EXTENDED REPORT

Anti-β₂GPI-antibody-induced endothelial cell gene expression profiling reveals induction of novel pro-inflammatory genes potentially involved in primary antiphospholipid syndrome

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Objective: To determine the effects of primary antiphospholipid syndrome (PAPS)-derived anti- β_2 GPI antibodies on gene expression in human umbilical vein endothelial cells (HUVEC) by gene profiling using microarrays.

Methods: Anti- β_2 GPI antibodies purified from sera of patients with PAPS or control IgG isolated from normal subjects were incubated with HUVEC for 4 h before isolation of RNA and processing for hybridisation to Affymetrix Human Genome U133A-2.0 arrays. Data were analysed using a combination of the MAS 5.0 (Affymetrix) and GeneSpring (Agilent) software programmes. For selected genes microarray data were confirmed by real-time PCR analysis or at the protein level by ELISA.

Results: A total of 101 genes were found to be upregulated and 14 genes were downregulated twofold or more in response to anti- β_2 GPI antibodies. A number of novel genes not previously associated with APS were induced, including chemokines CCL20, CXCL3, CX3CL1, CXCL5, CXCL2 and CXCL1, the receptors Tenascin C, OLR1, IL-18 receptor 1, and growth factors CSF2, CSF3 IL-6, IL1 β and FGF18. The majority of downregulated genes were transcription factors/signalling molecules including ID2. Quantitative real-time RT-PCR analysis confirmed the microarray results for selected genes (CSF3, CX3CL1, FGF18, ID2, SOD2, Tenascin C).

Conclusions: This study reveals a complex gene expression response in HUVEC to anti- β_2 GPI antibodies with multiple chemokines, pro-inflammatory cytokines, pro-thrombotic and pro-adhesive genes regulated by these antibodies in vitro. Some of these newly identified anti- β_2 GPI antibody-regulated genes could contribute to the vasculopathy associated with this disease.

Antiphospholipid syndrome (APS) is characterised by thrombosis, thrombocytopenia and recurrent foetal loss.¹ Two forms of the syndrome have been described; the "primary" syndrome (PAPS), where there is no evidence of any other underlying disease and "secondary" syndrome that is mainly associated with systemic lupus erythematosus (SLE). Elevated serum titres of antiphospholipid antibodies (aPL) correlate with thrombotic events in APS² and there is strong evidence that aPL display a pathogenic role in APS.^{3 4} β2glycoprotein I (β_2 GPI) binds to negatively charged phospholipids through a positively charged lysine-rich sequence of amino acids in its fifth domain⁵ and is now recognised as the primary aPL target in APS.⁵⁻⁸ Anti- β_2 GPI antibodies bind to the β_2 GPI protein adherent to the endothelial cell (EC) surface and induce EC activation.⁹

Anti- β_2 GPI antibodies might exert a direct pathogenic effect in APS by perturbing homeostatic reactions that take place on the surface of EC.¹⁰ A number of in vitro studies have reported that anti- β_2 GPI antibodies can activate EC as shown by early increases in monocyte adhesion and the expression of Eselectin, vascular cell adhesion molecule-1 (VCAM-1), and intracellular adhesion molecule-1 (ICAM-1).^{9 11 12} In vivo, aPL infused into naïve mice caused increased adhesion of monocytes and formation of sustained and larger thrombi when compared to normal control IgG.¹³

In addition, recent studies have reported that nuclear factor kappa B (NF- κ B) translocation, the myeloid differentiation primary response gene 88 (MyD88) pathway and p38 mitogen-activated protein kinase (MAPK) phosphorylation are involved in EC and monocyte activation by anti- β_2 GPI antibodies.¹⁴⁻¹⁶ However, the extent and diversity of anti- β_2 GPI-mediated gene

regulation in EC cells is not yet well characterised. The present study was undertaken to examine the profile and diversity of early gene regulation in EC in response to polyclonal patient-derived anti- β_2 GPI antibodies using Affymetrix microarray gene profiling.

