGTTGCCATG
481	*CASR	03q21	CCAGTGCCTGTAACAAGTGCCAGATGACT	TCTGGTCCAATGAGAACCACACTCCTGCAITGCCAAGGACATG

Indicated are the size of the expected PCR product in base pairs (bp), corresponding genes, chromosomal location, and probe sequences. In the probe sequences *HhaI* recognition sites are underlined. Control probes for genes lacking *HhaI* sites are indicated by asterisks.

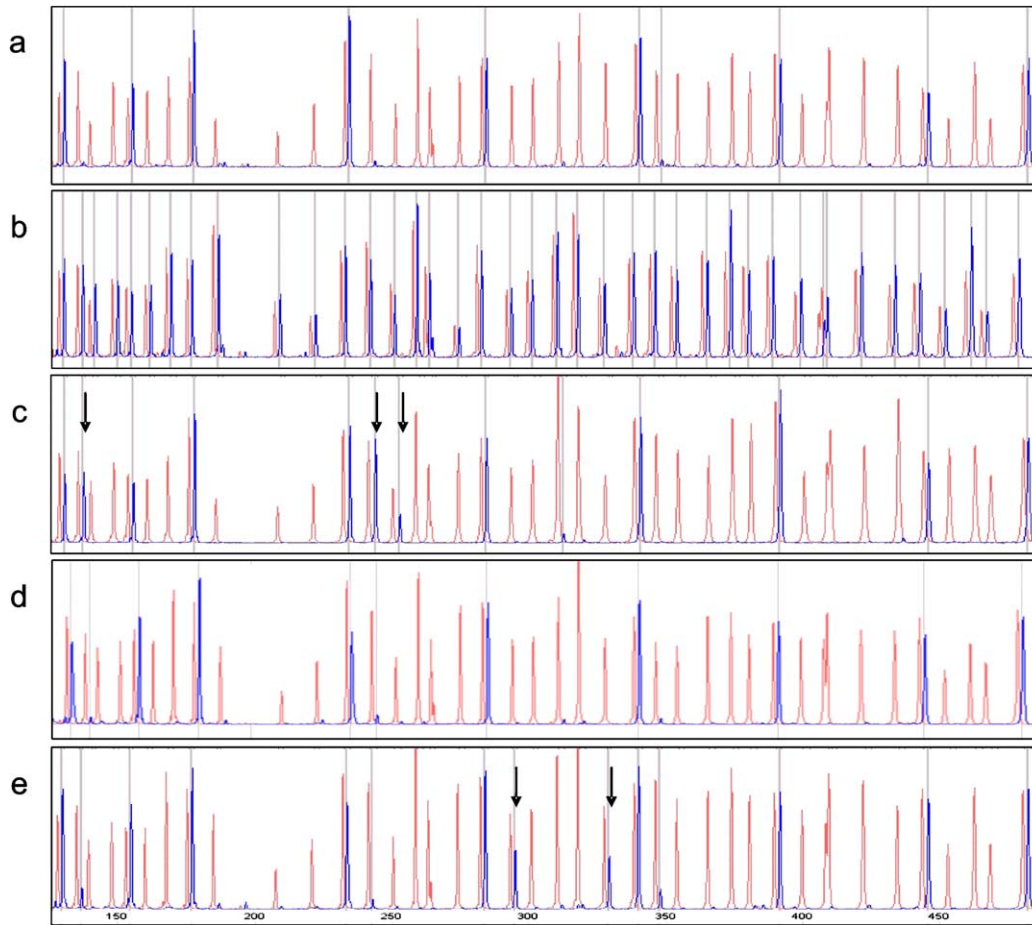


Fig. 1. Detection of aberrant methylation by MS-MLPA. MS-MLPA products were analyzed by capillary electrophoresis (CE). Profiles in red correspond with the undigested samples and blue with digested samples. MS-MLPA profiles are from (a) control genomic DNA without aberrant methylation, (b) SssI CpG methyltransferase treated control genomic DNA showing methylation of all target sequences, (c) genomic DNA derived from the CHR1-288 cell line, which shows *FANCL* methylation (blue peaks indicated by arrows), (d) genomic DNA from an AML sample without methylation and (e) genomic DNA from an AML sample showing *FANCC* methylation (blue peaks indicated by arrows).

