Functional Polymorphisms of the Coagulation Factor II Gene (*F2*) and Susceptibility to Systemic Lupus Erythematosus

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ABSTRACT. ***Objective.*** Two *F2* functional polymorphisms, rs1799963 (G20210A) and rs3136516 (A19911G), are known to be associated with elevated levels/activity of prothrombin (encoded by *F2*) and risk of thrombosis. Since patients with systemic lupus erythematosus (SLE) have high risk of thrombosis and accelerated atherosclerosis and also high prevalence of anti-prothrombin antibodies, we hypothesized that these two *F2* polymorphisms could affect risk of SLE.

Methods. We investigated these polymorphisms in 627 women with SLE (84% Caucasian Americans, 16% African Americans) and 657 female controls (78% Caucasian Americans, 22% African Americans).

Results. While the rs1799963 A allele was almost absent in African Americans, it was present at ~2% frequency in Caucasian Americans and showed no significant association with SLE. The rs3136516 G allele frequency was significantly higher in Caucasian SLE cases than in controls (48.4% vs 43.7%, respectively) with a covariate-adjusted odds ratio (OR) of 1.22 (95% CI 1.03–1.46, p = 0.023). The association was replicated in African Americans (rs3136516 G allele frequency 91.2% in cases vs 82.2% in controls) with an adjusted OR of 1.96 (95% CI 1.08–3.58, p = 0.022). Stratification of Caucasian SLE patients based on the presence or absence of cardiac and vascular events (CVE) revealed stronger association with the CVE-positive SLE subgroup than the CVE-negative SLE subgroup (OR 1.42 vs 1.20). Prothrombin activity measurements in a subset of SLE cases demonstrated higher activity in the carriers of the rs3136516 G allele.

Conclusion. Our results suggest a potential role for prothrombin and the crosstalk between hemostatic and immune/inflammatory systems in SLE and SLE-associated cardiovascular events, which warrants further investigation in independent samples. (J Rheumatol First Release Jan 15 2011; doi:10.3899/jrheum.100728)

Key Indexing Terms:
LUPUS PROTHROMBIN *F2* POLYMORPHISM A19911G G20210A

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Supported by the National Institutes of Health (R01-HL088648, R01-AR057028, R01-AR046588, K24-AR002213, K24-AR002138, P60-AR48098).

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Accepted for publication November 2, 2010.

Prothrombin is a vitamin K-dependent glycoprotein that is primarily synthesized in the liver and secreted into circulating plasma. Upon activation by the prothrombinase complex (activated factor X, factor V, calcium, and phospholipids), prothrombin (factor II) is converted to its enzymatically active form, thrombin (factor IIa). In the coagulation cascade, thrombin exerts its procoagulant activity by converting soluble fibrinogen into insoluble fibrin strands as well as by activating other coagulation factors[1]. Thrombin acts also as an indirect anticoagulant by activating protein C on the surface of endothelial cells in the presence of thrombomodulin. Thrombin is a multifunctional protein and, in addition to its well known role in the coagulation cascade, it is involved in platelet aggregation, thrombus formation and fibrinolysis, endothelial barrier integrity, immune cell adhesion/activation, inflammation, and tissue reparative processes[2,3,4]. Thrombin is among the key factors that mediate the extensive crosstalk between inflammation and hemostasis, the 2 major processes of defensive host response[5].

Systemic lupus erythematosus (SLE) is a chronic inflammatory autoimmune disease that predominantly targets women of reproductive age. Immunological and genetic studies suggest that SLE-related pathogenic mechanisms involve various abnormalities in both innate and adaptive immune responses[6,7,8]. It has been well recognized that patients with SLE are at high risk of thrombosis and premature atherosclerosis[9,10,11]. Elevated plasma prothrombin levels/activity are common in the general population and have been shown to be a risk factor for cardiac and vascular events, especially for venous thrombosis[12,13,14]. Moreover, prothrombin is among major antigens recognized by antiphospholipid antibodies that are also associated with cardiovascular thrombotic events in SLE and other conditions[15,16,17,18,19].