METHODS Patient group

Ethical approval for the collection of sera from PAPS patients was obtained prior to the initiation of the study from the St. Thomas' Hospital Research Ethics Committee. Following written patient consent, sera were collected from a total of five patients with PAPS. All 5 patients had high levels of IgG aPL and strong lupus anti-coagulant activity. Anticardiolipin activity in the patients was β_2 GPI dependent (data not shown). The clinical profiles of patients from whom polyclonal anti- β_2 GPI antibody preparations were isolated and used in this study are shown in table 1. All 5 patients fulfilled the Sapporo classification criteria for definitive PAPS.¹⁷

Purification of normal IgG and anti- $\beta_2 GPI$ antibodies from sera

IgG from patients or normal age and sex-matched subjects were purified using a HiTrap Protein G HP affinity column (GE Healthcare, Buckinghamshire, UK) as per the manufacturer's instructions. Purified human β_2 GPI protein was purchased from SCIPAC Ltd. (Sittingborne, Kent, UK.) The protein was coupled to a HiTrap NHS-activated HP column as recommended by the manufacturer (GE Healthcare). A 1/8 dilution of serum in starting buffer was applied to the column and affinitypurified antibody was eluted in 0.1 M glycine-HCL pH 2.7 and

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	Patient 1	Patient 2	Patient 3	Patient 4	Patient 5
Sex/age	F/33	F/53	F/54	F/38	F/59
Diagnosis Clinical features of APS	PAPS 1 DVT, 1 PE, PET, TIAs and stroke	PAPS 1 DVT, 3 PE	PAPS 1 DVT, 2 stillbirths, 1 PE, CVD, catastrophic APS	PAPS PVD, TIAs, brachial artery thrombosis	PAPS 3 Foetal losses, microinfarct CNS, MI, abnormal MR aortic stenosis
lgG aCL (GPL U/ml)	350	223	142	257	308
Lupus anticoagulant	+	+	+	+	+
Experimental procedures	Microarray, real time RT-PCR, ELISA	Microarray, real time RT-PCR, ELISA	Microarray, ELISA	Microarray, real time RT-PCR, ELISA	Real time RT-PCR

neutralised with 1 M Tris-HCL pH 9.0. The purification was carried out on an AKTA prime 3 system (GE Healthcare). Protein concentration of IgG and affinity purified antibodies was determined by Bicinchoninic protein assay (Sigma).

Characterisation of patient-derived anti- $\beta_2 GPI$ antibodies

Following isolation, patient-derived anti- β_2 GPI antibodies were tested for binding to β_2 GPI by enzyme-linked immunosorbant assay (ELISA) using a previously described method.¹⁸ All antibodies were also tested in an anti-cardiolipin ELISA.¹⁹

Human umbilical vein endothelial cell isolation and culture

Human umbilical cords were obtained from the Labour Ward at St. Thomas' Hospital London following ethical approval and written patient consent. Human umbilical vein endothelial cells (HUVEC) were isolated from normal full term umbilical cord vein using collagenase enzyme (Sigma) and cultured as previously described at 37°C in a humidified incubator.²⁰ For cell stimulation experiments HUVEC were incubated for 4 h with different antibody preparations. In all experiments, polymixin B (5 μ g/ml) was included to exclude the possibility of endotoxin effects as previously described.¹⁵

Isolation of RNA from HUVEC treated with anti- β_2 GPI antibodies or normal control IgG for microarray analysis

Confluent HUVEC at passage 3 were incubated with the four PAP-derived anti- β_2 GPI antibody preparations (P1, P2, P3, P4, 50 µg/ml) preparations or four normal control IgG (N1, N2, N3, N4, 50 µg/ml) for 4 h at 37°C in a humidified incubator. Total HUVEC RNA was then extracted using the RNeasy Kit (Qiagen, Crawley, West Sussex, UK). The quality of the RNA was checked using a 1% agarose gel. Three independent experiments using HUVEC from three different donors were carried out on different occasions.

Preparation of target biotinylated cRNA and hybridisation

cRNA samples for microarray hybridisation were prepared following the manufacturer's instructions (Affymetrix, Santa Clara, California). Fragmented cRNA was hybridised overnight to gene chip arrays at 45°C for 18 hours. Control cRNAs were then added to the hybridisation mix. Human Genome U133A-2.0 gene chips containing probe sets for 18 400 human transcripts were used. In one of the three independent experiments, one anti- β_2 GPI antibody (P2) treated sample and one control IgG treated (N2) sample were not processed beyond initial RNA quantitation due to low RNA yield.

