Factor 11 single-nucleotide variants in women with heavy menstrual bleeding

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Factor 11 single-nucleotide variants in women with heavy menstrual bleeding

Sophie Wiewel-Verschuerena,b, André B. Mulderc, Karina Mejiera and René Mulderc

Introduction

Factor XI (FXI 2014) deficiency, also known as haemophilia C, is an autosomal bleeding disorder characterised by reduced plasma levels of FXI with a high prevalence (about 9%) in the Ashkenazi Jewish population (Bolton-Maggs 2009). The prevalence of FXI deficiency in Caucasians is reported as low, but might be underestimated (Mitchell et al. 2006; Zadra et al. 2008). Women with low levels of FXI (<70%) are prone to excessive bleeding during menstruation. However, bleeding manifestations are not well correlated with plasma FXI levels and bleeding episodes can vary widely among patients with similar low FXI levels. In a previous study we showed that women with heavy menstrual bleeding (HMB) had normal, but on average, lower levels of FXI than controls.

In light of these findings, we performed F11 gene analysis to determine the single-nucleotide variants (SNVs) in women with HMB and performed an extensive literature search to determine the clinical significance of each SNV. By direct sequencing analysis of the F11 gene we found 29 different non-structural SNVs in 49 women with heavy menstrual bleeding. Remarkably, a number of these SNVs have previously been implicated in thrombosis. These findings have not helped to elucidate the molecular basis of HMB. They also question the specificity of previously reported F11 variations in patients with thrombosis. More studies are needed to explain the lower FXI levels seen in patients with HMB.

KEYWORDS
Heavy menstrual bleeding; factor XI; single-nucleotide variants

ABSTRACT
In a previous study it was shown that lower factor XI (FXI) levels in women with heavy menstrual bleeding (HMB). Our aim was to determine the single-nucleotide variants (SNVs) in the F11 gene in women with HMB. In addition, an extensive literature search was performed to determine the clinical significance of each SNV. Patients referred for HMB (PBAC-score >100) were included. With direct sequencing analysis of all 15 exons and flanking introns of the F11 gene, 29 different non-structural SNVs were detected in 49 patients with HMB. Interestingly, most of these SNVs have previously been associated with venous thrombosis instead of bleeding. These findings have not helped to elucidate the molecular basis of HMB. They also question the specificity of previously reported F11 variations in patients with thrombosis. More studies are needed to explain the lower FXI levels seen in patients with HMB.

Impact statement

- Women with mild deficiencies of factor XI (FXI) (<70%) are prone to excessive bleeding during menstruation. Bleeding manifestations are not well correlated with plasma FXI levels and bleeding episodes can vary widely among patients with similar low FXI levels. In a previous study we showed that women with heavy menstrual bleeding (HMB) had normal, but on average, lower levels of FXI than controls.
- In light of these findings, we performed F11 gene analysis to determine the single-nucleotide variants (SNVs) in women with HMB and performed an extensive literature search to determine the clinical significance of each SNV. By direct sequencing analysis of the F11 gene we found 29 different non-structural SNVs in 49 women with heavy menstrual bleeding. Remarkably, a number of these SNVs have previously been implicated in thrombosis.
- These findings have not helped to elucidate the molecular basis of lower FXI levels in HMB. They also question the specificity of previously reported F11 variations in patients with thrombosis. More studies are needed to explain the lower FXI levels seen in patients with HMB.
DNA was obtained from peripheral blood samples using the (20 pmol), 1.6
SNVs.
formed to determine the clinical relevance of the identified
with HMB. In addition, an extensive literature search was per-
to determine the single-nucleotide variants (SNVs) in women
et al. 1998), known bleeding disorder, use of any intrauterine	device within 2 months prior to inclusion and treatment with
fertility agents, progestagens or combined oral contraceptives.
Eligible women were asked to fill out a structured question-
tory agents, progestagens or combined oral contraceptives.

**Materials and methods**

**Inclusion**

Patients referred for heavy, regular menstrual periods were
included. Exclusion criteria were Pictorial Blood loss
Assessment Chart-score <100 (Higham et al. 1990; Janssen
et al. 1998), known bleeding disorder, use of any intrauterine
device within 2 months prior to inclusion and treatment with
antifibrinolytics, anticoagulants, non-steroidal anti-inflammatory
ter agents, progestagens or combined oral contraceptives.
Eligible women were asked to fill out a structured question-
aire for medical, obstetrical and gynaecological history,
including all items of the Tosetto bleeding score (Rodeghiero
et al. 2007). Eligible women were invited to our clinic and
gynaecological examination and pelvic ultrasonography in
the first week after the menstruation. The study was
approved by the Institutional Review Board of the University
Medical Center of Groningen. Informed consent was obtained
from all patients.