5'-TTAGTTTTGTGGATTTGAGGGTAAT-3' and *FANCL*-R 5'-TAAAACAAAACAAAAACACTAAC-3' for *FANCL*. PCR products were subcloned, isolated and analyzed by sequencing.

### 2.5. CFU assay and mitomycin C (MMC) sensitivity

To determine the number of Colony-Forming Units present in the total bone marrow of AML and ALL patients, samples were plated in duplicate in Methocult culture medium (Stemcell Technologies Inc., Vancouver, BC) at a concentration of 40,000, 100,000 and 400,000 cells/well. Colonies were counted after 7 days (37°C, 5% CO<sub>2</sub>, full humidity). MMC sensitivity was assessed by adding various concentrations of MMC (0, 5, 10 and 50 nM) to the cultures. Colonies were ex-

pressed as mean values from duplicate cultures and denoted as a percentage of the number of colonies in the wells without MMC.

## 3. Results

### 3.1. MS-MLPA

Using MS-MLPA with probes directed against 11 FA-BRCA genes we first analyzed 119 unselected adult AML bone marrow samples and 20 paediatric AML samples selected on the basis of an FA-AML like karyotype (complex rearrangements see materials and methods). Aberrant promoter methylation of the *FANCC* gene was detected in a single adult patient with biphenotypic AML (Fig. 1). Methylation was also