Therefore, a total of 22 chips were hybridised and scanned. Gene chips were washed and stained on the Gene Chip Fluidics Station 400 (Affymetrix). Fluorescent signals were detected using the HP G2500A Gene Array Scanner.

Statistical analysis of microarray data

After scanning the gene chips, images were analysed using the Affymetrix microarray suite (MAS) 5.0 (Affymetrix, Santa Clara, California, USA) to generate raw data in the form of ".cel" files. Further analysis was carried out using a combination of the MAS 5.0 and GeneSpring (Agilent Technologies, Santa Clara, California, USA) software programmes. The detection of a particular gene as "present, absent or marginal" was carried out using the MAS 5.0 software. The .cel files were imported into GeneSpring and normalised by GC-Robust Multichip Average (GCRMA), an algorithm that normalises the data by quantile normalisation, in order to minimise the biological variation between samples. Further analysis was carried out on genes identified as present or marginal. Genes with statistically different expression between the control IgG and the anti- β_2 GPI antibody treated cells (p<0.05) were identified by the Kruskal-Wallis test (non-parametric one way analysis of variance (ANOVA)) with the Benjamin and Hochberg multiple testing correction.²¹ Filtering the gene list on the criteria of a twofold or more increase or decrease in expression identified a panel of genes that were significantly changed in HUVEC by anti- β_2 GPI antibody treatment compared to normal control IgG treatment. Average-linkage hierarchical clustering (using the Pearson Correlation) was carried out separately on the genes and the samples generating a genetree and condition tree, respectively, to highlight any distinct patterns in gene expression and the relationships between the samples.

Quantitative real-time RT-PCR analysis of gene expression

Quantitative real time PCR was used to confirm the microarray results for the expression levels of selected genes. The primer pairs used for the following genes were: CSF3, forward 5'-CGCTCCAGGAGAAGCTGT-3' and reverse 5'-CCAGAGAGTGTC CGAGCAG-3', CX3CL1, forward 5'-ATCTCTGTCGTGGCTGCTC-3' and reverse 5'-TCACACCGTGGTGCTGTC-3', E-selectin, forward 5'-TGAAGCTCCCACTGAGTCCAA-3' and reverse 5'-GGTGCTAATGTCAGGAGGGAGA-3', FGF18, forward 5'-CTCTA CAGCCGGACCAGTG-3' and reverse 5'-CCGAAGGTGTCTGTCT CCAC-3', ID2, forward 5'-CAGCATCCTGTCCTTGCAG-3' and reverse 5'-AAAGAAATCATGAACACCGCTTA-3', SOD2, forward 5'-CAAATTGCTGCTTGTCCAAA-3' and reverse 5'-CGTGCTCC CACACATCAAT-3', Tenascin C, forward 5'-GCTCAAAGCAG CCACTCATT-3' and reverse, 5'-CCCATATCTGGAACCTCCTC-3', and β -actin, forward 5'-CCAAACGGGAAAGATGA-3' and

reverse 5'-CCAGAGGCGTACAGGGATAG-3'. B-Actin was used as an internal control as no changes were found in levels of expression of this housekeeping gene when cells were treated with anti-β₂GPI antibodies in microarray experiments. Primers for the genes were designed using the Roche universal probe library. One ug of total RNA from HUVEC incubated for 4 h in medium alone (blank), or with 2 normal control IgG preparations (N3, N4, 50 μ g/ml) or 4 anti- β_2 GPI antibody preparations (P1, P2, P4, P5, 50 µg/ml), or with TNFa was reverse transcribed into cDNA with the Ouantitect reverse transcription kit (Qiagen) using oligo-dT primers. Antibody preparations N3, N4, P1, P2 and P4 were previously used in the microarray experiments. Quantitative real-time PCR was carried out with the QuantiTect SYBR Green PCR Kit (Qiagen) in the ABI 7000 sequence detector (Applied Biosystems). Gene expression levels were calculated with the absolute quantitation method,²² and normalised to the β-actin level. All PCR reactions were carried out in duplicate, and repeated at least twice for each gene. The specificity of the PCR reactions was verified with dissociation curve analysis.