Prothrombin levels are under significant genetic influence, with heritability estimates reaching 50% and higher[20,21,22]. The gene encoding prothrombin (*F2*) spans ~21 kb on chromosome 11p11 and harbors 14 exons. Two functional *F2* single-nucleotide polymorphisms (SNP), rs3136516 (A19911G) and rs1799963 (G20210A), have been reported to be associated with elevated prothrombin levels/activity and increased risk of thrombosis, with the results being more consistent and stronger for the less common G20210A variant[12,23,24,25,26,27,28]. The rs1799963 (located at 3'UTR) minor allele A is believed to affect RNA metabolism by increasing the mRNA 3'-end formation efficiency (enhanced cleavage and processing) and mRNA stability[23,29,30]. An *in vitro* study[24] demonstrated that the rs3136516 polymorphism (located within the 13th intron, which is only 146 bp) is also functional through its effect on an intronic splicing enhancer motif (CAGGG); that is, the G allele was found to cause more efficient splicing of intron 13 than the A allele (~30% higher efficiency) due to the disruption of the intronic enhancer motif by the A allele.

The extensive crosstalk between hemostasis and inflammation, multiple functions of prothrombin/thrombin that are highly relevant to SLE and SLE-associated microvascular disease and/or cardiovascular events (increased risk of thrombosis and accelerated atherosclerosis), and the high prevalence of anti-prothrombin antibodies in patients with SLE strongly support the prothrombin/thrombin gene (*F2*) as a plausible candidate for susceptibility to SLE and related phenotypes. Previous studies investigated functional *F2* polymorphisms mainly for their effects on cardiovascular events in non-SLE individuals. Some reports examined the G20210A SNP in relation to SLE-associated cardiovascular events[31,32,33,34,35], although the sample sizes were underpowered to detect the effects of such an uncommon variant (1.5%–2% frequency in the general Caucasian population). To our knowledge, no study has previously examined both *F2* rs3136516 (A19911G) and rs1799963 (G20210A) SNP (the 2 well known genetic determinants of plasma prothrombin levels/activity) in relation to risk for SLE, which is the focus of this study.

MATERIALS AND METHODS

Subjects and data collection. A total of 1284 women (997 from Pittsburgh, PA, and 287 from Chicago, IL) were included in this study. The Pittsburgh sample comprised 474 women with SLE (417 Caucasian Americans and 57 African Americans, mean age 42.5 ± 11.3 SD yrs) and 447 age-matched female controls with no apparent history of SLE (411 Caucasian Americans and 36 African Americans, mean age 45.5 ± 13.5 yrs). In addition, 76 older female African American controls (mean age 67.1 ± 8.0 yrs) from Pittsburgh were included in the study in order to increase the African American sample size, after confirming that allele frequencies of the SNP of interest were almost identical in the 2 control age groups. The Chicago sample comprised 153 women with SLE (107 Caucasian Americans and 46 African Americans, mean 44.2 ± 10.5 yrs) and 134 age-matched female controls (102 Caucasian Americans and 32 African Americans, mean age 47.4 ± 10.0 yrs).

All SLE patients (≥ 18 yrs of age) met the 1982 or revised 1997 American College of Rheumatology classification criteria for SLE[36,37]. Data were collected at both recruitment sites using identical protocols and laboratory tests. Detailed description of the SLE sample can be found elsewhere[38,39,40]. Of the 524 Caucasian SLE women in this study, 332 were also characterized for the occurrence of cardiac and vascular events, of which 101 (30.4%) had experienced one or more of the following physician-confirmed events in medical records: myocardial infarction (5.5%), coronary artery bypass graft surgery (3.4%), percutaneous transluminal coronary angioplasty (5.8%), angina pectoris (13.4%), cardiac death (1.2%), stroke (5.5%), transient ischemic attack (6.4%), congestive heart failure (4.0%), blood clots (9.7%), or vascular surgery (0.9%).

All participants provided written informed consent for genetic research approved by the University of Pittsburgh and the Northwestern University institutional review boards.