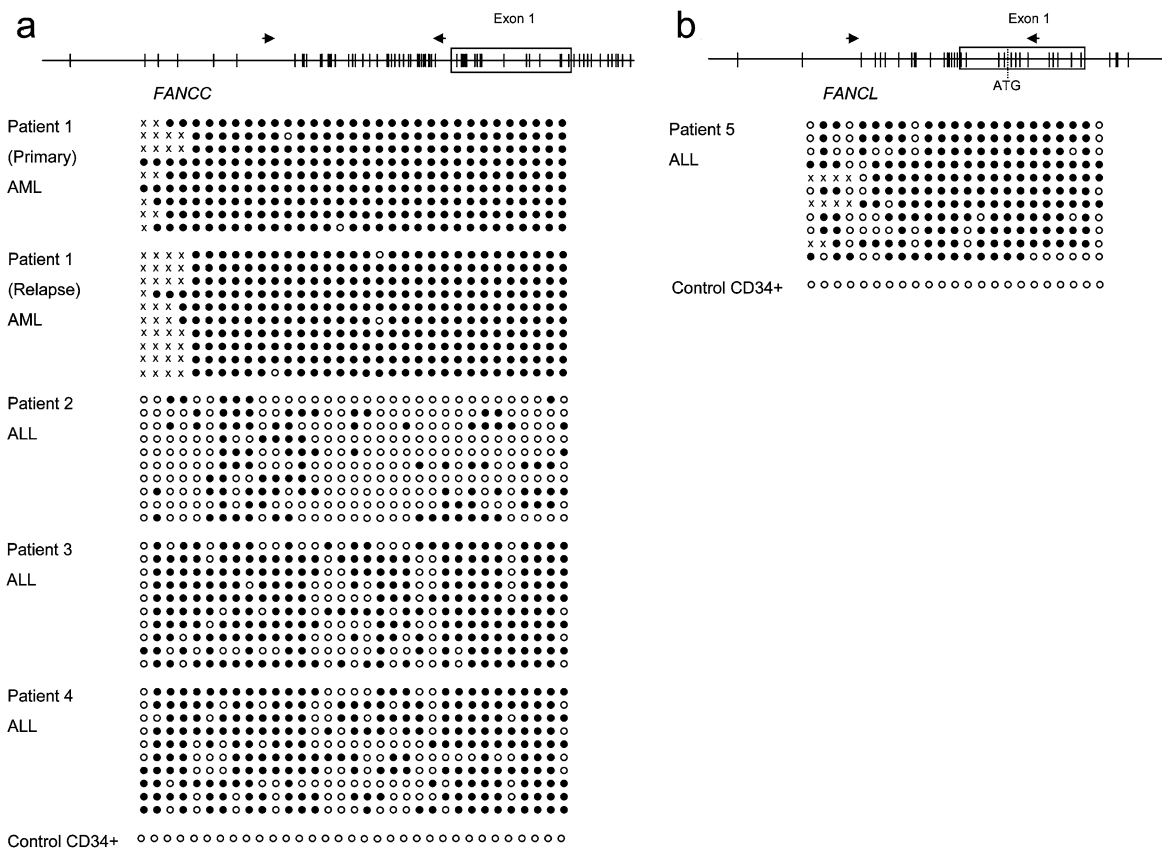


Fig. 2. Bisulphite sequence analysis of the *FANCC* and *FANCL* promoter regions in primary leukaemic samples. (a) Upper part: schematic representation of the *FANCC* gene's promoter region. The 33 assessed CpGs are situated upstream of exon 1, between the arrows; the translation start is in exon 2 (not shown). In the lower parts of the figure each row represents an individually cloned and sequenced allele following sodium bisulfite DNA modification, black and open circles representing methylated and unmethylated CpGs, respectively. Sequence data for a number of CpGs were ambiguous, indicated by an x. Arrows indicate sequences complementary to the primers used (patient 1, adult diagnosed with biphenotypic AML, patients 2, 3 and 4, paediatric patients diagnosed with ALL). (b) Methylation status of the 23 assessed CpGs in the promoter region of the *FANCL* gene, represented as described above. The translation start of the *FANCL* gene is located in the first exon (patient 5, adult diagnosed with ALL).

present in the relapse sample from this patient. To test whether FA-BRCA gene methylation was associated with the specific leukaemic phenotype, four additional biphenotypic AML samples, 15 adult ALL samples and 82 paediatric ALL samples were analyzed. One adult ALL sample showed *FANCL* promoter methylation, while *FANCC* promoter methylation was found in three paediatric ALL samples. All four patients had been diagnosed as having BCP-ALL with a hyperdiploid phenotype. In the biphenotypic subgroup we did not detect additional methylated cases.

### 3.2. Sodium bisulphite sequencing

Sodium bisulphite sequencing confirmed hypermethylation in all cases (Fig. 2). Analysis of the *FANCC*

promoter region from the adult biphenotypic AML sample (patient 1) at diagnosis and the corresponding relapse, showed equally dense methylation patterns. Similarly, *FANCC* hypermethylation was observed in the two paediatric ALL samples (patients 3 and 4). A third sample showed only partial methylation of the *FANCC* promoter region (patient 2). The methylation status of *FANCL* was determined in the adult ALL sample (patient 5) and showed dense methylation (Fig. 2b). No methylation of these genes was found in genomic DNA from control CD34+ cells.

### 3.3. Mitomycin C sensitivity

A CFU assay was performed to evaluate whether hypermethylation was associated with increased sen-

