European Journal of Human Genetics (2013) 21, 779–783

www.nature.com/ejhg

ARTICLE

A gene-centric analysis of activated partial thromboplastin time and activated protein C resistance using the HumanCVD focused genotyping array

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Activated partial thromboplastin time (aPTT) is an important routine measure of intrinsic blood coagulation. Addition of activated protein C (APC) to the aPTT test to produce a ratio, provides one measure of APC resistance. The associations of some genetic mutations (eg, factor V Leiden) with these measures are established, but associations of other genetic variations remain to be established. The objective of this work was to test for association between genetic variants and blood coagulation using a high-density genotyping array. Genetic association with aPTT and APC resistance was analysed using a focused genotyping array that tests approximately 50 000 single-nucleotide polymorphisms (SNPs) in nearly 2000 cardiovascular candidate genes, including coagulation pathway genes. Analyses were conducted on 2544 European origin women from the British Women's Heart and Health Study. We confirm associations with aPTT at the coagulation factor XII (*F12*)/G protein-coupled receptor kinase 6 (*GRK6*) and kininogen 1 (*KNG1*)/histidine-rich glycoprotein (*HRG*) loci, and identify novel SNPs at the *ABO* locus and novel locus kallikrein B (*KLKB1*)/*F11*. In addition, we confirm association between APC resistance and factor V Leiden mutation, and identify novel SNP associations with APC resistance in the *HRG* and *F5*/solute carrier family 19 member 2 (*SLC19A2*) regions. In conclusion, variation at several genetic loci influences intrinsic blood coagulation as measured by both aPTT and APC resistance.
European Journal of Human Genetics (2013) **21,** 779–783; doi:10.1038/ejhg.2012.242; published online 28 November 2012

Keywords: aPTT; coagulation; genotype; SNP

INTRODUCTION

Blood coagulation is an important process in preventing blood loss from damaged vessels, but can also be responsible for thrombosis leading to ischaemic heart disease, stroke or venous thromboembolism.[1] An informative measure of efficacy of the intrinsic coagulation pathway is activated partial thromboplastin time (aPTT), measured as time taken for a clot to form in plasma in the absence of tissue factor following introduction of an activator (eg, silica). An abnormally short aPTT can indicate a hypercoaguable state in acute coronary syndromes,[2] and is associated with increased risk of venous thrombosis,[3–5] whereas abnormally long aPTT may also indicate thrombotic risk in the case of the lupus anticoagulant.[6] Addition of activated protein C (APC), which deactivates factors Va and VIIIa, and calculation of an APC resistance provides one measure of APC resistance,[7] including effects of factor V Leiden mutation as its major determinant.[8,9] There is evidence to suggest aPTT is highly heritable,[10] thus meriting investigation of its genetic basis, but to date the only high-density genetic association study of aPTT was a recently reported genome-wide association study (GWAS) of aPTT in 1477 subjects from the Lothian Birth Cohorts, which identified three novel loci associated with aPTT, namely: coagulation factor XII (*F12*), kininogen 1 (*KNG1*) and histidine-rich glycoprotein (*HRG*).[11] The IL3581Thr variant in KNG1 has since been found to associate with risk of venous thrombosis as well as aPTT.[12] No GWAS has been reported for APC resistance.

MATERIALS AND METHODS

Subjects were from the British Women's Heart and Health Study, a prospective cohort study of heart disease in British women. Baseline recruitment was 1999–2001 (age 60–79 years), with blood samples for DNA, APC ratio and aPTT measurement taken from consenting individuals. Protocols and consents were approved by relevant research ethics committees.[13] aPTT measurements were available on 2962 women (mean age 68.8 years, SD 5.5), and APC resistance on 2953 women (mean age 68.8 years, SD 5.5). Data are not available where either insufficient blood was available to assay, consent was not given or assays failed in the laboratory.