DNA extraction and genotyping. Buffy coat samples from both recruitment sites were processed for genomic DNA isolation at the same laboratory (University of Pittsburgh Human Genetics Department) using QIAamp DNA Kits (Qiagen, Chatsworth, CA, USA). Genotyping of *F2* SNP was performed by TaqMan® allelic discrimination (Applied Biosystems, Foster City, CA, USA) using ready-made SNP Genotyping Assays (C__11661574_10 for rs3136516 and C___8726802_20 for rs1799963) and endpoint fluorescence readings on an ABI Prism 7900HT instrument (Applied Biosystems).

Prothrombin activity measurement. Plasma prothrombin activity measurements were available for analysis in a subset of Caucasian SLE women (n = 120) at the Pittsburgh site. Prothrombin activity was determined using a chromogenic assay (DiaPharma, West Chester, OH, USA). Briefly, 10 μl plasma was diluted 1:40 with Tris-BSA buffer and mixed with Ecarin to activate the prothrombin to meizothrombin, which in turn cleaved the thrombin selective chromogenic substrate S-2238. The absorbance, which is proportional to prothrombin activity in the sample, was measured at 405 nm. Serial dilutions of pooled human plasma (Innovative Research, Novi, MI, USA) were used as the standard.

Statistical methods. Allele and genotype frequencies were determined by direct counting. Allele frequencies were compared between cases and controls using a standard Z-test of 2 binomial proportions. Recruitment site and age were included as covariates in the logistic regression analysis of genotype distribution differences between cases and controls. Genotype associations were tested under the additive model for the common rs3136516 SNP and the dominant model for the uncommon rs1799963 SNP. Linear regression analysis of the effects of genotypes on prothrombin activity was also performed under the additive model, which included age, body mass index (BMI), and warfarin use as covariates. Association analyses were performed using R statistical software (available from: http://www.r-project.org) packages (SNPassoc, genetics, plotrix). Haplotype distribution was determined using Haploview (available from: http://www.broad.mit.edu/mpg/haploview/).

RESULTS

Association analyses of F2 rs3136516 and rs1799963 SNP with SLE risk in Caucasian Americans. The frequency of the rs3136516 G allele was higher in SLE patients than in controls at both Pittsburgh (47.9% vs 43.4%, respectively) and Chicago (50.0% vs 45.0%) sites. In the combined Pittsburgh + Chicago sample (Table 1), the rs3136516 G allele frequency was 48.4% in SLE cases versus 43.7% in controls (p = 0.034). The recruitment site- and age-adjusted OR for the rs3136516 G allele carriers (AA = 0, GA = 1, GG = 2) was 1.22 (95% CI 1.03–1.46, p = 0.023), indicating a modest effect. No significant association was observed for the rs1799963 SNP, which showed comparable allele frequencies between SLE cases and controls (A allele: 2.4% vs 2.0%; p = 0.593, in the combined sample). Haplotype analysis revealed 3 of the 4 expected haplotypes (GG, AG, AA); the fourth haplotype carrying the rs3136516 G and rs1799963 A alleles that are both associated with elevated prothrombin levels/activity was absent (D' = 1, r^2 = 0.019). The common haplotype carrying the rs3136516 risk allele G was overrepresented in cases (GG frequency: 0.484 in cases vs 0.437 in controls) whereas the one carrying the protective allele A was overrepresented in controls (AG frequency: 0.543 in controls vs 0.493 in cases).

Next, we wanted to determine whether the association of the rs3136516 SNP with SLE risk might have been influenced by the cardiovascular status of patients with SLE. For this purpose, we stratified the Caucasian patients with SLE who had been characterized for cardiac and vascular events (CVE) into 2 subgroups based on the presence or absence of CVE and compared them separately with the controls (Table 1). Although the association trend was present in both SLE subgroups, the association of the rs3136516 SNP was stronger with the CVE-positive group (n = 100, OR 1.42) than with the CVE-negative group (n = 228, OR 1.20) as compared to the healthy controls (n = 509) and remained significant (p = 0.024 vs p = 0.114) despite more dramatically reduced sample size. The comparison between SLE patients with and those without CVE did not yield a significant result, although the numbers were relatively small (100 vs 228 patients, respectively) for meaningful analysis considering the modest effect sizes observed in Caucasians.