Enzyme-linked immunosorbant assay to detect Eselectin and IL-8 expression levels in HUVEC

E-selectin cell surface expression was evaluated by a cell ELISA.⁹ Unstimulated cells were used as a negative control and TNF α (10 ng/ml, R&D Systems) was used a positive control stimulus.¹⁵ IL-8 levels in cell supernatants were determined

using a human IL-8 ELISA kit according to the manufacturer's instructions (BD Biosciences, Cowley, Oxon, UK).

Statistical analysis

The non-parametric Mann–Whitney U Test was used to compare E-selectin and IL-8 levels between cells incubated with anti- β_2 GPI antibodies and normal control IgG preparations in ELISA experiments.

RESULTS

Anti-B2GPI-induced gene expression in endothelial cells

Sera were collected from four PAPs patients and anti-B2GPI antibodies purified by protein G and B2GPI affinity column isolation. All patient derived anti-B2GPI antibodies bound to β_2 GPI by ELISA and were also positive in a modified anticardiolipin ELISA with but not without co-factor, carried out as previously described (data not shown).8 Following gene chip hybridisation and scanning, HUVEC were found to express 13 727 out of 18 400 transcripts. Genes that were significantly changed (p<0.05, up or down) twofold or more were filtered and categorised as anti- β_2 GPI antibody-regulated genes. A total of 101 genes were upregulated by at least twofold or more by anti- β_2 GPI antibodies (fig 1 and table 2). Figure 1 shows a hierarchical cluster analysis of upregulated and downregulated genes. Genes were clustered according to their patterns of expression (vertical axis) and also per condition (similarities between total gene expression profiles in different samples). It is noteworthy that in the dendrogram, similarities in level of

Expression

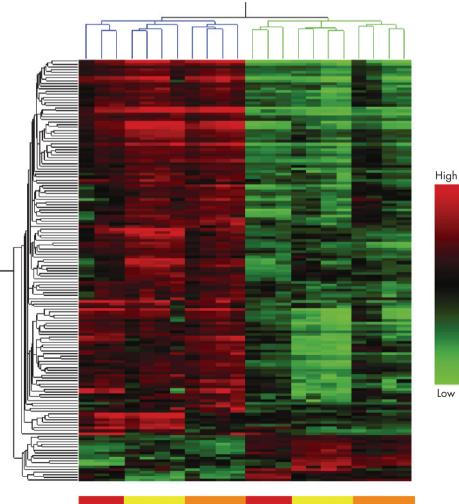


Figure 1 Hierarchical clustering of HUVEC genes changed twofold or more in expression (p<0.05) by treatment with anti- β_2 GPI antibodies. In three independent experiments on different HUVEC preparations, cells were incubated for 4 h with either anti- β_2 GPI antibodies (P1, P2, P3, P4, 50 µg/ml) or normal control IgG (N1, N2, N3, N4, 50 µg/ml). mRNA was isolated and processed for microarray hybridisation and analysis. A genetree and condition tree were created in GeneSpring software by average linkage hierarchical clustering using the Pearson Correlation. Each column represents results from an individual microarray chip (n = 22), each horizontal row represents a gene. Genes have been clustered according to similarities in patterns of expression (vertical axis) as well as per condition (horizontal axis). Branches are colour-coded for anti-B2GPI antibody treated (blue) and control IgG (green) treated samples. Coloured bars below figure also indicate location of results from the three independent experiments. Differences in expression level between anti- $\beta_2 \text{GPI}$ antibody treated HUVEC and those incubated with normal control IgG are

clearly distinguishable on the heat map. Genes with high expression levels are in red, intermediate-level expression in black and

low-level expression in green.

