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Genetic analysis of the M2/ANXA5 haplotype as adverse pregnancy outcomes risk factor- Evaluation in a Portuguese population group

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Genetic analysis of the M2/ANXA5 haplotype as adverse pregnancy outcomes risk factor- Evaluation in a Portuguese population group

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TABLE OF CONTENTS

TABLE INDEX	iii
FIGURE INDEX	iii
ABBREVIATIONS	iv
RESUMO	1
ABSTRACT	3
BACKGROUND	5
MATERIALS AND METHODS	8
Sample Selection	8
Ethical Statement	9
DNA Extraction	10
Polymerase Chain Reaction, Sequencing and Genotyping	10
Statistical Analyses	12
RESULTS	13
Population characteristics	13
Association of the ANXA5 M2 haplotype with APO	14
DISCUSSION AND CONCLUSIONS	17
CONFLICT OF INTEREST STATEMENT	20
AKNOWLEDGMENTS	20
REFERENCES	21

TABLE INDEX

Table 1: Demographic and clinical data of women with APO	13
Table 2: Characterization of APO in the case group	14
Table 3: Genotype frequencies of AMXA5 gene promoter haplotypes in APO cases gro	up
versus three different control groups	15
Table 4: Association between APO and the M2 haplotype in comparison with the cont	rol
groups	16

FIGURE INDEX

Figure 1: Location of the SNPs within the sequenced region of the ANXA5 promoter and
PCR analysis11
Figure 2: Electropherogram from Sanger sequencing

ABBREVIATIONS

- APO Adverse pregnancy outcome
- **BMI -** Body mass index
- CI Confidence interval
- FVL Factor V Leiden
- **GH** Gestational hypertension
- HELLP Hemolysis, elevated liver enzymes and low platelets
- HWE Hardy-Weinberg equilibrium
- **IUFD** Intrauterine fetal death
- IUGR Intrauterine growth restriction
- MCMC Monte Carlo Markov Chain
- **OR -** Odds ratio
- **PB** Premature birth
- PCR Polymerase chain reaction
- **PE** Pre-eclampsia
- **RPL** Recurrent pregnancy loss
- **RR** Relative risk
- **SGA -** Small for gestational age
- **SNP** Single nucleotide polymorphism
- $\ensuremath{\textbf{TE}}\xspace$ Thromboembolism
- VTE Venous thromboembolism
- $\mathbf{W}\mathbf{G}$ Week of gestation

RESUMO

Introdução: A gravidez induz um estado de hipercoaguabilidade fisiológica que pode predispor a complicações na gravidez, nomeadamente aborto recorrente (AR), hipertensão gestacional, pré-eclâmpsia (PE), restrição de crescimento intrauterino (RCIU), recém-nascido pequeno para a idade gestacional e tromboembolismo venoso. Os fatores de risco hereditários para trombofilia têm sido identificados como possíveis causas e extensamente investigados. Recentemente, foi identificado um novo fator de risco hereditário para estas complicações, uma variação na sequência da região promotora do gene que codifica a Anexina A5 (*ANXA5*), denominado haplótipo M2. Assim, este estudo pretende avaliar a frequência do haplótipo M2 numa amostra populacional de mulheres portuguesas e averiguar a sua associação com o risco de ocorrência de complicações na gravidez.

Metodologia: Realizou-se um estudo retrospetivo caso-controlo com 102 casos de mulheres portuguesas com antecedentes de complicações na gravidez, incluindo AR, aborto precoce, morte fetal *in* útero, RCIU, PE, eclâmpsia e síndrome HELLP (*hemolysis, elevated liver enzymes and low platelets*). Este grupo foi comparado com um grupo controlo de mulheres portuguesas sem história de complicações na gravidez (n=84), e com dois grupos controlo independentes, previamente usados em estudos semelhantes: os *Münster controls* (n=500) e os *PopGen controls* (n=533). A região promotora do gene da *ANXA5* foi genotipada para a presença dos haplótipos M1 e M2 por PCR/sequenciação de Sanger. Foram estimadas as frequências alélicas, avaliada a conformidade com o equilíbrio Hardy-Weinberg e testada a associação entre os haplótipos da *ANXA5* e a ocorrência de complicações na gravidez utilizando o teste exato de Fisher, cálculo do OR (*odds ratio*), intervalos de confiança (IC) de 95% e valores de p, recorrendo ao *software* Graphpad.