Association analysis of F2 rs3136516 SNP with SLE risk in African Americans. Following the observation of a significant association of the rs3136516 SNP with SLE in Caucasian Americans, we sought a similar association in African Americans. As in Caucasian Americans, the rs3136516 G allele frequency was higher in African American women with SLE than in controls at both Pittsburgh (92.9% vs 82.0%) and Chicago (89.1% vs 82.8%) sites. In the combined sample (Table 1), the rs3136516 G allele frequency was 91.2% in SLE cases versus 82.2% in controls (p = 0.003). The OR for the rs3136516 G allele carriers (AA = 0, GA = 1, GG = 2) was 1.96 (95% CI 1.08–3.58; p = 0.022) after adjustment for the effects of the recruitment site and age. Only 2 African American individuals were found to carry the rs1799963 A allele (in the heterozygous state), thus the association analysis was not feasible for this SNP in the African American sample.

Association analysis of F2 rs3136516 SNP with plasma prothrombin activity in Caucasian American SLE cases. Among Caucasian American SLE cases with available prothrombin activity measurements at the Pittsburgh site, the rs3136516 G allele was significantly associated with a modest increase in plasma prothrombin activity (p = 0.039 after adjustment for age, BMI, and warfarin use; Table 2). The effect of the rs3136516 G allele remained significant (p = 0.015) after excluding the cases carrying the rs1799963 A allele (by evaluating only the individuals with wild-type GG genotype for rs1799963).

DISCUSSION

Since first reported in 1996[12], the uncommon *F2* variant, rs1799963 (G20210A), has been established as a risk factor for hyperprothrombinemia and venous thrombosis in Caucasian populations. The relationship between this poly-

Table 1. Allele frequencies and association statistics for *F2* rs3136516 SNP in SLE women compared to control women. Only data for successfully genotyped individuals were included in the table.

rs3136516	Caucasian Americans				African Americans	
	Controls, n = 509	All Cases, n = 519	CVE Negative Cases*, n = 228	CVE Positive Cases*, n = 100	Controls, n = 143	All Cases, n = 102
Alleles						
A	0.563	0.516	0.515	0.470	0.178	0.088
G	0.437	0.484	0.485	0.530	0.822	0.912
p**	—	0.034	0.091	0.016	—	0.003
OR† (95% CI; p†)	—	1.22 (1.03–1.46; 0.023)	1.20 (0.96–1.49; 0.114)	1.42 (1.05–1.92; 0.024)	—	1.96 (1.08–3.58; 0.022)

* Caucasian SLE cases with available cardiovascular data were stratified by the occurrence of cardiac and vascular events (CVE): myocardial infarction, coronary artery bypass graft surgery, percutaneous transluminal coronary angioplasty, angina pectoris, cardiac death, stroke, transient ischemic attack, congestive heart failure, blood clots, or vascular surgery. ** Comparison of the allele frequencies between cases and controls using a standard Z-test of 2 binomial proportions. † Odds ratios and p values under additive genetic effect model (AA = 0, GA = 1, GG = 2), adjusted for recruitment site and age.

Table 2. Relation between *F2* rs3136516 genotypes and plasma prothrombin activity (PPA) in a subset of Caucasian SLE cases (analysis was performed regardless of *F2* rs1799963 status and only in individuals with wild-type GG genotype for rs1799963). Only data for successfully genotyped individuals with available PPA measurements were included in the table.

rs3136516	Caucasian Americans: All Cases, n = 117 PPA mean ± SE*	Caucasian Americans: Cases with GG Genotype for rs1799963, n = 111 PPA mean ± SE*
Genotypes		
AA	15.17 ± 0.88 (86.69 ± 5.05)	14.79 ± 0.88 (84.53 ± 5.00)
GA	15.65 ± 0.46 (89.45 ± 2.61)	15.62 ± 0.47 (89.28 ± 2.69)
GG	17.70 ± 1.01 (101.12 ± 5.76)	17.73 ± 1.00 (101.30 ± 5.73)
p*	0.039	0.015

* Mean and p values adjusted for age, body mass index, and warfarin use; p values under additive genetic effect model. Mean values are presented in National Institutes of Health (NIH) U/ml; percentages of normal activity are given in parentheses.

morphism and arterial thrombosis risk (i.e., myocardial infarction and stroke) was also evaluated, but yielded inconsistent results[14]. More recently, a common *F2* SNP (rs3136516, A19911G) was also reported to be associated with increased plasma prothrombin activity and thrombosis risk in Caucasians, although at a lesser degree[27,28,41]. Large studies and metaanalysis suggested that the rs3136516 G allele is associated with a slight increase in prothrombin activity and thrombotic risk[26,42,43]. Previous studies[13,26,27,28] indicated that chromosomes carrying the rs1799963 A allele almost always had the rs3136516 A allele, which was also confirmed in our study.