DNA was extracted from whole blood using a salting-out procedure.[14] Genotyping was successfully performed on 3445 of 3838 available samples using the Illumina HumanCVD Beadchip.[15] Principal components analysis was used to check self-reported ancestry, with 32 individuals excluded to avoid stratification issues, leaving 3413 samples for analysis. aPTT and APC resistance were assayed in an automated coagulometer (MDA-180, Organon Teknika, Cambridge, UK) using reagents and standards from the manufacturer as previously described.[16] APC ratio was assayed without factor V-deficient plasma. Citrated plasma samples were stored at −80 °C for a maximum of 12 months before assay. Genotype and phenotype data were available on 2618

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Received 5 April 2012; revised 12 September 2012; accepted 11 October 2012; published online 28 November 2012

women for aPTT (mean age 68.9 years, SD 5.5) and 2610 women for APC resistance (mean age 68.9 years, SD 5.5).

Analysis of genetic association was performed using linear regression without covariables (adjustment for age had little effect; whereas clotting phenotypes are age dependent this cohort are all post-menopausal and within the relatively narrow age-range 60–79 years) using PLINK.[17] Single-nucleotide polymorphisms (SNPs) out of Hardy–Weinberg equilibrium ($P<0.0001$) were excluded, as were any with a minor allele frequency below 0.1%, leaving 36 529 SNPs for analysis. Both traits were natural log transformed, outliers >2.5 SD from the mean were removed (on the basis that extreme values may represent either technical errors or biological abnormalities unrelated to common polymorphic variants, which are the focus of our analyses), and warfarin users excluded, leaving 2510 participants with non-missing data for aPTT (arithmetic mean 30.06 s, SD 1.103 s) and 2500 with non-missing data for APC resistance (arithmetic mean 2.924, SD 1.134). Exclusion of women on hormone replacement therapy (shown to associate with these measures[16]) was evaluated, but did not substantially change the results. A stringent (given non-independence of many SNPs) Bonferroni correction for 36 529 tests gives a threshold of $P=1.37\times10^{-6}$ as equivalent to a single-test $P=0.05$. Variable selection was performed in R using Akaike Information Criterion (AIC)[18] with the stepAIC function of the 'MASS' library.

RESULTS

Results of the HumanCVD BeadArray-wide association analysis with aPTT and APC resistance are presented in Table 1, with results of variable selection presented in Table 2. The SNPs most significantly associated with aPTT are in or near the *F12* gene on chromosome 5. The top SNP rs2545801 is a non-coding SNP upstream of *F12*, $P=1.39\times10^{-59}$), with an (antilogged) per-allele effect of 1.05 s on aPTT (95% CI 1.04–1.06). Other gene regions showing association include the *HRG*/*KNG1* region on chromosome 3 (top hit SNP rs710446, $P=2.68\times10^{-19}$), the ABO blood group (*ABO*) locus on chromosome 9 (rs657152, $P=2.45\times10^{-11}$) and the kallikrein B (*KLKB1*) region on chromosome 4 (rs4253304, $P=1.67\times10^{-7}$). Variable selection identified multiple statistically independent signals at each locus except *KLKB1* (Table 2).