Resultados: O haplótipo M2 estava presente em 31,4% das mulheres com complicações na gravidez (frequência alélica 0,167) e em 15,5% dos controlos portugueses (frequência alélica

0,083). As portadoras do haplótipo M2 apresentavam um risco relativo de ocorrência de complicações na gravidez 1,32 vezes superior ao das não portadoras (OR 2,15, 95% CI 1,13-4,30; p=0,0280), quando comparadas com os controlos portugueses, um risco relativo 1,74 vezes superior quando comparadas com os *PopGen controls* (OR 2,04, 95% CI 1,32-3,10; p<0,0015), e um risco relativo 2,36 vezes superior em comparação com os *Münster controls* (OR 3,27, 95% CI 2,06-5,15; p<0,0001). O haplótipo M1 não estava significativamente associado ao risco de ter complicações na gravidez.

Conclusão: Os resultados obtidos sugerem que o haplótipo M2 pode ser um fator de risco relevante para o desenvolvimento de complicações na gravidez nesta amostra populacional de mulheres portuguesas. Assim, a genotipagem do gene da *ANXA5* para a presença do haplótipo M2, parece ser um procedimento prognóstico adequado em mulheres com complicações na gravidez de causa desconhecida, podendo auxiliar a estabelecer medidas terapêuticas preventivas.

Palavras-chave: Anexina A5, Haplótipo M2, Gravidez, Complicações na gravidez, Fator de risco.

ABSTRACT

Background: Pregnancy alters the hemostatic system into a physiological state of hypercoagulability, which can predispose to adverse pregnancy outcomes (APO), namely recurrent pregnancy loss (RPL), gestational hypertension (GH), pre-eclampsia (PE), intrauterine growth restriction (IUGR), small-for gestational age and venous thromboembolism. Inherited risk factors for thrombophilia have been largely explored as a cause of these APO. Recently a new hereditary risk factor for APO was identified, a sequence variation in the promoter region of the gene encoding annexin A5 (ANXA5), called the M2 haplotype. Therefore, we intend to evaluate the frequency of the M2 haplotype in a Portuguese women population sample with a previous history of APO and to assess the association between the M2 haplotype and the risk of APO.

Materials and Methods: A retrospective case-control study was conducted with a case group of 102 Portuguese women with history of unexplained APO including RPL, early miscarriage, IUFD, IUGR, PE, eclampsia and hemolysis, elevated liver enzymes and low platelets (HELLP) syndrome. This group was compared with a control group of Portuguese women without history of APO (n=84), and two independent control groups, previously recruited in similar studies: the Münster controls (n=500) and the PopGen controls (n=533). The *ANXA5* gene promoter region was genotyped by PCR/Sanger sequencing for the presence of the M1 and M2 haplotypes. GraphPad software was used to determine the allelic frequencies, concordance with Hardy-Weinberg equilibrium and the association between the *ANXA5* haplotypes and APO through the Fisher's exact test, estimating OR with 95% confidence intervals (95% CI) and p-values.

Results: The M2 haplotype was found in 31.4% of women with APO (allele frequency 0.167) and in 15.5% of the Portuguese controls (allele frequency 0.083). Carriers of the M2 haplotype were found to exhibit a relative risk of APO 1.32 higher than non-carriers (OR

2.15, 95% CI 1.13-4.30; p=0.0280), when compared to the Portuguese controls, a 1.74 higher risk when compared to the PopGen controls (OR 2.04, 95% CI 1.32-3.10; p<0.0015) and a 2.36 higher risk in comparison to the Münster controls (OR 3.27, 95% CI 2.06-5.15; p<0.0001). The M1 haplotype was not significantly associated with the risk of APO.