While no significant effect of the uncommon rs1799963 variant on SLE was observed in our study, a significant association of the common rs3136516 SNP with SLE susceptibility was detected in both Caucasian and African Americans (Table 1). The rs3136516 G allele frequency was significantly higher in Caucasian American SLE cases than in controls (48.4% vs 43.7%, respectively) with a covariate-adjusted OR of 1.22 (95% CI 1.03–1.46, p = 0.023) indicating a modest effect size. The effect seemed to be stronger in the CVE-positive SLE subgroup than in the CVE-negative SLE subgroup (OR 1.42 vs 1.20), which warrants further confirmation in larger SLE samples characterized for CVE. The association was replicated in the African American sample, where the rs3136516 G allele frequency was also significantly higher in SLE cases than in controls (91.2% vs 82.2%), with an adjusted OR of 1.96 (95% CI 1.08–3.58, p = 0.022). In public databases (dbSNP and HapMap), African populations show absence or varying low frequencies of the rs3136516 A allele, suggesting that the G allele is the ancestral allele and that the presence of the A allele may be due to varying degrees of Caucasian admixture. Interestingly, a major SLE locus was identified on the short arm of chromosome 11 by genome-wide linkage scan of African American families[44], although the maximum LOD score was reported at a marker (D11S1392, 11p13) located ~12.1 Mb telomeric to *F2* (11p11). It may still be worthwhile to evaluate *F2* in these families given that the location estimates may vary substantially in linkage studies of complex disorders, with 95% confidence intervals covering tens of cM, even in samples including relatively large numbers of families[45].

The mechanism of action of the *F2* rs3136516 SNP on SLE risk remains to be determined. The rs3136516 G allele, which was shown to cause more efficient RNA splicing than the A allele, was reported to cause slightly higher prothrombin activity. Consistently, we found in our SLE cases that the rs3136516 G allele was associated with higher plasma prothrombin activity and its effect remained significant after excluding the cases carrying the rs1799963 A allele, which is an established genetic determinant of elevated prothrombin levels and activity (Table 2). The rs1799963 A allele did not appear to increase SLE risk in our sample, although our study was underpowered to detect a small to moderate effect of this uncommon variant, thus its effect on SLE still remains a possibility. Alternatively, the rs3136516 SNP may be influencing the SLE risk by another currently unknown mechanism (i.e., not only affecting the splicing efficiency but also changing the splicing behavior and yielding different isoforms). A direct analysis of the RNA samples from primary liver cells of individuals carrying different rs3136516 genotypes will be necessary to unravel the exact functional effect of this SNP. Another possibility is that the rs3136516 SNP may not be causative itself, but may simply be in strong linkage disequilibrium (LD) with a true causative (yet to be identified) variant residing in *F2* or a nearby gene. Current information in the literature[13] and public databases (SeattleSNPs and HapMap) does not indicate the presence of other *F2* common SNP strongly correlated with the rs3136516 SNP. Comprehensive resequencing-based analysis of the entire *F2* gene and its flanking regions, in conjunction with analysis of prothrombin activity and levels, will help to characterize the true SLE-related causative effects.

The role of prothrombin/thrombin in hemostasis, thrombosis, and occurrence of antiphospholipid antibodies (that are also associated with increased thrombosis risk) has long been recognized. Studies increasingly emphasize that prothrombin has actually a plethora of biological functions that also include an important role in inflammation and immune activation[2,3,5]. Thrombin, the active form of prothrombin, was shown to be chemotactic for monocytes and neutrophils and can induce several inflammatory responses, including cytokine production and apoptosis[5,46]. A number of biological pathways are being implicated in SLE pathogenesis and our study indicates that the "hemostasis and its crosstalk with immunity and inflammation" can be added to this growing list.