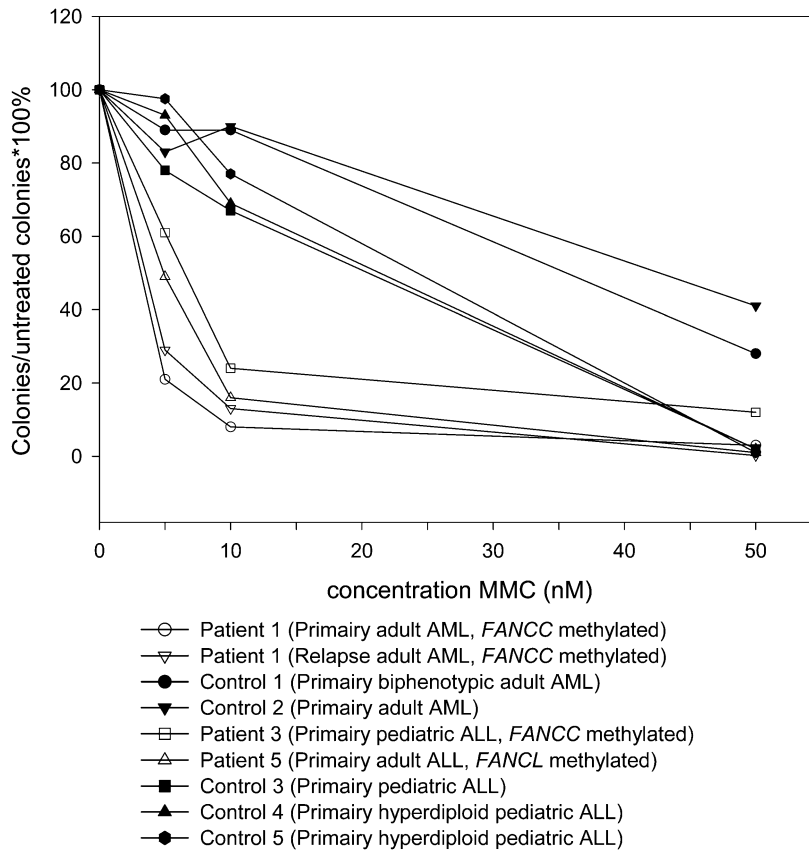


Fig. 3. Mitomycin C (MMC) sensitivity in Colony Forming Units (CFU) assay. Number of colonies scored following a 7-day culture in Methocult culture medium with increasing concentrations (5, 10 and 50 nM) of MMC, expressed as percentage of the number of scored colonies in the untreated (0 nM MMC) fraction. Open symbols, patients with FA-BRCA gene promoter methylation (patient 1, biphenotypic AML, *FANCC* methylated; patient 3, paediatric ALL, *FANCC* methylated; patient 5, adult ALL, *FANCL* methylated). Black symbols, controls (control 1, biphenotypic adult AML, control 2, primary adult AML, control 3, primary paediatric ALL, controls 4 and 5, primary hyperdiploid adult ALL).

sensitivity towards mitomycin C (MMC), a hallmark of cells defective in the FA-BRCA pathway. From two paediatric ALL samples with *FANCC* hypermethylation no colonies were obtained in the CFU assay. The other four methylated samples were on average 6.9-fold more sensitive to MMC (median  $IC_{50}$  4.6 nM) than controls (median  $IC_{50}$  32.1 nM), see Fig. 3, an extent of hypersensitivity commonly observed in cells carrying biallelic FA gene defects. This suggests that the observed hypermethylation in these samples indeed is associated with an FA-like cellular phenotype of DNA cross-linker sensitivity.

#### 4. Discussion

This is the first report showing epigenetic alterations of the *FANCC* and *FANCL* promoter regions in malignant cells. Furthermore, we show here for the first time

evidence for FA-BRCA gene hypermethylation in primary sporadic leukaemia samples.

We had anticipated to enrich for AML samples carrying a defect in the FA-BRCA pathway by selecting paediatric AML samples with cytogenetic abnormalities that are frequently found in FA patients [14, 15]. However, no aberrant FA-BRCA gene methylation was detected in these samples using MS-MLPA for the detection of methylation in 11 FA-BRCA genes. In a larger series of sporadic leukaemia samples, a relative higher incidence of FA-BRCA gene methylation was observed in ALL samples (4/97) compared to AML samples (1/143). This is somewhat surprising, since ALL is rarely observed in FA-patients [14] except for the FA subtype associated with a defect in the *FANCD1/BRCA2* gene [16]. If methylation of the FA-BRCA genes is causally involved in the occurrence of sporadic leukaemia our data suggest that this accounts for a small proportion of these cases. On the

other hand the presented data may be an underestimate due to a number of reasons. First, MS-MLPA detects the presence of methylation only for a limited number of CpGs. Samples which are methylated but in which these specific CpGs are not will be missed. Second, silencing of the FA-BRCA pathway is predicted to be only necessary temporarily for the accumulation of tumourigenic alterations. Loss of *FANCF* methylation in vitro has been shown to occur [17]. Third, we have analyzed 11 of the 13 genes known to cause Fanconi anaemia. Not included were the recently identified *FANCN/PALB2* [18,19] and *FANCI* [20–22] genes.