Table 1 Associations between SNPs and either aPTT or APC resistance

Trait	*SNP*	*Chr*[a]	*Position*[b]	*Gene symbol*[c]	*Tested allele*	*N*	*Ln effect*[d] *(95% CI)*	*Effect in seconds*[e] *(95% CI)*	P-*value*[f]
aPTT	rs2545801	5	176773945	*F12*	A	2498	0.05 (0.04, 0.06)	1.05 (1.04, 1.06)	1.39×10^{-59}
aPTT	rs1801020	5	176769138	*F12*	A	2505	0.05 (0.05, 0.06)	1.05 (1.05, 1.06)	1.55×10^{-59}
aPTT	rs17876032	5	176763233	*F12*	G	2507	0.04 (0.03, 0.04)	1.04 (1.03, 1.04)	1.40×10^{-37}
aPTT	rs710446	3	187942621	*KNG1*	G	2501	−0.03 (−0.03, −0.02)	0.97 (0.97, 0.98)	2.68×10^{-19}
aPTT	rs2228243	3	187877807	*HRG*	G	2503	0.03 (0.02, 0.04)	1.03 (1.02, 1.04)	1.35×10^{-17}
aPTT	rs16860992	3	187876732	*HRG*	C	2503	0.03 (0.02, 0.04)	1.03 (1.02, 1.04)	4.37×10^{-17}
aPTT	rs5030062	3	187936874	*KNG1*	C	2506	−0.02 (−0.03, −0.02)	0.98 (0.97, 0.98)	3.55×10^{-15}
aPTT	rs1621816	3	187921867	*KNG1*	G	2500	0.02 (0.02, 0.03)	1.02 (1.02, 1.03)	2.33×10^{-14}
aPTT	rs5030028	3	187928448	*KNG1*	A	2502	0.03 (0.02, 0.03)	1.03 (1.02, 1.03)	3.78×10^{-14}
aPTT	rs5030023	3	187927338	*KNG1*	A	2508	0.03 (0.02, 0.03)	1.03 (1.02, 1.03)	4.16×10^{-14}
aPTT	rs3856930	3	187941016	*KNG1*	A	2506	−0.02 (−0.03, −0.02)	0.98 (0.97, 0.98)	6.90×10^{-14}
aPTT	rs1624230	3	187921629	*KNG1*	A	2499	0.02 (0.02,0.03)	1.02 (1.02, 1.03)	9.47×10^{-14}
aPTT	rs657152	9	135129086	*ABO*	A	2507	−0.02 (−0.03, −0.01)	0.98 (0.97, 0.99)	2.45×10^{-11}
aPTT	rs266723	3	187929741	*KNG1*	C	2501	0.02 (0.01, 0.02)	1.02 (1.01, 1.02)	3.31×10^{-10}
aPTT	rs7447593	5	176756743	*F12*	C	2504	−0.02 (−0.02, −0.01)	0.98 (0.98, 0.99)	1.81×10^{-09}
aPTT	rs7381103	5	176770918	*F12*	G	2510	0.05 (0.03, 0.07)	1.05 (1.03, 1.07)	4.35×10^{-09}
aPTT	rs651007	9	135143696	*ABO*	A	2502	−0.02 (−0.03, −0.01)	0.98 (0.97, 0.99)	5.97×10^{-09}
aPTT	rs1042445	3	187878130	*HRG*	A	2508	−0.02 (−0.03, −0.01)	0.98 (0.97, 0.99)	2.27×10^{-08}
aPTT	rs1624569	3	187932763	*KNG1*	G	2499	0.02 (0.01, 0.02)	1.02 (1.01, 1.02)	5.15×10^{-08}
aPTT	rs2062632	3	187943875	*KNG1*	G	2503	0.02 (0.01, 0.02)	1.02 (1.01, 1.02)	1.04×10^{-07}
aPTT	rs2287694	5	176792899	*GRK6*	G	2508	0.02 (0.02, 0.03)	1.02 (1.02, 1.03)	1.39×10^{-07}
aPTT	rs4253304	4	187410565	*KLKB1*	C	2498	−0.01 (−0.02, −0.01)	0.99 (0.98, 0.99)	1.67×10^{-07}
aPTT	rs13177732	5	176789531	*GRK6*	C	2500	−0.02 (−0.02, −0.01)	0.98 (0.98, 0.99)	2.56×10^{-07}
aPTT	rs9898	3	187873321	*HRG*	A	2505	0.02 (0.01, 0.02)	1.02 (1.01, 1.02)	2.61×10^{-07}
aPTT	rs2304595	4	187409274	*KLKB1*	A	2507	−0.01 (−0.02, −0.01)	0.99 (0.98, 0.99)	3.60×10^{-07}
aPTT	rs5030091	3	187943571	*KNG1*	G	2507	0.01 (0.01, 0.02)	1.01 (1.01, 1.02)	7.29×10^{-07}
APC-R	rs6025	1	1.68E+08	*F5*	A	2500	−0.28 (−0.31, −0.26)	0.76 (0.73, 0.77)	4.2×10^{-104}
APC-R	rs6682179	1	1.68E+08	*F5*	A	2499	−0.08 (−0.1, −0.07)	0.92 (0.9, 1.07)	1.43×10^{-28}
APC-R	rs6427196	1	1.68E+08	*F5*	C	2500	−0.08 (−0.1, −0.07)	0.92 (0.9, 1.07)	2.11×10^{-28}
APC-R	rs6009	1	1.68E+08	*F5*	A	2500	−0.08 (−0.1, −0.07)	0.92 (0.9, 1.07)	1.24×10^{-27}
APC-R	rs16860992	3	1.88E+08	*HRG*	C	2492	0.04 (0.03, 0.04)	1.04 (1.03, 1.04)	2.29×10^{-15}
APC-R	rs2228243	3	1.88E+08	*HRG*	G	2492	0.03 (0.03, 0.04)	1.03 (1.03, 1.04)	9.55×10^{-15}
APC-R	rs9898	3	1.88E+08	*HRG*	A	2496	0.02 (0.02, 0.03)	1.02 (1.02, 1.03)	5.26×10^{-11}
APC-R	rs2038024	1	1.68E+08	*SLC19A2*	C	2496	−0.03 (−0.04, −0.02)	0.97 (0.96, 0.98)	1.75×10^{-09}