Experiment

Table 2Anti- β_2 GPI antibody-induced gene expression in HUVEC

Gene	Induction (-fold)	Accession no.	Gene description	Gene	Induction (-fold)	Accession no.	Gene description
Apoptosis/a BCL2A1	anti-apoptosis 14.4	NM_004049	BCL2-related protein A1	Metabolism SLC7A5	4.7	AB018009	Solute carrier family 7 (cationic amino acid
TNAIP8	3.8	NM_014350	Tumour necrosis factor α-induced	PPAP2B	4.2	AB000889	transporter) Phosphatidic acid
TNFAIP3	3.6	NM_006290	protein 8 Tumour necrosis factor α-induced	ASNS	3.5	NM_001673	phosphatase type 2B Asparagine synthetase
TRAF1	3.5	NM_005658	protein 3 TNF receptor-associated factor	INDO	3.3	M34455	Indoleamine-pyrrole 2,3
BIRC3	3.4	U37546	Baculoviral IAP repeat-containing 3	GCH1	2.9	NM_000161	dioxygenase GTP cyclohydrolase 1 (dopa-responsive
CARD15	3.0	NM_022162	Caspase recruitment domain	\$100A3	2.8	NM_002960	dystonia) S100 calcium binding
RIPK2	2.5	AF027706	family, member 15 Receptor-interacting	SDC4	2.6	NM_002999	protein A3 Syndecan 4 (amphiglyca
TRIB3	2.3	NM_021158	serine-threonine kinase 2 Tribbles homolog 3 (Drosophila)	MSCP	2.5	BE677761	ryudocan) Solute carrier family 25,
				GFPT2	2.5	NM_005110	member 37 Glutamine-fructose-6-
Adhesion m TNFAIP6	iolecules/rece 21.3	ptors NM_007115	Tumour necrosis factor a-induced	MT1X MTIE	2.3 2.3	NM_002450 BF217861	phosphate transaminase Metallothionein 1X Metallothionein 1E
TNFRSF1	5.0	NM_002546	protein 6 Tumour necrosis factor receptor	PDLM4	2.3	AF153882	(functional) PDZ and LIM domain 4
LLT 1	4.7	NM_013269	superfamily, member 11b C-type lectin domain family 2,	LIPG	2.3	NM_006033	Lipase, endothelial
BDKRB2	4.7	NM_000623	member D Bradykinin receptor B2	KCNMB1	2.2	U61536	Potassium large conductance calcium-
TNC	4.5	NM_002160	Tenascin C (hexabrachion)	OASL	2.2	NM_00373	activated channel 2'-5'-Oligoadenylate synthetase-like
TNFRSF9	4.4	NM_001561	Tumour necrosis factor receptor superfamily, member 9	Miscellaneous			-,
OLR1	4.4	AF035776	Oxidised low density lipoprotein (lectin-like) receptor 1	TNFAIP2	9.7	NM_006291	Tumour necrosis factor o induced protein 2
IL18R1	4.3	NM_003855	Interleukin 18 receptor 1	DD1T4	2.8	NM_019058	DNA-damage-inducible transcript 4
E-Selectin	3.8	NM_000450	Selectin E (endothelial adhesion molecule 1)	IFIT3	2.5	NM_001549	Interferon-induced protein with tetratricopeptide
ICAM	3.4	NM_000201	Intercellular adhesion molecule 1 (CD54)	IFIT2	2.3	BE888744	repeats 3 Interferon-induced protei with tetratricopeptide
ICOSL CCRL2	3.1 3.0	AL355690 AF015524	Inducible T-cell co-stimulator ligand Chemokine (C-C motif)	MOX2 ZC3HV1	2.2 2.2	H23979 NM_020119	repeats 2 CD200 antigen Zinc finger CCCH-type,
PDZK3	2.8	AF338650	receptor-like 2 PDZ domain containing 3	CDC42	2.1	AI754416	antiviral 1 CDC42 effector protein
CD69	2.6	L07555	CD69 antigen (p60, early T-cell activation antigen)	MSCP	2.1	NM_018579	(Rho GTPase binding) 3 Solute carrier family 25, member 37
IFRG28 JAG1	2.5 2.3	NM_022147 U61276	28kD Interferon responsive protein Jagged 1 (Alagille syndrome)	AIMI CHST5	2.1 2.1	U83115 N32257	Absent in melanoma 1 Carbohydrate metabolisr N-acetylglucosamine metabolism
PTHLH EB13	2.2 2.2	BC005961 NM_005755	Parathyroid hormone-like hormone Epstein-Barr virus induced gene 3	NAV3 ST5	2.0 2.0	NM_014903 NM_005418	Neuron navigator 3 Suppression of tumourigenicity 5
VCAM	2.2	NM_001078	Vascular cell adhesion molecule 1	FLJ23231	2.0	NM_025079	Zinc finger CCCH-type
CD83	2.1	NM_004233	CD83 antigen (immunoglobulin				containing 12A
PDGFRA	2.1	NM_006206	superfamily) Platelet-derived growth factor	Transcription fo	actors/signalling		
HRH1	2.1	D28481	receptor α polypeptide Histamine receptor H1	NKX31	6.3	AF247704	Transcription factor related, locus 1
IL1R1	2.1	NM_000877	Interleukin 1 receptor, type I	SOD2	5.7	AL050388	(Drosophila) Superoxide dismutase 2,
				CEBPD	5.6	NM_005195	mitochondrial CCAAT/enhancer bindir
Coagulatior	1			HIVER2	4.4	AL023584	protein (C/EBP), delta Human immunodeficienc virus type I enhancer
F3	3.3	NM_001993	Coagulation factor III (tissue factor)	DSCR1	3.7	NM_004414	binding protein 2 Down syndrome critical region gene 1