To our knowledge, this is the first study to evaluate the role of *F2* rs3136516 common SNP in relation to susceptibility for SLE. The significant and consistent association of the rs3136516 G allele with SLE risk in both Caucasians and African Americans suggests that this *F2* polymorphism might play a role in SLE pathogenesis. Its effect size seems to be modest, although more pronounced among SLE patients who had experienced cardiac and/or vascular events. Nevertheless, replication by independent groups is essential in establishing genetic associations with complex disorders due to various factors that may lead to false-positive associations (i.e., by chance, power issues, population stratification). Our study had more than 60% but less than 80% power to detect the odds ratios reported in our Caucasian and African American samples. Although our sample size was reasonable in Caucasians, it was relatively small in African Americans. The rs3136516 SNP was neither part of the high-density genotyping panels used by recently published genome-wide association studies of SLE[47,48,49] nor strongly correlated with any common *F2* SNP included in those panels. Therefore, other groups will need to genotype this SNP in their independent large samples in order to replicate our findings, and the cardiovascular status of the participants (cases and controls) is likely to influence the results.

REFERENCES

1. Amengual O, Atsumi T, Koike T. Antiprothombin antibodies and the diagnosis of antiphospholipid syndrome. Clin Immunol 2004;112:144-9.
2. Narayanan S. Multifunctional roles of thrombin. Ann Clin Lab Sci 1999;29:275-80.
3. Strukova SM. Thrombin as a regulator of inflammation and reparative processes in tissues. Biochemistry (Mosc) 2001;66:8-18.
4. Szaba FM, Smiley ST. Roles for thrombin and fibrin(ogen) in cytokine/chemokine production and macrophage adhesion in vivo. Blood 2002;99:1053-9.
5. Cicala C, Cirino G. Linkage between inflammation and coagulation: an update on the molecular basis of the crosstalk. Life Sci 1998;62:1817-24.
6. Mok CC, Lau CS. Pathogenesis of systemic lupus erythematosus. J Clin Pathol 2003;56:481-90.
7. Crow MK. Collaboration, genetic associations, and lupus erythematosus. N Engl J Med 2008;358:956-61.
8. Rahman A, Isenberg DA. Systemic lupus erythematosus. N Engl J Med 2008;358:929-39.
9. Manzi S, Meilahn EN, Rairie JE, Conte CG, Medsger TA Jr, Jansen-McWilliams L, et al. Age-specific incidence rates of myocardial infarction and angina in women with systemic lupus erythematosus: comparison with the Framingham Study. Am J Epidemiol 1997;145:408-15.
10. Manzi S, Selzer F, Sutton-Tyrrell K, Fitzgerald SG, Rairie JE, Tracy RP, et al. Prevalence and risk factors of carotid plaque in women with systemic lupus erythematosus. Arthritis Rheum 1999;42:51-60.
11. Meesters EW, Hansen H, Spronk HM, Hamulyak K, Rosing J, Rowshani AT, et al. The inflammation and coagulation cross-talk in patients with systemic lupus erythematosus. Blood Coagul Fibrinol 2007;18:21-8.