Conclusion: The obtained results suggest that the M2 haplotype may be a relevant risk factor for APO in this Portuguese women population sample. Thus, genotyping *ANXA5* gene for the M2 haplotype status seems to be a well oriented approach in the prognosis of women with unexplained APO and may guide adequate preventive therapeutic measures.

Key-words: Annexin A5, M2 haplotype, Pregnancy, Pregnancy complications, Risk factor.

BACKGROUND

It is well known that pregnancy is a physiological state of hypercoagulability characterized by a progressive increase in the procoagulant activity, which is maximal around term, while the anticoagulant and fibrinolytic activities are impaired, in order to protect the mother against the bleeding challenges associated with miscarriage and childbirth.¹ On the other hand, these hemostatic changes predispose both the mother and fetus, to adverse pregnancy outcomes (APO), such as recurrent pregnancy loss (RPL), premature birth (PB), intrauterine growth restriction (IUGR), small for gestational age (SGA), intrauterine fetal death (IUFD), gestational hypertension (GH), pre-eclampsia (PE), placental abruption and venous thromboembolism (VTE).² These APO collectively complicate up to 15% of pregnancies and are the leading causes of maternal and fetal morbimortality in developed countries,³ which is in accordance with a Portuguese report, where coagulopathy, hemorrhagic disorders and gestational hypertension were the major maternal death causes (49.6%).⁴

These risks are higher in women with acquired or inherited hypercoagulation disorders that promote venous thrombosis. Amongst the non-inherited predisposing factors, some are considered strong/moderate [odds ratio (OR) >2] provoking factors, such as, major trauma, immobilization, auto-immune diseases, pregnancy or puerperium, hormone replacement therapy and oral contraception.⁵ Regarding the inherited risk factors, they have a strong heritability, estimated around 50%.⁶ Amongst these, there are classical factors, such as, rare deficiencies in natural coagulation inhibitors (antithrombin, protein C and protein S), Factor V Leiden (*FVL*) and prothrombin G20120A variants.⁶ The association between these variants and APO have been widely studied.⁷⁻⁹ However, while case-control studies suggested the existence of this association, large cohort studies failed to demonstrate it, or when established, it was weak and translated into a small absolute increased risk.^{2,8,10,11}

Annexin A5, a member of the annexin family of calcium-dependent phospholipid binding proteins, functions as an inhibitor of coagulation due to its ability to bind to anionic phospholipids, and most avidly to phosphatidylserine, exposed on the surface of platelets,¹² thereby inhibiting aggregation and/or down-regulating the cell surface presentation of tissue factor.¹³ Annexin A5, originally named "placental anticoagulant protein", is abundantly found on the apical surface of placental syncytiotrophoblast,¹⁴ the interface between maternal and fetal circulation. Therefore, it has been proposed that Annexin A5 builds an antithrombotic shield, covering the exposed phosphatidylserine content, and thus contributing to the maintenance of blood fluidity in the placenta.^{15,16} Most recently, it was found that Annexin A5 functions as an endogenous membrane repair protein essential for the placental integrity.¹⁷ Bogdanova et al. identified the presence of two variant haplotypes in the promoter region of the ANXA5 gene, in addition to the wild-type, termed M1 and M2 haplotypes. The M2 haplotype is a group of single nucleotide polymorphisms (SNP), which comprises of four consecutive nucleotide substitutions (-19G/A, 1A/C, 27T/C and 76G/A), while in the M1 haplotype only two of the four nucleotide substitutions were present (1A/C and 27T/C).¹⁸ Reporter gene assays have demonstrated a reduction in the activity of the ANXA5 promoter region when the M2 haplotype is present, which was 37-42% of the wild-type promoter.^{18,19} The decrease was less pronounced for M1 (57-62% activity).¹⁸ Since the syncytiotrophoblast, which carries the Annexin A5 protein at its surface, is of fetal origin and has both a halfmaternal and half-paternal genome, it has been proved that reduced ANXA5 expression was independent of M2 allele parental origin, making the M2 haplotype the first case of a hereditary factor causing pregnancy pathology by affecting embryonic-induced anticoagulation.^{19,20} Moreover, it was shown that there is no genetic compensation through the wild-type allele in heterozygous placentas.¹⁹ It was thus reasonable to speculate that carriage of the M2 haplotype leads to a reduced Annexin A5 cover of the exposed phosphatidylserine