Induction (-fold)	Accession no.	Gene description	Gene	Induction (-fold)	Accession no.	Gene description
			Transcription factors signalling continued RAPGEF5	3.4	NM_012294	Rap guanine nucleotide exchange factor (GEF) 5
chemokines			STC2	3.2	BC000658	Stanniocalcin 2
27.0	NM_004591	protein- MIP-3	NCF4	2.9	NM_013416	Neutrophil cytosolic facto 4, 40 kDa
14.7	NM_002090	ligand 3	APOL3	2.7	NM_014349	Apolipoprotein L3
11.6	M11734	(granulocyte-macrophage)	SNFT	2.6	NM_018664	Jun dimerisation protein p21SNFT
10.5	NM_002996	Fractalkine	RND1	2.6	U69563	Rho family GTPase 1
		(granulocyte)			NM_005204	Mitogen-activated protein kinase kinase kinase 8
6.0	NM_000600	Interleukin 6 (interferon β2)	FOXF1	2.5	NM_001451	Forkhead box F1
5.6	AK026546	ligand 5	IRF1	2.5		Interferon regulatory factor 1
5.1	NM_000576		MSC	2.4	AF060154	Musculin (activated B-cel factor-1)
4.1	M57731					
4.1		ő	RGS2			Regulator of G-protein signalling 2, 24 kDa
4.0	NM_001511	Chemokine (C-X-C motif) ligand 1	STAT5A	2.2	NM_003152	Signal transducer and activator of transcription 5A
3.6	NM_002309	Leukaemia inhibitory factor (cholinergic differentiation factor)	MEOX1	2.2	NM_004527	Mesenchyme homeo box
3.3	NM_001565	Chemokine (C-X-C motif) ligand 10	NFKB1	2.2	M55643	Nuclear factor of kappa light polypeptide gene enhancer
2.3	AF030514	Chemokine (C-X-C motif) ligand 11	ISG20	2.2	NM_002201	Interferon stimulated exonuclease gene 20 kD
2.3	NM_002341	Lymphotoxin β (TNF superfamily, member 3)	ABTB2	2.2	AL050374	Ankyrin repeat and BTB (POZ) domain containing 2
2.2	AF043337	Interleukin 8				
2.1	NM_002985	Chemokine (C-C motif) ligand 5				
2.1						
	(-fold) chemokines 27.0 14.7 11.6 10.5 6.9 6.0 5.6 5.1 4.1 4.1 4.1 4.0 3.6 3.3 2.3 2.3 2.3 2.3 2.2 2.1	(-fold) Accession no. 27.0 NM_004591 14.7 NM_002090 11.6 M11734 10.5 NM_0002996 6.9 NM_000759 6.0 NM_000600 5.6 AK026546 5.1 NM_000576 4.1 M57731 4.1 NM_003862 4.0 NM_001511 3.6 NM_001565 2.3 AF030514 2.3 NM_002985 2.1 NM_002985 2.1 AI984980 2.0 BF575514	(-fold)Accession no.Gene descriptionchemokines27.0NM_004591Macrophage inflammatory protein- MIP-314.7NM_002090Chemokine (C-X-C motif) ligand 311.6M11734Colony stimulating factor 2 (granulocyte-macrophage)10.5NM_0029966.9NM_0007596.0NM_000600Interleukin 6 (interferon β 2)5.6AK026546Chemokine (C-X-C motif) ligand 55.1NM_0005764.1M577314.0NM_0015113.6NM_0015556.0NM_0015117.1Chemokine (C-X-C motif) ligand 13.6NM_0023091.3Leukaemia inhibitory factor (cholinergic differentiation factor)3.3NM_0015652.2AF0305142.2AF0433372.1NM_0029852.1AIM_0029852.1AIM_0029852.0BF575514Pre-B-cell colony enhancing factor 1	(fold)Accession no.Gene descriptionGene $Transcriptionfactors signallingcontinuedRAPGEF5Transcriptionfactors signallingcontinuedRAPGEF527.0NM_004591Macrophage inflammatoryprotein- MIP-3NCF414.7NM_002090Chemokine (C-X-C motif)(granulocyte-macrophage)APOL311.6M11734Colony stimulating factor 2(granulocyte-macrophage)SNFT10.5NM_002996Fractalkine(granulocyte)RND16.9NM_000759Colony stimulating factor 3(granulocyte)MAP3K86.0NM_000600Interleukin 6 (interferon β2)Interleukin 6 (interferon β2)FOXF15.6AK026546Chemokine (C-X-C motif)ligand 5IRF11.1NM_000576Interleukin 1βMSC4.1M57731Chemokine (C-X-C motif) ligand 2(cholinergic differentiation factor)RGS24.0NM_001511Chemokine (C-X-C motif) ligand 1STAT5A3.6NM_002309Leukaemia inhibitory factor(cholinergic differentiation factor)MEOX12.3AF030514Chemokine (C-X-C motif) ligand 11ISG202.3NM_002341Lymphotoxin β (TNF superfamily,member 3)ABTB22.2AF0433372.1Interleukin 8Chemokine (C-C-C motif) ligand 52.1AP043337Chemokine (C-C-C motif) ligand 82.0BF5755142.3AF0433372.1Interleukin 8Pre-8-cell colony enhancing factor 1ABTB2$	$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$

