Association of the R67X and W303X non-sense polymorphisms in the protein Z-dependent protease inhibitor gene with idiopathic recurrent miscarriage

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ABSTRACT: Protein Z-dependent protease inhibitor (ZPI) is a 72 kDa single-chain serpin which inhibits the activated coagulation factors X and XI. Two non-sense polymorphisms of ZPI, R67X and W303X, were recently identified, and were linked with a prothrombotic state. Here, we investigated the association of the R67X (728C>T) and W303X (1438G>A) variants in the ZPI gene with recurrent spontaneous miscarriage (RSM). This was a case–control study involving a total of 288 women with a history of two consecutive or ≥3 non-consecutive pregnancy losses between 8 and 12th week of gestation, along with 304 age-matched and ethnically matched multiparous control women, with no personal or family history of pregnancy complications. The minor allele frequency of R67X (P = 0.003) and W303X (P = 0.014) were higher in RSM cases than in control women. Both single-nucleotide polymorphisms were significantly associated with RSM under the dominant genetic association model, and were in moderate linkage disequilibrium (D' = 0.412; P < 0.001). Taking the common 728C/1438G haplotype as reference, multivariate analysis confirmed the positive association of 728T/1438G (P = 0.043; odds ratio (OR) = 2.25; 95% confidence interval (CI) = 1.03–4.90) and 728T/1438A (P = 0.022; OR = 3.93; 95% CI = 1.23–12.59) haplotypes with increased RSM risk. These differences remained significant after controlling for some covariates. These results demonstrate that both ZPI R67X and W303X non-sense variants and specific ZPI haplotypes are significantly associated with RSM.

Key words: haplotype / protein Z-dependent protease inhibitor / recurrent miscarriage / genetic association

Introduction

The protein Z (PZ)-dependent protease inhibitor (ZPI) is a 72 kDa single chain anti-coagulant glycoprotein (Han et al., 1999), belonging to the serpin superfamily of protease inhibitors (Han et al., 1999, 2000; Rezaie et al., 2008; Vass, 2011). ZPI is synthesized in the liver (Han et al., 2000; Vass, 2011), and mediates its anti-coagulant effects by two distinct mechanisms (Vass, 2011). ZPI exerts its effects by binding the 62 kDa PZ cofactor, resulting in the formation of PZ/ZPI complex, which in turn inactivate coagulation factor Xa in a Ca²⁺– and phospholipid-dependent manner (Corral et al., 2007; Vass, 2011). The significance of the PZ-ZPI formation on factor Xa inhibition was highlighted by the findings that the absence of PZ reduces ZPI inhibitory effects by 1000 folds, resulting in a specific, but poor, factor Xa inhibition (Huang et al., 2011). ZPI also directly inhibits coagulation factor Xa in a PZ-independent fashion, by binding heparin (Rezaie et al., 2008; Huang et al., 2011).

Successful pregnancy depends on maintaining a fine balance between pro- and anti-coagulant mechanisms (Isermann et al., 2003; Zygmunt et al., 2003), and the maintenance of early pregnancy is tightly linked with placental growth and differentiation (Demir et al., 2007; Blois et al., 2011). Defective maternal haemostatic responses, leading to thrombosis of the utero-placental circulation and subsequent fetal loss, was described as a major cause of recurrent spontaneous miscarriage (RSM), a common reproductive problem affecting 1–3% of pregnancies (Brown, 2008; Warren and Silver, 2008). While very early pregnancy loss was attributed to chromosomal abnormalities, later losses were attributed to altered vascular permeability of the placenta. In this regard, it was shown that pregnancy, delivery and post-partum are associated with differential changes in the levels of
of coagulation factors (Szecsi et al., 2010) favoring a hypercoagulable state associated with increased clotting factors, decreased fibrinolytic activity and reduction in anti-coagulant levels (Brenner, 2004; D’Uva et al., 2008; Thornton and Douglas, 2010). This becomes more apparent in RSM (Rai, 2003; D’Uva et al., 2008), whereby a significant proportion of RSM women present with identifiable prothrombotic risk factors (Krause et al., 2005; Sottoliata et al., 2006), thereby posing greater risk state of miscarriage in future pregnancies.