[a]Chromosome ('Chr').
[b]Chromosomal position.
[c]Mapped gene.
[d]Logged effect sizes (as tested by regression).
[e]Anti-logged effect sizes (for direct interpretation), where effect is change in trait per tested allele.
[f]*P*-value indicates strength of evidence against the null hypothesis as tested by linear regression of trait on number of tested alleles.
Both aPTT and APC resistance ('traits') are presented in this table.

Table 2 Variable selection results

Genomic region[a]	*Location*[b]	*Phenotype*	*SNPs*	*Estimate*	*Individual P-value*[c]	*Overall P-value*[d]
F12 and *GRK6*	5q33-35	aPTT	rs2545801	−0.02950	0.041	$< 2.2 \times 10^{-16}$
			rs1801020	−0.022793	0.1303	
HRG and *KNG1*	3q27	aPTT	rs1042445	0.010413	0.00704	$< 2.2 \times 10^{-16}$
			rs2062632	0.007951	0.02904	
			rs2228243	0.018532	2.34×10^{-05}	
			rs710446	−0.021965	2.96×10^{-12}	
			rs9898	−0.014528	6.23×10^{-05}	
KLKB1	4q35	aPTT	rs4253304	0.015523	6.15×10^{-08}	6.15×10^{-08}
ABO	9q34	aPTT	rs657152	0.015269	0.000263	1.269×10^{-10}
			rs651007	0.006843	0.154113	
F5 and *SLC19A2*	1q23	APC resistance	rs6025	0.28882	$<2 \times 10^{-16}$	$< 2.2 \times 10^{-16}$
HRG	3q27	APC resistance	rs16860992	−0.116523	0.043113	2.2×10^{-16}
			rs2228243	−0.088207	0.125584	
			rs9898	−0.014962	0.000618	

[a]Genomic regions are represented by gene names.
[b]Location is cytogenetic location.
[c]The individual *P*-value gives an indication of the statistical independence of a SNP from others included in the model.
[d]The overall *P*-value indicates the strength of the combined evidence against the null hypothesis when all SNPs are included.
For each SNP in a genomic region the estimate gives an indication of the independent effect of that SNP on the trait. Akaike Information Criterion was used to identify SNPs with a significant independent contribution to the phenotype of interest in a step-wise multiple regression of significantly associated SNPs in each genomic region.

Table 1 also presents genetic association results for APC resistance. The most strongly associated SNP with APC resistance is the factor V Leiden mutation (rs6025, $P = 4.2 \times 10^{-104}$) in the factor V (*F5*) gene on chromosome 1. The other region associated with APC resistance is the *HRG* region on chromosome 3 (top SNP rs16860992, $P = 2.29 \times 10^{-15}$).

Variable selection (Table 2) suggests that all association with APC resistance in the *F5* and solute carrier family 19 member 2 (*SLC19A2*) region on chromosome 1 is attributable to the functional factor V Leiden mutation, with no evidence of statistically independent effects for other SNPs. In the *HRG* region on chromosome 3 there are three potentially independent SNPs.

DISCUSSION

Although the HumanCVD array is a candidate gene array, the coagulation pathway is well represented, with SNPs in the genes for the majority of intrinsic and extrinsic pathway proteins (Table 3). We confirmed previous reports[11] of effects in *F12* (our 'top hit' rs2545801 is the best HumanCVD tag of rs2731672, HapMap $r^2 = 0.935$[19]), *KNG1* ('top hit' rs710446) and *HRG* (rs9898, significantly associated, but not our top hit at this locus). We also found positive associations with aPTT at the G protein-coupled receptor kinase 6 (*GRK6*) gene, genomically adjacent to the *F12* gene, although low LD between the 'top hit' SNPs at each locus suggests that these are marking independent effects (even if both the effects are actually in the *F12* gene). GRK6 deactivates G protein-coupled receptors, and thus may potentially also have a biological effect in the clotting mechanism. The results of variable selection suggest that there may be more than one causal site at each of the three main loci (excluding *KLKB1*).