**Blood collection and sample preparation**

Venous blood was taken from all patients in the first week
after the menstruation. The blood samples were taken before
the gynaecological examination. Blood samples were anticoa-
gulated with a 1:10 volume of 0.109 M trisodium citrate.
Platelet-poor plasma was prepared by centrifugation at
2500×g for 15 min, aliquoted and immediately frozen at
−80°C, and analysed after rapid thawing at 37°C. Genomic
DNA was obtained from peripheral blood samples using the
Qiagene system.

**FXI assay**

FXI activity levels were determined by a one-stage clotting
assay (Siemens, Marburg, Germany). Reference interval was
65–150%.

**PCR amplification and sequencing**

PCRs were performed for each of the 15 exons and flanking
introns. Primers are indicated in Table 1. Reactions (25 μl) for
all PCRs except for exon 9 and 14 contained 1 μl of primer
(20 pmol), 1.6 μl of MgCl2 (25 mM), 0.3 μl of dNTPs (25 mM),
0.4 μl of Faststart Taq (5U/μl), 5 μl of 5× GC-rich solution,
2.5 μl of 10× PCR-buffer (−MgCl2), 11.2 μl of DEPC H2O and
2 μl of DNA (10 ng). For exons 9 and 14, 1 μl instead of 1.6 μl
of MgCl2 (25 mM) was used. The PCR protocol for exons 9
and 14 started with denaturation for 5 min at 94°C, followed
by 40 cycles at 94°C for 30 s, 55°C for 30 s and 70°C for
1 min. The cycling protocol of the remaining exons was
almost the same, only the annealing temperature was 49°C
instead of 55°C, and the amount of cycles was 35 instead of
40. M13-tailed primers enabled the use of standardised ampli-
fication conditions for the sequencing PCR (96°C for 1 min,
30 cycles at 96°C for 30 s, 55°C for 15 s and 60°C for 2 min).
The sequencing PCR was performed on both strands using
Big Dye terminators V1.1 and an ABI 3130xl analyser. The
chromatograms were analysed with CLC main workbench.

**Nomenclature**

The nomenclature was according to the guidelines of the
Human Genome Variation Society. For cDNA numbering,
nucleotide 1 is the A of the ATG translation initiation codon
(c.1). For amino acid numbering, the ATG initiation codon
corresponds to the first amino acid (p.1).

**Literature search**

To determine the clinical significance of each SNV, a search
in PubMed was performed to identify all relevant references
for each SNV. More specifically, references were included if a
significant clinical association was reported, if molecular gen-
etic analysis was performed to identify causal F11 gene
defects, if structural features of a specific variant were ana-
lysed, or if haplotype analysis was performed with specific
variants. Based on these criteria, references were selected in
association studies and molecular analysis.
Table 2. Patient characteristics.

<table>
<thead>
<tr>
<th>Patient characteristics</th>
<th>Patients (n = 49)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age in years, median (range)</td>
<td>44 (26 to 54)</td>
</tr>
<tr>
<td>PBAC-score in points, median (Q1–Q3)</td>
<td>272 (204 to 557)</td>
</tr>
<tr>
<td>FXI level in %, median (Q1–Q3)</td>
<td>96 (88 to 118)</td>
</tr>
<tr>
<td>FXI level &lt;100%, n (%)</td>
<td>26 (53)</td>
</tr>
<tr>
<td>Tosetto bleeding score in points, median (range)</td>
<td>0 (–2 to 7)</td>
</tr>
</tbody>
</table>

PBAC: Pictorial Blood Loss Assessment Chart; FXI: Factor XI.

Results

49 patients were included with a median age of 44 years (range: 26–54). Median FXI level was 96% (range 61%–155%); vs 124% in our previously published menstrual cycle-matched controls (Knol et al. 2013). In 53% of the patients, the FXI level was <100% (Table 2). In 2 patients FXI levels below the normal range of 65% were found. One patient (number 46 in the supplementary table S1) had a level of 61% factor XI, which was in the normal range (83%) when the measurement was repeated and one patient had a FXI of 64%, which was not repeated. None of these 49 patients had a history of deep venous thrombosis. In total, 29 different non-structural SNVs were identified in 49 patients (Table 3).