surfaces, allowing coagulation factors to compete for phospholipid binding, and consequently leading to a prothrombotic placental environment, which in turn may induce the development of APO.¹⁵ In fact, the M2 haplotype frequency was found to be significantly higher in German patients who had experienced RPL than among controls, and women with de M2 haplotype had about a twofold higher risk of RPL than non-carriers.¹⁸ Subsequent studies confirmed the M2/ANXA5 association with RPL among Italian, German, Bulgarian, UK white European, Japanese and Malay populations.²¹⁻²⁶ The M2 haplotype has also been associated with other APO such as GH and PE,^{20,21,27,28} as well as a risk factor for IUGR²⁹ and SGA,^{21,27,28,30} PB²⁸ and VTE.³¹ However, no significant association was noted between the M1 haplotype and APO when compared with different control groups.^{18,21-23,25,26,28,30}

The aims of the present study were i) to determine the frequency of the M2 haplotype in a Portuguese women population sample and ii) to assess the association between the M2 haplotype and the risk of APO, in order to address the unclear causes of APO and predictive value of the *ANXA5* genotyping in pregnancy.

MATERIALS AND METHODS

Sample Selection

The case group included 102 women (mean age of 33.5 years, range 17-41) referred to the Pregnancy and Thrombophilia Consultation Center incorporated by clinicians of both departments - Bissaya Barreto Maternity Hospital and Clinical Hematology department, from Centro Hospitalar e Universitário de Coimbra - in Portugal, between January 2012 and December 2015, with at least one previous episode of unexplained APO including RPL, early miscarriage, IUFD, IUGR, PE, eclampsia and hemolysis, elevated liver enzymes and low platelets (HELLP) syndrome.

RPL was defined as the occurrence of three or more consecutive pregnancy losses before the 22nd week of gestation (WG), early miscarriage was defined as those occurred before the 12th WG,³² while IUFD was defined as having a fetal loss after completing the 24th WG.^{21,33} IUGR was defined as an estimated fetal weight below the 10th percentile for gestational age.^{32,34} PE was defined as the occurrence of GH (blood pressure \geq 140/90 mmHg in at least two different measurements, more than 6 hours apart, in a previously normotensive woman) and proteinuria (\geq 300 mg/24 h urine specimen), after the 20th WG.³² Eclampsia was defined as the presence of new-onset seizures in a woman with PE, and HELLP syndrome was defined by a laboratory documentation of hemolysis with increased lactate dehydrogenase (>600 U/L), elevated liver enzymes (aspartate aminotransferase>70 U/L) and low platelet counts (<10000/µL).³²

Detailed previous medical history was reviewed, including obstetric and reproductive history, as well as information on medical conditions known to increase the risk for thromboembolism (TE) (i.e. smoking habits, obesity, dyslipidemia, hypertension and diabetes *mellitus*) was obtained.

In order to maximize our ability to detect an association, we excluded APO cases with known risk factors such as: antiphospholipid syndrome, auto-immune diseases, deficiency of antithrombin, protein C or protein S, *FVL* or prothrombin G20120A variants, uterine anomalies and polycystic ovaries. These data were collected retrospectively from the patients' hospital records. Clinically relevant features of the cases are provided in Table 1.

We recruited a total of 84 Portuguese control women (mean age of 42 years, range 26-60) from our Center with at least one successful pregnancy, no documented history of infertility or APO and without TE risk factors (Portuguese controls). We also used as a control population two independent control groups previously recruited in other studies:^{18,22,23,28,35} a cohort of fertile women (n=500) from the registry of the Institute of Human Genetics, University Clinic Münster (Münster controls),¹⁸ and a female control sample (n=533) drafted from PopGen biobank at University Hospital Schesleswig-Holstein, Kiel (PopGen controls).³⁶ The Münster fertile control sample had a northern German origin and was selected along the same criteria as the fertile controls sample. The PopGen population controls were from northwest Germany and were unselected healthy subjects identified through official population registers.