12. Poort SR, Rosendaal FR, Reitsma PH, Bertina RM. A common genetic variation in the 3'-untranslated region of the prothrombin gene is associated with elevated plasma prothrombin levels and an increase in venous thrombosis. Blood 1996;88:3698-703.
13. Reiner AP, Carlson CS, Rieder MJ, Schwartz SM, Siscovick DS. Common genomic sequence variation of the prothrombin gene and risk of non-fatal myocardial infarction in white women. J Thromb Haemost 2005;3:2809-11.
14. Boekholdt SM, Kramer MH. Arterial thrombosis and the role of thrombophilia. Semin Thromb Hemost 2007;33:588-96.
15. Galli M, Beretta G, Daldossi M, Bevers EM, Barbui T. Different anticoagulant and immunological properties of anti-prothrombin antibodies in patients with antiphospholipid antibodies. Thromb Haemost 1997;77:486-91.
16. De Groot PG, Horbach DA, Simmelink MJ, Van Oort E, Derksen RH. Anti-prothrombin antibodies and their relation with thrombosis and lupus anticoagulant. Lupus 1998;7:S32-36.
17. Afeltra A, Vadacca M, Conti L, Galluzzo S, Mitterhofer AP, Ferri GM, et al. Thrombosis in systemic lupus erythematosus: congenital and acquired risk factors. Arthritis Rheum 2005;53:452-9.
18. Nojima J, Iwatani Y, Suehisa E, Kuratsune H, Kanakura Y. The presence of anti-phosphatidylserine/prothrombin antibodies as risk factor for both arterial and venous thrombosis in patients with systemic lupus erythematosus. Haematologica 2006;91:699-702.
19. Bizzaro N, Ghirardello A, Zampieri S, Iaccarino L, Tozzoli R, Ruffatti A, et al. Anti-prothrombin antibodies predict thrombosis in patients with systemic lupus erythematosus: a 15-year longitudinal study. J Thromb Haemost 2007;5:1158-64.
20. Rosendaal FR, Bovill EG. Heritability of clotting factors and the revival of the prothrombotic state. Lancet 2002;359:638-9.
21. Vossen CY, Hasstedt SJ, Rosendaal FR, Callas PW, Bauer KA, Broze GJ, et al. Heritability of plasma concentrations of clotting factors and measures of a prethrombotic state in a protein C-deficient family. J Thromb Haemost 2004;2:242-7.
22. Warren DM, Soria JM, Souto JC, Comuzzie A, Fontcuberta J, Blangero J, et al. Heritability of hemostasis phenotypes and their correlation with type 2 diabetes status in Mexican Americans. Hum Biol 2005;77:1-15.
23. Gehring NH, Frede U, Neu-Yilik G, Hundsdoerfer P, Vetter B, Hentze MW, et al. Increased efficiency of mRNA 3' end formation: a new genetic mechanism contributing to hereditary thrombophilia. Nat Genet 2001;28:389-92.
24. Von Ahsen N, Oellerich M. The intronic prothrombin 19911 A>G polymorphism influences splicing efficiency and modulates effects of the 20210 G>A polymorphism on mRNA amount and expression in a stable reporter gene assay system. Blood 2004;103:586-93.
25. Van Der Putten HH, Bertina RM, Vos HL. Is the prothrombin 19911 A>G polymorphism a functional noncoding variant? Blood 2005;105:2995.
26. Chinthammitr Y, Vos HL, Rosendaal FR, Doggen CJ. The association of prothrombin A19911G polymorphism with plasma prothrombin activity and venous thrombosis: results of the MEGA study, a large population-based case-control study. J Thromb Haemost 2006;4:2587-92.
27. Martinelli I, Battaglioli T, Tosetto A, Legnani C, Sottile L, Ghiotto