We also found significant associations between aPTT and SNPs at the *ABO* and *KLKB1* loci. Blood group O versus non-O becomes associated with lower levels of factor VIII and von Willebrand factor (vWF) during childhood[20] and continues into adulthood.[21] Assuming this relationship is causal, and given that aPTT is prolonged with both severe von Willebrand Disease (vWF deficiency in type 1 and 3) and Haemophilia A (factor VIII deficiency), we hypothesise that *ABO* genotype could associate with aPTT through alteration of levels of vWF or factor VIII. There is also a previous report describing association of ABO OO genotype with aPTT using a combined linkage and association approach.[22] Our highest *ABO* locus association is with rs657152, which is in high linkage disequilibrium (LD, $r^2 = 0.98$)[23]

Table 3 Representation of coagulation factor genes on the HumanCVD array

Coagulation factor	*Gene symbol*	*Number of SNPs*
Fibrinogen	*FGA*	23
Fibrinogen	*FGB*	28
Fibrinogen	*FGG*	20
Prothrombin	*F2*	36
Tissue factor	*F3*	38
Factor V	*F5*	126
Factor VII	*F7*	34
Factor VIII	*F8*	19
Factor IX	*F9*	18
Factor X	*F10*	20
Factor XI	*F11*	20
Factor XII	*F12*	19
Factor XIII	*F13A1*	133
Factor XIII	*F13B*	9
Von Willebrand factor	*VWF*	128
Prekallikrein	*KLKB1*	21
Fibronectin	*FN*	0
Antithrombin III	*SERPINC1*	9
Heparin cofactor II	*SERPIND1*	5
Protein C	*PROC*	8
Protein S	*PROS1*	8
Protein Z	*PROZ*	6
Protein Z-related protease inhibitor (ZPI)	*SERPINA10*	11
Plasminogen	*PLG*	35
Alpha 2-antiplasmin	*SERPINF2*	7
Tissue plasminogen activator	*PLAT*	19
Plasminogen activator	*PLAU*	6
Plasminogen activator inhibitor-1	*SERPINE1*	33
Plasminogen activator inhibitor-2	*SERPINB2*	16

For each of the main proteins in the coagulation cascade the corresponding gene(s) is/are shown, along with the number of SNPs included in the HumanCVD array for that gene.

with rs8176719 (the O/non-O variant), and thus rs657152 closely marks the association of O blood group with clotting. SNP rs657152 is also in high LD ($r^2 = 0.93$) with the myocardial infarction risk SNP reported by Reilly *et al*,[24] and hence likely to tag the functional mechanism of that risk. *KLKB1* encodes plasma kallikrein B (Fletcher factor) 1, a glycoprotein, which is involved in the intrinsic coagulation pathway,[25] and also neighbours the *F11* locus, encoding the factor XI protein, an important factor in the intrinsic coagulation pathway.

We also present results for genetic associations with APC resistance. The HumanCVD array directly assays the factor V Leiden mutation (rs6025), which is known to influence the APC resistance.[26] This mutation shows the strongest genetic association with APC resistance in our data set ($P = 4.2 \times 10^{-104}$). Although our other association signals in the *F5* gene are with SNPs in little LD with rs6025 (eg, $r^2 = 0.104$), the magnitude of signal with rs6025 and results of variable selection (Table 2) suggest these SNPs are simply showing a 'bystander' effect. The other locus containing SNPs associating with APC resistance is *HRG* (same SNPs as with aPTT, and showing consistent direction of effect on both tests). HRG has a complex role in coagulation, with both anticoagulant and antifibrinolytic properties reported.[27,28] In our data, we observe concordant effects of *HRG* genotype on both aPTT (clotting speed) and APC resistance (response to inhibition). Although there is a SNP in *SLC19A2* (the gene for solute carrier family 19 (thiamine transporter), member 2) this is physically close to the *F5* gene on chromosome 1, so may simply tag functional variation in *F5*. Although variable selection excludes the *SLC19A2* SNP (Table 2), the LD between all our top hits in *F5* (including rs6025) and the *SLC19A2* SNP is very low ($r^2 < 0.006$), suggesting this may either mark an independent effect in the *F5* gene, or a biological relevance of thiamine transport in coagulation.