Several variants in the ZPI gene were previously reported (van de Water et al., 2004; Vossen et al., 2004), of which the two non-sense polymorphisms, R67X and W303X, were associated with venous thromboembolism (VTE) in New Zealand (van de Water et al., 2004), likely due to altered ZPI levels given their location within structurally important sites within the ZPI gene, as was suggested (van de Water et al., 2004). Other studies reported lack of association of the ZPI variants with venous (Razzari et al., 2006; Fabbrro et al., 2007; Dentali et al., 2008) or arterial (Refaai et al., 2006) thrombosis and an ethnic contribution of the ZPI variants (W303X) to venous thrombosis was proposed (Gonzalez-Conjero et al., 2005; Fabbrro et al., 2007). While previous studies have documented a link between altered PZ levels in normal pregnancy (Quack Loetscher et al., 2005), and pregnancy complications (Erez et al., 2007; Kusanovic et al., 2007), no single study has investigated the association between changes in ZPI levels and the ZPI variants to the risk of RSM. Here, we investigate the association of the R67X and W303X ZPI non-sense variants to RSM in 288 women with confirmed RSM and 304 age-matched and ethnically matched control women.

Materials and Methods

Subjects

A total of 288 women with confirmed RSM (mean age 31.6 ± 5.2 years) were consecutively recruited from the outpatient OB/GYN clinics in Manama, Bahrain for assessment of idiopathic RSM, as per the Royal College of Obstetricians and Gynaecologists Guidelines (http://www.aetna.com/cpb/medical/data/300_399/0348.html), which were consistent with ACOG Guidelines. These included endometrial biopsies for evaluating luteal phase defect, pelvic ultrasound scan to assess ovarian morphology and the uterine cavity, hysterosalpingography, hysteroscopy or sonohysteroscopy to evaluate uterine anatomic abnormality (Fallopian tubes openness, any evidence of peritoneal cavity scarring); all cases or sonohysteroscopy to evaluate uterine anatomic abnormality (Fallopian tubes openness, any evidence of peritoneal cavity scarring); all cases.

Statistical analyses

Data were expressed as mean ± SD for continuous variables, or as percent for categorical variables. Intergroup significance was assessed by Student’s t-test (continuous variables), and χ² test (categorical variables). Allele frequencies were calculated by the gene-counting method; each single-nucleotide polymorphisms (SNP) was tested for Hardy–Weinberg equilibrium using χ² goodness-of-fit test by HPLus 2.5 (http://cdsweb01.ficr.org/HPLus). The power was calculated for each SNP (http://pngu.mgh.harvard.edu/~purcell/gpc/cc2.html) At α = 0.05, this sample size provided 88.28 and 73.32% power for R67X and W303X, respectively. Pairwise linkage disequilibrium (LD) values were calculated with SNPStats (http://bioinf.iconcologia.net/snpstats); R67X and W303X were in moderate LD (ρ = 0.571) and smoking prevalence (P = 0.001). Haplotype estimation was done by the expectation maximization method with the HPLus 2.5. Logistic regression analysis was performed to calculate specific P values, odds ratios (ORs), 95% confidence intervals (CIs) after controlling for age, BMI and menstrual history.

Results

Study subjects

The demographics and clinical characteristics of study subjects are reported in Table 1. Although age (P = 0.571) and smoking prevalence (P = 0.776) were comparable between RSM cases and control women, significant differences were seen with regard to BMI (P = 0.003) and obesity (P = 0.005), menarche (P = 0.001), irregular menstrual history (P = 0.011) and gravida (P < 0.001). Accordingly, the latter were the covariates that were controlled for in subsequent analysis.
Association studies

Table 2 illustrates the association between ZPI SNPs studied and RSM in cases and controls. Genotype distribution of R67X (P = 1.00) and W303X (P = 1.00) were in Hardy–Weinberg equilibrium among control women. The minor allele frequency (MAF) of R67X (P = 0.003; OR, 2.66; 95% CI, 1.40–4.87) and W303X (P = 0.014; OR, 2.44; 95% CI, 1.21–4.71) were significantly associated with RSM, and both SNPs were in moderate linkage disequilibrium (LD) (P < 0.001; D’ = 0.412; r = 0.375). This association remained significant after applying the Bonferroni correction for multiple testing.

Table 3 summarizes the association between R67X and W303X ZPI variants and RSM. In the virtual absence of homozygous carriers, these were analyzed under the dominant genetic model. Both ZPI SNPs showed a significant association with RSM under the model selected. This association remained significant after adjusting for BMI and menarche. Neither R67X (MAF: 0.065 versus 0.043; P = 0.060), nor W303X (MAF: 0.043 versus 0.063; P = 0.084) were associated with the status of miscarriage (primary/childless or secondary/at least one live birth). However, R67X (MAF: 0.106 versus 0.052; P = 0.037), more so than W303X (MAF: 0.083 versus 0.032; P = 0.058), was associated with fetal miscarriages (>10 weeks gestation).