Ethical Statement

Written Informed Consent for genetic studies was obtained prior to the participation in this study from each individual, in accordance with the Declaration of Helsinki. The Ethics Committee of the Faculty of Medicine of the University of Coimbra (Coimbra, Portugal) approved all research methodology.

DNA Extraction

Peripheral blood samples were collected from all participants and genomic DNA was extracted from EDTA whole blood by automatic isolation on iPrepTM instrument, using a gDNA Blood Kit (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's instructions.

Polymerase Chain Reaction (PCR), Sequencing and Genotyping

The promoter region, exon 1 and intronic boundaries of the ANXA5, which comprises of four consecutive nucleotide substitutions (-19G/A, 1A/C, 27T/C and 76G/A) (Figure 1-A), were described amplified by PCR, using primers as previously: P+ex1.F -CCG AGCCCTGGACAGCTCCCCA; P+ex1.R -GCCCCGCGACCACGCTCTCC TCT.¹⁸ PCR reactions were done in a final volume of 25 µL, and the reaction mix contained the following: 2,5 µL of 10x Taq DNA Polymerase PCR buffer (20 mM Tris HCl (pH 8), 40 mM NaCl, 2 mM Na₂HPO₄, 0,1 mM EDTA, 1 mM DTT), 2 µL of dNTP's (2,5 mM) (Invitrogen, Ca, USA), 3.5 µL of forward and reverse primers (50 ng/µL) (Tib Molbiol, Berlin, Germany), 0,75 µL of MgCl₂ (50 mM), 1U of Platinium[®] Taq (Invitrogen, Ca, USA), 1,25 µL of 5% DMSO, 5 μ L of betaine (1M), 1,5 μ L of DNA (100 ng/ μ L), 9,05 μ L of double-distilled H₂O. PCR amplifications were performed using a Tpersonal Thermal Cycler (Biometra, Göttingen, Germany). The PCR cycling conditions were 3 min at 94°C (initial denaturation), followed by 33 cycles of 20 seconds at 94°C (denaturation), 30 seconds at 61°C (annealing) and 1 min at 72°C (extension). In the last cycle, we performed a final extension at 72°C for 5 min. PCR products were run on a 2% agarose gel electrophoresis. The DNA fragments were stained with SYBR[®] Safe DNA Gel Stain (Invitrogen, CA, USA), exposed to UV light and visualized using a transilluminator (Vilber Lourmat, Frane) (Figure 1-B).

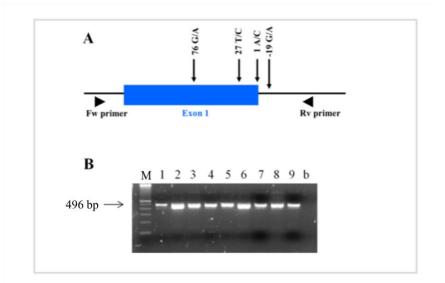


Figure 1. Location of the SNPs within the sequenced region of the *ANXA5* **promoter and PCR analysis.** (A) The SNPs positions were given according to the first *ANXA5* haplotypes detection study.¹⁸ The exon 1 is indicated by a blue box; vertical arrows indicate the SNPs location; triangles indicate the position recognized by primers used to amplify the promoter region. (B) The photo shows an agarose gel electrophoresis of the 496 bp PCR products (lines 1-9). Line M indicates the 100 bp DNA size marker; line b indicates the negative control without DNA.

After the amplification, the Sanger sequencing was performed according to the manufacturer's instructions: products were purified using a cleanup reagent ExoSAP-ITTM, the purified amplicons were then sequenced using BigDye[®] Terminator Cycle Sequencing Kit (Applied Biosystems, CA, USA), and the sequencing products were run on a 3130 Genetic Analyzer (Applied Biosystems, CA, USA) through capillary electrophoresis. Traces were examined and compared using Seqscape[®] software v2.5. (Applied Biosystems, CA, USA) to available DNA sequences in the GenBank database³⁷ (Figure 2).