With the exception of the factor V Leiden mutation (rs6025), already known to influence APC resistance,[26] the majority of these results represent relatively small genetic effects on aPTT and APC resistance. They therefore have very limited *predictive* value (especially as individual variants), but instead offer additional insight into the functional pathways underlying blood coagulation.

Our study has three principal limitations: (i) the HumanCVD array is not 'genome-wide'. Although even genome-wide arrays do not capture all genetic variation they offer a relatively unbiased representation of the genome. Table 3 illustrates the extent to which this candidate gene array represents coagulation system genes. (ii) The population we have analysed is female, of European ancestry, and represents a fairly narrow age-range (post-menopausal, 60–79 years). The results may therefore not be generalisable to other ancestries, males or younger people. Further studies are needed to examine the associations of newly identified genotypes with risk of venous and arterial thrombosis. (iii) These phenotypes (in particular APC resistance) are infrequently measured on a cohort scale, and we were unable to identify a suitable replication cohort with both these measures and appropriate genotyping data. Appropriate caution should therefore be applied in interpreting results close to our significance threshold. Our replication of published aPTT GWAS results[11] and the very strong statistical evidence (most of our reported *P*-values several orders of magnitude below the nominal HumanCVD significance threshold of 1×10^{-6}) support the reliability of these findings.

In conclusion, we have both confirmed previous reports that *F12/GRK6*, *KNG1* and *HRG* are associated with aPTT[11] and identified new SNPs at *ABO* and new genomic locus *KLKB1* associated with aPTT. We also present the first high-density genetic association analysis of APC resistance, and identify signals in the *F5* and *HRG* genomic regions. Our findings suggest that *KLKB1* and *HRG* may have potentially important roles in blood coagulation.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ACKNOWLEDGEMENTS

We thank all participants and the GPs, nurses and staff who supported data collection and preparation. The British Women's Heart and Health Study has been supported by funding from the British Heart Foundation and the Department of Health Policy Research Programme (England). Genotyping work was funded by the BHF (PG/07/131/24254). TRG, DAL and INMD work in a centre that receives core funding from the UK Medical Research Council (G0600705) and the University of Bristol.