Non-synonymous variants

Two non-synonymous variants were identified: rs5969 (p.Gln244Arg) and rs202061241 (p.Val615Met). Rs5969 is the result of an A to G substitution at nucleotide 731 in exon 7. This mutation was first described by Martincic et al. (Martincic et al. 1998; Erratum 1999). This paper reports on the genetic analysis of F11 gene in two African–American patients with mild FXI deficiency and one patient of European Jewish ancestry with severe FXI deficiency (patient 3). This last patient was included in the study as an abnormal control. The propositus, a 9-year-old boy with a history of excessive bleeding and mild FXI deficiency, was compound heterozygous for rs5969 and rs145168351 (p.Ser266Asn). His mother was heterozygous for rs145168351, and also experienced excessive bleeding. Besides being compound heterozygous for type II (rs121965063, p.Glu135Ter) and type III (rs121965064, p.Phe301Leu) variants, the abnormal control did not contain the other two non-synonymous variants. The binding affinity between FXI and FIX (Km) differed considerably from wild-type FXI (Sun et al. 2001). However, rs5969 was associated with FXI activity levels comparable to wild-type when tested in an APTT-based assay (Martincic et al. 1998). In line with this, the catalytic efficiency (kcat) for FIX activation was shown to be comparable to that of wild-type FXI, thus normalising the APTT result (Sun et al. 2001).

Various clinical studies as well as studies that examined the structural features of rs5969 have confirmed the minimal effect (Mitchell et al. 1999; Mitchell et al. 2003; O’Connell et al. 2005; Mitchell et al. 2006; Saunders et al. 2009). Therefore, our findings were in accordance with the normal FXI level (83%) was found in our patient. Rs202061241 is caused by a G to A substitution at nucleotide 1843 in exon 15, which is located in the protease domain. To our knowledge, no clinical data on this mutation has been reported. Therefore, PROVEAN (2014) (http://provean.jcvi.org/index.php) was used to determine the functional effects of this mutation. With a score of −0.276, this mutation was said to be neutral (default threshold −2.5). This finding supports the FXI level (93%) found in this patient.

Synonymous variants

Our study detected six synonymous variants. One patient (FXI level: 96%) was heterozygous for a SNV in exon 5 (c.423 G > A), maintaining the threonine at amino acid position 141 in the second apple domain (p.Thr141=). This variant had no reference ID, though it was found in the Exome Aggregation Consortium (Exac) Browser (http://exac.broadinstitute.org/), with an allele frequency of 0.000008243.

A missense mutation at this position, resulting in a threonine to methionine substitution has been described in combination with the nonsense mutation p.Glu135Ter in a severe FXI-deficient patient from the Abruzzo region in Italy (Castaman et al. 2008).

The five other synonymous variants (rs5973, rs5974, rs5970, rs5971 and rs5976) have been extensively used as markers for haplotype analysis (Bolton-Maggs et al. 2004; Quelin et al. 2004; Zadra et al. 2004; Zadra et al. 2008; Kim et al. 2012; Bicocchi et al. 2013), which is not surprising as three (rs5973, rs5974 and rs5970) are in marked linkage disequilibrium with one another (Tarumi et al. 2000). These three neutral variants were initially reported by Martincic et al. (1998).

Non-coding variants

Twenty-one SNVs were located in the non-coding regions of the F11 gene. Based on the literature search (Table 3), these variants have mostly been mentioned in the context of the risk of venous thrombosis. Among these variants, rs2289252 was most frequently reported to be independently associated with venous thrombosis. Furthermore, rs2289252 was associated with miscarriages, decreased APTT and high FXI levels.
<table>
<thead>
<tr>
<th>dbsnp</th>
<th>Base change</th>
<th>AA change</th>
<th>Region</th>
<th>Trait</th>
<th>Association</th>
<th>Reference</th>
<th>Causal</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs2425410</td>
<td>c.485 + 181T &gt; C</td>
<td>Intron 5</td>
<td>NR</td>
<td>NR</td>
<td>(Bezemer et al. 2008)</td>
<td>N</td>
<td>(Bezemer et al. 2008)</td>
<td></td>
</tr>
<tr>
<td>rs2425414</td>
<td>c.485-88G &gt; C</td>
<td>Intron 5</td>
<td>VTE</td>
<td>N</td>
<td>(Bezemer et al. 2008)</td>
<td>N</td>
<td>(Bezemer et al. 2008)</td>
<td></td>
</tr>
</tbody>
</table>