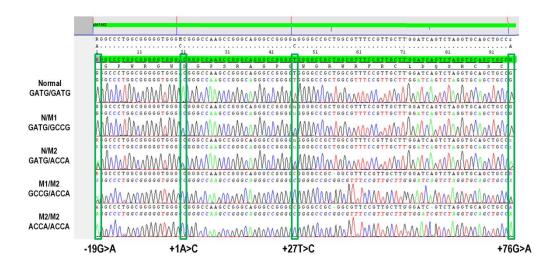


Figure 2. Electropherogram from Sanger sequencing. The figure shows the four different SNP's which comprises the *ANXA5* haplotypes (M1 and M2) and all the possible genotypes.

Statistical Analyses

The allele frequencies were estimated by simple counting and deviations from the Hardy-Weinberg equilibrium (HWE) were performed using a Monte Carlo Markov chain (MCMC) implementation of an exact test.³⁸ The distribution of the *ANXA5* haplotypes between the studied groups was analyzed using Fisher's exact test. OR with 95% confidence intervals (CI) were calculated. Tests were assumed significant whenever p<0.05. All these statistical analyses were performed using GraphPad Prism 6.02 for Windows (GraphPad Software, La Jolla, CA, USA, <u>www.graphpad.com</u>).

RESULTS

Population characteristics

The case group included 102 women with previous history of unexplained APO. 101 women were Caucasian and one was African. They had a mean age of 33.5 years (17-41), a median number of pregnancies of 2 (0–7) and a median parity of 1 (0–2). Mean body mass index (BMI) was 24.62 ± 3.98 Kg/m² (mean ±SD). Acquired risk factors for TE were distributed as following: smoking habit 13.7% (n=14), obesity 13.7% (n=14), dyslipidemia 11.7% (n=12), hypertension 2.9% (n=3) and only 1 had previous history of diabetes (Table 1).

Table 1. Demographic and chinical data of women with AI O.				
Characteristics	Cases (n=102)			
Demographic data				
Age, mean (range)	33.5 (17-41)			
Number of pregnancies, median (range)	2 (0-7)			
Parity, median (range)	1 (0-2)			
Acquired TE risk factors, n (%)				
Smoking habit	14 (13.7%)			
Obesity	14 (13.7%)			
Dyslipidemia	12 (11.7%)			
Hypertension	3 (2.9%)			
Diabetes mellitus	1 (0.9%)			

Table 1: Demographic and clinical data of women with APO.

TE – Thromboembolism; n – Number.

The diverse APO summarized in Table 2 evidence that almost half of the pregnant women showed pregnancy-related hypertensive disorders, and 48 had experienced a median of 3 pregnancy losses (range 1-5), with a total of 108 pregnancy losses, 91% in the first trimester. We highlight that some women had more than one subtype of APO.

Subtype of APO	n (%)
Pregnancy-related hypertensive disorders (PE/HELLP syndrome/eclampsia)	50 (49.02)
Pregnancy losses	48 (47.05)
Early miscarriages (<12 WG) - 37 (77.08%)	
<i>RPL (≥3)</i> - 24 (50%)	
IUGR	28 (27.45)
IUFD (27-39 WG)	10 (9.8)

Table 2: Characterization of APO in the case group.

PE – Pre-eclampsia; HELLP – Hemolysis, elevated liver enzymes, and low platelets; RLP – Recurrent pregnancy loss; WG – Week of gestation; IUGR – Intrauterine growth restriction; IUFD – Intrauterine fetal death; n – Number.

Association of the ANXA5 M2 haplotype with APO

When comparing the study case group with the Portuguese control group, the allele frequency of the M2 haplotype was found to be substantially higher in APO cases (0.167) than among Portuguese controls (0.083) (Table 3). Consequently, a relative risk of 1.32 for APO was observed in the M2 carriers *versus* non-carriers (OR 2.15, 95% CI 1.13-4.30; p=0.0280), when compared with the Portuguese controls (Table 4). The Portuguese control group and cases group were in HWE for the *ANXA5* haplotypes (MCMC p=0.797 and p=0.857, respectively). The frequency of the M2 allele was also higher in the APO cases (0.167) in comparison to the Münster controls (0.051) and the PopGen controls (0.082). The M2 haplotype contributes to a relative risk of 2.36 for APO (OR 3.27, 95% CI 2.06-5.15; p<0.0001), when compared with the Münster controls, and contributes to a relative risk of 1.74 (OR 2.04, 95% CI 1.32-3.10; p<0.0015), when compared with the PopGen controls. In the Münster control group, a significant deviation from the HWE was observed (MCMC

p<0.0001), which was mainly owing to the excess of M2 homozygotes (10 observed *versus* 1.4 expected). The PopGen control group was in HWE for the ANXA5 haplotypes (MCMC p=0.409).