1 Lowe GDO: Can haematological tests predict cardiovascular risk? The 2005 Kettle Lecture. *Br J Haematol* 2006; **133**: 232–250.
2 Abdullah WZ, Moufak SK, Yusof Z, Mohamad MS, Kamarul IM: Shortened activated partial thromboplastin time, a hemostatic marker for hypercoagulable state during acute coronary event. *Transl Res* 2010; **155**: 315–319.
3 Lowe GD, Haverkate F, Thompson SG *et al*: Prediction of deep vein thrombosis after elective hip replacement surgery by preoperative clinical and haemostatic variables: the ECAT DVT Study. European Concerted Action on Thrombosis. *Thromb Haemost* 1999; **81**: 879–886.
4 Tripodi A, Chantarangkul V, Martinelli I, Bucciarelli P, Mannucci PM: A shortened activated partial thromboplastin time is associated with the risk of venous thromboembolism. *Blood* 2004; **104**: 3631–3634.
5 Korte W, Clarke S, Lefkowitz JB: Short activated partial thromboplastin times are related to increased thrombin generation and an increased risk for thromboembolism. *Am J Clin Pathol* 2000; **113**: 123–127.
6 Alving BM, Baldwin PE, Richards RL, Jackson BJ: The dilute phospholipid APTT: a sensitive assay for verification of lupus anticoagulants. *Thromb Haemost* 1985; **54**: 709–712.
7 Dahlbäck B, Carlsson M, Svensson PJ: Familial thrombophilia due to a previously unrecognized mechanism characterized by poor anticoagulant response to activated protein C: prediction of a cofactor to activated protein C. *Proc Natl Acad Sci USA* 1993; **90**: 1004–1008.
8 De Stefano V, Leone G: Resistance to activated protein C due to mutated factor V as a novel cause of inherited thrombophilia. *Haematologica* 1995; **80**: 344–356.
9 Dahlbäck B, Hildebrand B: Inherited resistance to activated protein C is corrected by anticoagulant cofactor activity found to be a property of factor V. *Proc Natl Acad Sci USA* 1994; **91**: 1396–1400.
10 Warren DM, Soria JM, Souto JC *et al*: Heritability of hemostasis phenotypes and their correlation with type 2 diabetes status in Mexican Americans. *Hum Biol* 2005; **77**: 1–15.
11 Houlihan LM, Davies G, Tenesa A *et al*: Common variants of large effect in F12, KNG1, and HRG are associated with activated partial thromboplastin time. *Am J Hum Genet* 2010; **86**: 626–631.
12 Morange P-E, Oudot-Mellakh T, Cohen W *et al*: KNG1 Ile581Thr and susceptibility to venous thrombosis. *Blood* 2011; **117**: 3692–3694.
13 Lawlor DA, Day INM, Gaunt TR *et al*: The association of the PON1 Q192R polymorphism with coronary heart disease: findings from the British Women's Heart and Health cohort study and a meta-analysis. *BMC Genet* 2004; **5**: 17.
14 Miller SA, Dykes DD, Polesky HF: A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Res* 1988; **16**: 1215.
15 Keating BJ, Tischfield S, Murray SS *et al*: Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. *PLoS ONE* 2008; **3**: e3583.
16 Lowe GD, Rumley A, Woodward M, Reid E, Rumley J: Activated protein C resistance and the FV:R506Q mutation in a random population sample–associations with cardiovascular risk factors and coagulation variables. *Thromb Haemost* 1999; **81**: 918–924.
17 Purcell S, Neale B, Todd-Brown K *et al*: PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* 2007; **81**: 559–575.
18 Akaike H: A new look at the statistical model identification. *Automatic Control, IEEE Transactions on* 1974; **19**: 716–723.
19 The International HapMap Consortium. A haplotype map of the human genome. *Nature* 2005; **437**: 1299–1320.
20 Klarmann D, Eggert C, Geisen C *et al*: Association of ABO(H) and I blood group system development with von Willebrand factor and Factor VIII plasma levels in children and adolescents. *Transfusion* 2010; **50**: 1571–1580.

21 Gill JC, Endres-Brooks J, Bauer PJ, Marks Jr WJ, Montgomery RR: The effect of ABO blood group on the diagnosis of von Willebrand disease. *Blood* 1987; **69**: 1691–1695.
22 Souto JC, Almasy L, Muñiz-Diaz E *et al*: Functional effects of the ABO locus polymorphism on plasma levels of von Willebrand factor, factor VIII, and activated partial thromboplastin time. *Arterioscler Thromb Vasc Biol* 2000; **20**: 2024–2028.
23 Teupser D, Baber R, Ceglarek U *et al*: Genetic regulation of serum phytosterol levels and risk of coronary artery disease. *Circ Cardiovasc Genet* 2010; **3**: 331–339.
24 Reilly MP, Li M, He J *et al*: Identification of ADAMTS7 as a novel locus for coronary atherosclerosis and association of ABO with myocardial infarction in the presence of coronary atherosclerosis: two genome-wide association studies. *Lancet* 2011; **377**: 383–392.
25 Saito H: *Haemostasis & Thrombosis*, In Bloom AL, Forbes CD, Thomas DP, Tuddenham EGD (eds). Edinburgh: Churchill Livingstone, 1994; 289–308.
26 Bertina RM, Koeleman BP, Koster T *et al*: Mutation in blood coagulation factor V associated with resistance to activated protein C. *Nature* 1994; **369**: 64–67.
27 Tsuchida-Straeten N, Ensslen S, Schäfer C *et al*: Enhanced blood coagulation and fibrinolysis in mice lacking histidine-rich glycoprotein (HRG). *J Thromb Haemost* 2005; **3**: 865–872.
28 Poon IKH, Patel KK, Davis DS, Parish CR, Hulett MD: Histidine-rich glycoprotein: the Swiss Army knife of mammalian plasma. *Blood* 2011; **117**: 2093–2101.