Haplotype analysis

Two-locus (R67X and W303X) ZPI haplotypes were constructed based on the prevalence of individual SNPs and LD between them. Taking the common 728C/1438G as reference (OR = 1.00), multivariate analysis confirmed the association of the 728T-containing haplotypes 728T/1438G (P = 0.043; OR, 2.25; 95% CI, 1.03–4.90), and 728T/1438A (P = 0.022; OR, 3.93; 95% CI, 1.23–12.59) haplotypes with RSM, thus conferring disease susceptibility nature to these haplotypes (Table 4).

Discussion

In this case–control study, we investigated the association of the R67X and W303X non-sense ZPI variants as risk factors for RSM, and found strong association of R67X (OR = 2.66), and to a lower extent W303X (OR = 2.44), ZPI variants with RSM risk. Of

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**Table I** Clinical characteristic of patients and controls.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Controls (304)</th>
<th>Patients (288)</th>
<th>P*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean age (years)</td>
<td>31.8 ± 4.5</td>
<td>31.6 ± 5.2</td>
<td>0.571</td>
</tr>
<tr>
<td>Smoking</td>
<td>29 (10.6)</td>
<td>27 (11.9)</td>
<td>0.776</td>
</tr>
<tr>
<td>Mean BMI (kg/m²)</td>
<td>24.8 ± 3.9</td>
<td>26.1 ± 5.3</td>
<td>0.003</td>
</tr>
<tr>
<td>Obesity (BMI &gt;30 kg/m²)</td>
<td>31 (10.2)</td>
<td>56 (19.4)</td>
<td>0.005</td>
</tr>
<tr>
<td>Menarche</td>
<td>12.7 ± 1.0</td>
<td>12.2 ± 1.0</td>
<td>0.001</td>
</tr>
<tr>
<td>Irregular menstrual history</td>
<td>25 (8.2)</td>
<td>35 (12.2)</td>
<td>0.011</td>
</tr>
<tr>
<td>Gravida</td>
<td>3.5 ± 1.0</td>
<td>4.3 ± 1.1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Live births</td>
<td>3.5 ± 1.0</td>
<td>0.95 ± 1.1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Abortion</td>
<td>0.0 ± 0.0</td>
<td>3.7 ± 1.3</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

*aStudent’s t-test for continuous variables, Pearson’s χ² test for categorical variables.  
*bNumber of subjects (percent of total).

**Table II** Minor allele frequencies of the ZPI SNPs analyzed.

<table>
<thead>
<tr>
<th>SNP</th>
<th>Gene position</th>
<th>HWE</th>
<th>Alleles</th>
<th>Controls b</th>
<th>Cases b</th>
<th>P-value c</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>R67X</td>
<td>728C&gt;T</td>
<td>1.00</td>
<td>C : T</td>
<td>14 (0.02)</td>
<td>34 (0.06)</td>
<td>0.003</td>
<td>2.66 (1.40–4.87)</td>
</tr>
<tr>
<td>W303X</td>
<td>1438G&gt;A</td>
<td>1.00</td>
<td>G : A</td>
<td>12 (0.02)</td>
<td>27 (0.05)</td>
<td>0.014</td>
<td>2.44 (1.21–4.71)</td>
</tr>
</tbody>
</table>

HWE, Hardy–Weinberg equilibrium.  
*bMinor allele defined based on frequency in controls.  
*aA total of 288 RSM cases and 304 control women were genotyped. Values indicate number of alleles (frequency)  
*bObserved P-value.