R, et al. Prothrombin A19911G polymorphism and the risk of venous thromboembolism. J Thromb Haemost 2006;4:2582-6.
28. Castoldi E, Simioni P, Tormene D, Thomassen MC, Spiezia L, Gavasso S, et al. Differential effects of high prothrombin levels on thrombin generation depending on the cause of the hyperprothrombinemia. J Thromb Haemost 2007;5:971-9.
29. Carter AM, Sachchithananthan M, Stasinopoulos S, Maurer F, Medcalf RL. Prothrombin G20210A is a bifunctional gene polymorphism. Thromb Haemost 2002;87:846-53.
30. Pollak ES, Lam HS, Russell JE. The G20210A mutation does not affect the stability of prothrombin mRNA in vivo. Blood 2002;100:359-62.
31. Topaloglu R, Akierli C, Bakkaloglu A, Aydintug O, Ozen S, Besbas N, et al. Survey of factor V leiden and prothrombin gene mutations in systemic lupus erythematosus. Clin Rheumatol 2001;20:259-61.
32. Brouwer JL, Bijl M, Veeger NJ, Kluin-Nelemans HC, van der Meer J. The contribution of inherited and acquired thrombophilic defects, alone or combined with antiphospholipid antibodies, to venous and arterial thromboembolism in patients with systemic lupus erythematosus. Blood 2004;104:143-8.
33. Pullmann R Jr, Skerenova M, Lukac J, Hybenova J, Melus V, Kubisz P, et al. Factor V Leiden and prothrombin G20210A mutations and the risk of atherothrombotic events in systemic lupus erythematosus. Clin Appl Thromb Hemost 2004;10:233-8.
34. Sallai KK, Nagy E, Bodo I, Mohl A, Gergely P. Thrombosis risk in systemic lupus erythematosus: the role of thrombophilic risk factors. Scand J Rheumatol 2007;36:198-205.
35. Vaya A, Santaolaria M, Mico L, Calvo J, Oropesa R, Villa P, et al. Thrombotic events in systemic lupus erythematosus. Its association with acquired and inherited thrombophilic defects. Clin Hemorheol Microcirc 2008;40:79-87.
36. Tan EM, Cohen AS, Fries JF, Masi AT, McShane DJ, Rothfield NF, et al. The 1982 revised criteria for the classification of systemic lupus erythematosus. Arthritis Rheum 1982;25:1271-7.
37. Hochberg MC. Updating the American College of Rheumatology revised criteria for the classification of systemic lupus erythematosus. Arthritis Rheum 1997;40:1725.
38. Demirci FY, Manzi S, Ramsey-Goldman R, Kenney M, Shaw PS, Dunlop-Thomas CM, et al. Association study of Toll-like receptor 5 (TLR5) and Toll-like receptor 9 (TLR9) polymorphisms in systemic lupus erythematosus. J Rheumatol 2007;34:1708-11.
39. Rhew EY, Manzi SM, Dyer AR, Kao AH, Danchenko N, Barinas-Mitchell E, et al. Differences in subclinical cardiovascular disease between African American and Caucasian women with systemic lupus erythematosus. Transl Res 2009;153:51-9.
40. Suresh S, Demirci FY, Jacobs E, Kao AH, Rhew EY, Sanghera DK, et al. Apolipoprotein H promoter polymorphisms in relation to lupus and lupus-related phenotypes. J Rheumatol 2009;36:315-22.
41. Ceelie H, Bertina RM, Van Hylckama Vlieg A, Rosendaal FR, Vos HL. Polymorphisms in the prothrombin gene and their association with plasma prothrombin levels. Thromb Haemost 2001;85:1066-70.
42. Gohil R, Peck G, Sharma P. The genetics of venous thromboembolism. A meta-analysis involving approximately 120,000 cases and 180,000 controls. Thromb Haemost 2009;102:360-70.
43. Reiner AP, Lange LA, Smith NL, Zakai NA, Cushman M, Folsom AR. Common hemostasis and inflammation gene variants and venous thrombosis in older adults from the Cardiovascular Health Study. J Thromb Haemost 2009;7:1499-505.
44. Nath SK, Namjou B, Kilpatrick J, Garriott CP, Bruner GR, Scofield RH, et al. A candidate region on 11p13 for systemic lupus erythematosus: a linkage identified in African-American families. J Invest Dermatol Symp Proc 2004;9:64-7.
45. Roberts SB, MacLean CJ, Neale MC, Eaves LJ, Kendler KS. Replication of linkage studies of complex traits: an examination of variation in location estimates. Am J Hum Genet 1999;65:876-84.
46. Levi M, Keller TT, Van Gorp E, Ten Cate H. Infection and inflammation and the coagulation system. Cardiovasc Res 2003;60:26-39.
47. Graham RR, Cotsapas C, Davies L, Hackett R, Lessard CJ, Leon JM, et al. Genetic variants near TNFAIP3 on 6q23 are associated with systemic lupus erythematosus. Nat Genet 2008;40:1059-61.
48. Hom G, Graham RR, Modrek B, Taylor KE, Ortmann W, Garnier S, et al. Association of systemic lupus erythematosus with C8orf13-BLK and ITGAM-ITGAX. N Engl J Med 2008;358:900-9.
49. International Consortium for Systemic Lupus Erythematosus Genetics (SLEGEN), Harley JB, Alarcon-Riquelme ME, Criswell LA, Jacob CO, Kimberly RP, et al. Genome-wide association scan in women with systemic lupus erythematosus identifies susceptibility variants in ITGAM, PXK, KIAA1542 and other loci. Nat Genet 2008;40:204-10.