gene expression are grouped (see branching) per independent experiment (that is per separate HUVEC population) rather than per antibody preparation. This implies that the greatest source of variation, in terms of genes regulated by anti- β_2 GPI antibody, is determined by individual HUVEC populations rather than between individual anti- β_2 GPI antibody preparations. It is likely that inter-experiment variation masked any subtle differences in the upregulation/downregulation of genes by anti- β_2 GPI antibody from different patients.

Confirmation of microarray data by real-time RT-PCR and ELISA

Real-time RT-PCR analysis was carried out for selected novel anti- β_2 GPI antibody regulated genes, covering a range of different levels of regulation. Genes included in this analysis were CSF3, CX3CL1, FGF18, SOD2 and Tenascin C plus E-selectin as a positive control gene. We also included the downregulated gene ID2 in these experiments. The results of these experiments are shown in fig 2. All six upregulated genes (CSF3, CX3CL1, E-Selectin, FGF18, Tenascin C and SOD2) were also found to be upregulated by real time PCR analysis. Levels of upregulation were variable, but CX3CL1 was the highest-fold upregulated gene of the six selected genes by microarray analysis (fig 2A). ID2 was downregulated 2.3-fold by microarray analysis and this was very similar to the level of downregulation by real-time PCR analysis. (fig 2B). In the present study increased mRNA levels of E-selectin and IL-8 following anti- β_2 GPI antibody

treatment and microarray analysis were consistent with increased protein levels following antibody treatment (figs 1, 2C, D).