**Table III** RSM association for ZPI SNPs adjusted for BMI and menarche.

<table>
<thead>
<tr>
<th>SNP</th>
<th>Genotype</th>
<th>Controls</th>
<th>Cases</th>
<th>P-value</th>
<th>aOR (95% CI) d</th>
</tr>
</thead>
<tbody>
<tr>
<td>R67X (728C&gt;T)</td>
<td>CC</td>
<td>290 (0.95) b</td>
<td>255 (0.89)</td>
<td>0.005</td>
<td>1.00 (Reference)</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>14 (0.05)</td>
<td>32 (0.11)</td>
<td>2.68 (1.40–5.12); C/T-T/T versus C/C</td>
<td></td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>0 (0.00)</td>
<td>1 (0.01)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>W303X (1438G&gt;A)</td>
<td>GG</td>
<td>292 (0.96) b</td>
<td>263 (0.91)</td>
<td>0.025</td>
<td>1.00 (Reference)</td>
</tr>
<tr>
<td></td>
<td>GA</td>
<td>12 (0.04)</td>
<td>23 (0.08)</td>
<td>2.31 (1.14–4.70); G/A-A/A versus G/G</td>
<td></td>
</tr>
<tr>
<td></td>
<td>AA</td>
<td>0 (0.00)</td>
<td>2 (0.007)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Analyzed by SNPstats software.  
*bNumber of subjects (frequency).  
*cOR, adjusted odds ratios, covariates controlled for included BMI and menarche. Analysis conducted under dominant genetic model.  
*dAnalysis conducted under dominant genetic model.
Table IV  Haplotype frequencies across the ZPI SNPs analyzed.

<table>
<thead>
<tr>
<th>Haplotypea</th>
<th>Totalb</th>
<th>Controlsb</th>
<th>Casesb</th>
<th>P-value</th>
<th>aOR (95% CI)c</th>
</tr>
</thead>
<tbody>
<tr>
<td>728C/1438G</td>
<td>0.941</td>
<td>0.964</td>
<td>0.918</td>
<td>—</td>
<td>1.00 (Reference)</td>
</tr>
<tr>
<td>728T/1438G</td>
<td>0.026</td>
<td>0.017</td>
<td>0.036</td>
<td>0.043</td>
<td>2.25 (1.03–4.90)</td>
</tr>
<tr>
<td>728C/1438A</td>
<td>0.018</td>
<td>0.013</td>
<td>0.023</td>
<td>0.210</td>
<td>1.71 (0.74–3.94)</td>
</tr>
<tr>
<td>728T/1438A</td>
<td>0.015</td>
<td>0.006</td>
<td>0.024</td>
<td>0.022</td>
<td>3.93 (1.23–12.59)</td>
</tr>
</tbody>
</table>

aZPI haplotype construction was done using SNPstats software.
bHaplotype frequency.
caOR, adjusted odds ratios, covariates controlled for included BMI and menarche.

significance was the finding that R67X, and to a lesser extent W303X, was associated with fetal, but not embryonic miscarriages. To the best of our knowledge, this is the first report investigating the contribution of these polymorphisms to increased RSM risk.

In contrast to pre-embryonic/embryonic pregnancy losses, which occur secondary to chromosomal abnormalities or intrauterine infections (Porter and Scott, 2005), later losses are due to altered maternal vascular permeability, resulting from constitutional defective homeostatic mechanisms (Paidas et al., 2005; Porter and Scott, 2005). In our study, which comprised 288 women with confirmed RSM diagnosis and 304 age-matched and ethnically matched control women, patients were excluded if they had systemic or autoimmune diseases and other maternal factors previously implicated in pregnancy losses in the fetal period (Davis and Olson, 2007; Metwally et al., 2010).

We reasoned that since pregnancy is associated with increased levels of clotting factor (Szecci et al., 2010), and reduced fibrinolysis and levels of a number of anti-coagulants (Brenner, 2004; D’Uva et al., 2008; Thornton and Douglas, 2010), which is more evident in RSM (Rai, 2003; D’Uva et al., 2008), the presence of inherited prothrombotic risk factors, including ZPI mutations, significantly increases the risk of miscarriage in future pregnancies.

It is noteworthy that the MAF of the R67X (2%) and W303X (2%) were generally comparable to prevalence rates established for Italians (Al-Shanqeeti et al., 2005; Corral et al., 2005) and New Zealanders (van de Water et al., 2010), and that it was limited to Bahraini Arabs, thereby necessitating follow-up studies in RSM cases from different ethnic groups. Furthermore, while we adjusted for a number of conventional RSM risk factors, we cannot exclude the possible contribution of other unmeasured risk factors, and given the modest OR associated with either SNP, this questions the potential for clinical utility of our findings. Large independent prospective population-based studies with different ethnicity are needed to confirm the contribution of ZPI polymorphisms to the risk of RSM.

Authors’ roles

F.S.A. performed the genotyping assays and analysis of results and contributed toward the drafting of the manuscript. R.R.F. participated in patient careening and referral. A.W.A. contributed toward specimens preparation and performed genotyping assays. F.E.M. participated in patient screening and referral. W.Y.A. was the project leader and contributed toward data analysis and manuscript preparation.

References