In conclusion, FA-BRCA gene hypermethylation is observed in a small portion of primary sporadic acute leukaemia samples. These samples appeared hypersensitive to DNA cross-linking agents. The data suggests that methylation of these genes resulted in chromosomal instability which may have contributed to the accumulation of oncogenic alterations eventually leading to leukaemia. Since the role of cross-linking agents in the treatment of leukaemia's is limited in general, determining FA-BRCA gene hypermethylation may have clinical consequences, as such leukaemias are predicted to be particularly sensitive to regimens containing the cross-linking agents cyclophosphamide, cisplatin, or busulfan.

## References

- [1] M. Levitus, H. Joenje and J.P. de Winter, The Fanconi anemia pathway of genomic maintenance, *Cell. Oncol.* **28**(1/2) (2006), 3–29.
- [2] L.J. Niedernhofer, A.S. Lalai and J.H. Hoeijmakers, Fanconi anemia (cross)linked to DNA repair, *Cell* **123**(7) (2005), 1191–1198.
- [3] A. Lyakhovich and J. Surrallés, Disruption of the Fanconi anemia/BRCA pathway in sporadic cancer, *Cancer Lett.* **232**(1) (2006), 99–106.
- [4] T. Taniguchi and A.D. D'Andrea, Molecular pathogenesis of Fanconi anemia: recent progress, *Blood* **107**(11) (2006), 4223–4233.
- [5] O.I. Olopade and M. Wei, *FANCF* methylation contributes to chemoselectivity in ovarian cancer, *Cancer Cell* **3**(5) (2003), 417–420.
- [6] G. Narayan, H. Arias-Pulido, S.V. Nandula, K. Basso, D.D. Sugi-tharaj, H. Vargas, M. Mansukhani, J. Villella, L. Meyer, A. Schneider, L. Gissmann, M. Durst, B. Pothuri and V.V. Murty, Promoter hypermethylation of *FANCF*: disruption of Fanconi anemia-BRCA pathway in cervical cancer, *Cancer Res.* **64**(9) (2004), 2994–2997.
- [7] C.J. Marsit, M. Liu, H.H. Nelson, M. Posner, M. Suzuki and K.T. Kelsey, Inactivation of the Fanconi anemia/BRCA pathway in lung and oral cancers: implications for treatment and survival, *Oncogene* **23**(4) (2004), 1000–1004.
- [8] A. Condie, R.L. Powles, C.D. Hudson, V. Shepherd, S. Bevan, M.R. Yuille and R.S. Houlston, Analysis of the Fanconi anaemia complementation group A gene in acute myeloid leukaemia, *Leuk. Lymph.* **43**(9) (2002), 1849–1853.
- [9] M. Tischkowitz, N. Ameziane, Q. Waisfisz, J.P. de Winter, R. Harris, T. Taniguchi, A. D'Andrea, S.V. Hodgson, C.G. Mathew and H. Joenje, Bi-allelic silencing of the Fanconi anaemia gene *FANCF* in acute myeloid leukaemia, *Br. J. Haematol.* **123**(3) (2003), 469–471.
- [10] M.W. Lensch, M. Tischkowitz, T.A. Christianson, C.A. Reifsteck, S.A. Speckhart, P.M. Jakobs, M.E. O'Dwyer, S.B. Olson, M.M. Le Beau, S.V. Hodgson, C.G. Mathew, R.A. Larson and G.C. Bagby, Jr., Acquired *FANCA* dysfunction and cytogenetic instability in adult acute myelogenous leukemia, *Blood* **102**(1) (2003), 7–16.
- [11] M.D. Tischkowitz, N.V. Morgan, D. Grimwade, C. Eddy, S. Ball, I. Vorechovsky, S. Langabeer, R. Stoger, S.V. Hodgson and C.G. Mathew, Deletion and reduced expression of the Fanconi anemia *FANCA* gene in sporadic acute myeloid leukemia, *Leukemia* **18**(3) (2004), 420–425.
- [12] S. Meyer, D.J. White, A.M. Will, T. Eden, A. Sim, R. Brown and G. Strathdee, No evidence of significant silencing of Fanconi genes *FANCF* and *FANCB* or Nijmegen breakage syndrome gene *NBS1* by DNA hyper-methylation in sporadic childhood leukaemia, *Br. J. Haematol.* **134**(1) (2006), 61–63.
- [13] A.O. Nygren, N. Ameziane, H.M. Duarte, R.N. Vijzelaar, Q. Waisfisz, C.J. Hess, J.P. Schouten and A. Errami, Methylation-specific MLPA (MS-MLPA): simultaneous detection of CpG methylation and copy number changes of up to 40 sequences, *Nucleic Acids Res.* **33**(14) (2005), e128.
- [14] D.I. Kutler, B. Singh, J. Satagopan, S.D. Batish, M. Berwick, P.F. Giampietro, H. Hanenberg and A.D. Auerbach, A 20-year perspective on the International Fanconi Anemia Registry (IFAR), *Blood* **101**(4) (2003), 1249–1256.
- [15] M. Tischkowitz and I. Dokal, Fanconi anaemia and leukaemia – clinical and molecular aspects, *Br. J. Haematol.* **126**(2) (2004), 176–191.
- [16] B.P. Alter, P.S. Rosenberg and L.C. Brody, Clinical and molecular features associated with biallelic mutations in *FANCD1/BRCA2*, *J. Med. Genet.* **44**(1) (2007), 1–9.
- [17] T. Taniguchi, M. Tischkowitz, N. Ameziane, S.V. Hodgson, C.G. Mathew, H. Joenje, S.C. Mok and A.D. D'Andrea, Disruption of the Fanconi anemia-BRCA pathway in cisplatin-sensitive ovarian tumors, *Nat. Med.* **9**(5) (2003), 568–574.
- [18] S. Reid, D. Schindler, H. Hanenberg, K. Barker, S. Hanks, R. Kalb, K. Neveling, P. Kelly, S. Seal, M. Freund, M. Wurm, S.D. Batish, F.P. Lach, S. Yetgin, H. Neitzel, H. Ariffin, M. Tischkowitz, C.G. Mathew, A.D. Auerbach and N. Rahman, Biallelic mutations in *PALB2* cause Fanconi anemia subtype FA-N and predispose to childhood cancer, *Nat. Genet.* **39**(2) (2007), 162–164.
- [19] B. Xia, J.C. Dorsman, N. Ameziane, Y. de Vries, M.A. Rooimans, Q. Sheng, G. Pals, A. Errami, E. Gluckman, J. Llera, W. Wang, D.M. Livingston, H. Joenje and J.P. de Winter, Fanconi anemia is associated with a defect in the *BRCA2* partner *PALB2*, *Nat. Genet.* **39**(2) (2007), 159–161.