No association between carriage status for the M2 haplotype and the subtype of APO was identified. No other differences in age, BMI, TE risk factors were identified when comparing the M2 carriers *versus* non-carriers.

Genotype M1/M1 was absent in the APO cases group and in the Portuguese control group, thus no significant association of the M1 haplotype with APO was noted when comparing with different control groups.

Genotype	Cases		Portuguese	e controls	Münster co	ontrols	PopGen co	ntrols
	Observed n (%)	Expected	Observed n (%)	Expected	Observed n (%)	Expected	Observed n (%)	Expected
N/N	58 (56.9)	58.1	52 (61.9)	53.4	356 (71.2)	343.6	415 (77.9)	413.3
N/M1	12 (11.8)	12.1	19 (22.6)	16.0	87 (17.4)	99.5	35 (6.6)	47.8
M1/M1	0 (0)	0.6	0 (0)	1.2	16 (3.2)	7.2	1 (0.2)	1.5
N/M2, M1/M2	30 (29.4)	28.4	12 (14.3)	12.8	31 (6.2)	48.4	77 (14.4)	69.0
M2/M2	2 (2.0)	2.8	1 (1.19)	0.6	10 (2)	1.4	5 (0.9)	1.4
Total	102	102	84	84	500	500	533	533
M2 carriage (%)	31.4		15,5		8.2		15.4	
M2 AF	0.167		0.083		0.051		0.082	

Table 3: Genotype frequencies of *ANXA5* gene promoter haplotypes in APO cases group *versus* three different control groups.

 $\label{eq:expected-genotype frequency expected at the Hardy-Weinberg equilibrium; AF-allele frequency; n-Number.$

Index category	Cases (n=102)	Cases (n=102)	Cases (n=102)		
Reference category	Portuguese controls (n=84)	Münster controls (n=500)	PopGen controls (n=533)		
RR	1.32	2.36	1.74		
OR	2.15	3.27	2.04		
95% CI	1.13-4.30	2.06-5.15	1.32-3.10		
p value	0.0280	< 0.0001	0.0015		

Table 4: Association between APO and the M2 haplotype in comparison with the control groups.

RR – Relative risk; OR – Odds ratio; CI – Confidence interval; N – number.

DISCUSSION AND CONCLUSIONS

In this work we report a study of the M2 *ANXA5* promoter haplotype, previously found associated with APO in several different ethnic populations. Prior studies using controls with a German, Italian, Bulgarian and UK white European origin, with at least one successful pregnancy and no former history of APO, conveyed a M2 carriage rate of 15-17%,^{18,21-23} which is in agreement with the frequency of 15.5% found in our control population sample of Portuguese origin. In contrast, a lower frequency of 11% has been observed in Japanese populations,^{20,24} whereas in Northern European populations the reported carrier rate was about 23.4%-27%³⁹ and 35% in Malay populations.²⁵