(continued)
This SNV is located in intron 12 (c.1481–188) and the result of a C>T substitution. Eight other SNVs, including rs1593, rs3822057, rs925451, rs42534230, rs4253414, rs4253399, rs3733403 and rs3822056 also showed an association with venous thrombosis. Interestingly, all these SNVs are in linkage disequilibrium with rs2289252 (SNAP, 1000 genomes, Bioinformatics).

It is tempting to speculate that an overexpression of these variants could compensate for low FXI level in these patients and may reset the haemostatic balance to a less-haemophilic phenotype. To test this hypothesis, the allele frequencies of all SNVs between high (>100%) and low (<100%) FXI levels were compared using the Fisher Exact probability test in a 2 × 3 contingency table. A p value of less than .05 indicated significance. No significant difference was observed between both the groups. Moreover, even when the lowest percentile was taken and compared to the rest this difference remained non-significant.

Two identified SNVs in high LD (rs373403 and rs3822056) are located in the promoter region of the F11 gene. In our cohort, nine patients had one or both of these SNVs with a median FXI level of 96% (range 61%–129%). Rs373403, a variant that is caused by a C to G base change at c.-316, has been shown to negatively affect the transcription binding (Tarumi et al. 2003). However, the overall effect is probably low, because a region between 381 and 363 bp upstream of exon 1, is responsible for maximum promoter activity in HepG2 hepatocellular carcinoma cells (Tarumi et al. 2002).

This region contains the sequence ACTTTG that has been identified in several gene promoters of coagulation factors for being the binding site for transcription factor hepatocyte nuclear factor 4 (HNF4) (Reijnen et al. 1992; Erdmann and Heim 1995; Hung and High 1996). Also, no variant was located at the binding site for miR-181a-5p, a microRNA which is inversely correlated with F11 mRNA levels (Salloum-Asfar et al. 2014).

**Discussion**

This study was performed because it was shown (Knol et al. 2013) that women with HMB had lower mean FXI levels than menstrual cycle-matched controls. 29 different non-structural SNVs were detected in 49 patients with HMB.

Additionally, the SNVs found in our patient group were also compared with the literature. Literature shows that F11 gene analysis is mainly carried out in the context of the risk of deep venous thrombosis and elevated levels of FXI. Most SNVs that were found are therefore already described in relationship with either venous thrombo-embolism, stroke, decreased APTT, hypertensive disorders in pregnancy, higher FXI levels or miscarriages. Remarkably, our results show that these SNVs are also present in women with HMB and thus in a group with increased bleeding tendency. Noteworthy is that none of the women in our study had a previous VTE. This result directly undermines the assumed relationship between these SNVs and venous thrombosis.

A limitation of our study is that the patient group is small. As a consequence it was impossible to provide haplotype data and multiple comparisons could not be made. Nonetheless, this is the first study which gives an overview of the molecular background of the F11 gene, as found in patients with HMB. Therefore, our group can serve as a reference group for future studies. Another limitation is that it
was not possible to compare the patients with a control group of women with a normal amount of blood loss during their menstruation. However, it was possible to compare the FXI levels of our patients with a control group from our previous study (Knol et al. 2013). In addition, because most of the SNVs that were found have previously been described, an extensive literature search was performed to determine the clinical significance of each SNV.

Conclusions

By direct sequencing analysis of the F11 gene, 29 different non-structural SNVs were found in 49 women with HMB. These findings have not helped to elucidate the molecular basis of HMB. They also question the specificity of previously reported F11 variations in patients with thrombosis. More studies are needed to explain the lower FXI levels seen in patients with HMB.

Disclosure statement

K.M. reports grants and other from Baxter, Bayer and Sanquin; other from Pfizer and Boehringer Ingelheim, outside the submitted work. S.W.-V. reports travel support from CSL Behring, outside the submitted work. The remaining authors have nothing to disclose. The authors alone are responsible for the content and writing of the paper.

References