- [20] J.C. Dorsman, M. Levitus, D. Rockx, M.A. Rooimans, A.B. Oostra, A. Haitjema, S.T. Bakker, J. Steltenpool, D. Schuler, S. Mohan, D. Schindler, F. Arwert, G. Pals, C.G. Mathew, Q. Waisfisz, J.P. de Winter and H. Joenje, Identification of the Fanconi anemia complementation group I gene, *FANCI*, *Cell. Oncol.* **29**(3) (2007), 211–218.
- [21] A.E. Sims, E. Spiteri, R.J. Sims, 3rd, A.G. Arita, F.P. Lach, T. Landers, M. Wurm, M. Freund, K. Neveling, H. Hanenberg, A.D. Auerbach and T.T. Huang, *FANCI* is a second monoubiquitinated member of the Fanconi anemia pathway, *Nat. Struct. Mol. Biol.* **14**(6) (2007), 564–567.
- [22] A. Smogorzewska, S. Matsuoka, P. Vinciguerra, E.R. McDonald, 3rd, K.E. Hurov, J. Luo, B.A. Ballif, S.P. Gygi, K. Hofmann, A.D. D'Andrea and S.J. Elledge, Identification of the *FANCI* protein, a monoubiquitinated *FANCD2* paralog required for DNA repair, *Cell* **129**(2) (2007), 289–301.