Portuguese women with history of APO had a higher M2 allele frequency compared to women with uncomplicated pregnancies with the same origin (0.167 versus 0.083) and also, when compared with two independent control groups previously recruited in other studies, the Münster controls group (0.051) and the PopGen controls (0.082) of German origin.^{18,22,23,28,35} Both control groups, the Portuguese controls and the PopGen controls, were in HWE for the M2 haplotype. Thus, our selected control group could be viewed as a representative sample of the Portuguese population. However, a deviation from HWE was observed in the Münster controls like in previous studies, owing to an excess of M2 homozygotes. A possible explanation to this is the positive ascertainment bias resulting from the Münster controls group consisting entirely of women who had no history of APO, whereas APO usually occurs in up to 15% of women worldwide.^{3,23} We have shown that carriers of the M2 have a higher APO risk than non-carriers, with an estimated OR close to 2 for M2 carriers when compared to controls, which strengthens the significant association of the M2 haplotype of ANXA5 with APO, already demonstrated in European and Asian APO cohorts, with OR for the M2 carriers ranging between 1.4 and 3.1.^{18,21-25,28,30,31} Although these findings were in disagreement with the Northern European population-based study, where a lower M2 carriage rate was detected among the APO patients compared to the controls (15%-18% versus 23.4-27%).³⁹ However, it is important to bear in mind that the differences between studies may arise from different aspects, such as differences in selection criteria for APO subjects and controls, experimental setup or study design.³⁹

The M2 haplotype frequency was very similar among early miscarriage, RPL, pregnancyrelated hypertensive disorders, IUGR and IUFD, which was in agreement with the previously obtained results for these APO,^{21,28} except for IUFD, which has not been significantly associated with the M2 haplotype.²¹ In fact, it has been suggested that ANXA5 plays a more important role before de 15th WG,^{21-23,25,26} which relates to a time in the course of pregnancy when embryonic implantation²¹ and placental vascular remodeling happens²², in contrast to the *FVL* and prothrombin G20120A variants reported to lead to adverse events after the 10th WG.^{8,10,40}

The diagnostic protocol in Bissaya Barreto Maternity Hospital for women with history of unexplained APO, involves the screening of antiphospholipid antibodies and the more common inherited risk factors for thrombophilias (*FVL* and prothrombin G20120A variants), or others if there is a documented family history. However the screening of inherited risk factors for thrombophilias in women with history of unexplained APO, but without personal or family history of VTE, is controversial since large cohort studies failed to demonstrate a significant association between them and APO.^{2,8,10,11} In contrast, we found a significant association between the M2 haplotype and APO, besides the fact that the M2 haplotype carriage rate in the Portuguese control sample was equal or about 3 times higher than the frequency of the *FVL* in the European population.^{32,41} Thus, we consider that genetic testing for *ANXA5* haplotypes could be considered in the thrombophilic risk assessment algorithm of women who previously suffered from an unexplained APO, mainly if it occurs in early pregnancy stages. The usefulness of screen *ANXA5* haplotypes is even more supported by the

fact that there are biological reasons for supposing that M2 carriers may benefit from lowmolecular-weight heparin treatment starting before a new clinical pregnancy is confirmed.⁴² Recent studies conducted with couples with history of APO, rather than mothers alone, had demonstrated that paternal M2 carriage confers a similar relative risk for APO as maternal M2 carriage^{20,22,23,25,35,43} so on the basis of the findings from these studies, screening for M2 carriage on both partners in APO couples should be considered.

Some limitations of the present study need to be taken into account when interpreting the results obtained. Indeed, the cases group included some women with known acquired risk factors for TE, which may have functioned as confounding factors, distorting the M2/ANXA5 APO association studied. This was a small population-based study, with a small patient number for each APO. Even though the Hardy-Weinberg analysis did not reveal any evidence of population disequilibrium in the Portuguese controls and cases groups, the diminished total size sample does not allow the generalizability of the study results. The clinical data was retrospectively collected, thus there may be some confounding factors that were not possible to control within the study. To overcome these limitations, further studies prospectively conducted with a larger total sample size and for each APO, are required. Moreover, as already done in studies conducted in other countries, would be also interesting to verify the role of paternal M2 carriage and the relation of M2 carriage to the timing of APO in the Portuguese population, in order develop a thrombophilic risk assessment algorithm for couples with history of unexplained APO.

In conclusion, our results suggest that the M2 haplotype of the *ANXA5* gene may contribute to the risk of APO in Portuguese women carriers of this haplotype. Considering the estimated high general frequency of the M2 haplotype, the data collected emphasizes the usefulness of the incorporation of M2 carrier status screening in risk APO assessment models for women with history of unexplained APO.

CONFLICT OF INTEREST STATEMENT

There are no conflicts of interest in this paper.

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