We assigned the 101 upregulated genes to the following APS relevant functional groups; cell receptors/adhesion molecules, cytokines/chemokines, coagulation genes, apoptosis/anti-apoptosis, transcription factors/signalling, metabolism and miscellaneous genes (table 2). Of particular note are the high level of induction of the chemokines CCL20, CXCL3, CX3CL1, CXCL5, CXCL2 and CXCL1 as well as genes classically associated with pro-inflammatory cytokine $\mbox{TNF}\alpha$ signalling such as TNFAIP6, TNFAIP2, TNFAIP8, TNFAIP3 and the anti-apoptotic gene BCL2A1. Cell receptors induced included Tenascin C, OLR1 (oxLDL receptor) and IL-18 receptor 1. Other induced genes of interest included growth factors CSF2, CSF3, IL-6, IL-1β and FGF18. The list of upregulated genes includes some previously identified anti-β₂GPIinduced genes such as E-selectin, Tissue Factor (TF), ICAM-1 and VCAM-110 but the majority of the genes we have identified represent anti-β₂GPI-induced genes not previously reported.

Anti-β₂GPI-mediated downregulation of gene expression in endothelial cells

A smaller panel of anti- β_2 GPI antibody-regulated genes in EC were downregulated (fig 2 and table 3). None of these genes has previously been reported to be anti- β_2 GPI antibody-regulated genes in EC. The majority of the 14 downregulated

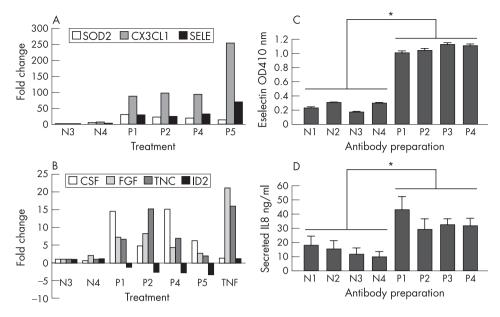


Figure 2 Quantitative real-time RT-PCR and ELISA analysis of anti-β2GPI antibody mediated gene regulation in HUVEC. Cells were incubated with different anti- β_2 GPI antibody preparations (P1, P2, P4, P5, 50 µg/ml) or with control normal IgG (N3, N4, 50 μ g/ml) or, TNF α for 4 h and total RNA isolated and processed for real-time PCR analysis. Antibody preparations N3, N4, P1, P2 and P4 were previously used in the microarray experiments. Gene expression levels were normalised to the β actin mRNA level. The results show change in expression level relative to control normal IgG (N3) level and represent the mean of duplicate samples from two independent experiments. (A) shows data for SOD2 CX3CL1 and E-selectin. TNFa induced highlevel expression of these genes but induction levels were off the scale and omitted from the figure, (B) shows data for CSF, FGF, Tenascin C (TNC) and ID2. TNFα-regulated changes in levels of expression are included for comparison. The effect of four control normal IgG and four APS-derived anti- β_2 GPI antibody preparations (used in microarray experiments) on E-selectin expression (C) and IL-8 secretion (D) was determined by ELISA. Antibodies were incubated with the cells for 4 h at 50 μ g/ml. Results show mean \pm SEM of triplicate samples from a representative experiment (one of three). = p < 0.03 as determined by two-tailed Mann-Whitney U Test. TNFa also induced high levels of E-selectin and IL-8 in HUVEC as measured by ELISA (data not shown).

genes encode signalling and transcription factors/signalling molecules. Two receptor/adhesion molecules were also down-regulated. GJA4 (connexin 37) is a gap junctional protein and OCLN (Occludin) is a structural protein of tight junctions.

DISCUSSION

The most striking feature of this study is the extent and diversity of anti- β_2 GPI antibody regulated genes in EC. The results reveal induction of a complex pro-inflammatory, as well as, a pro-adhesive and pro-coagulant milieu by these antibodies, which could potentially be involved in the pathogenesis of PAPs.

It is intriguing that many of the most highly upregulated genes in the present study are chemokines such as CCL20, CXCL3, CX3CL1 (fractalkine), CXCL5, CXCL2 and CXCL1, which are involved in recruitment, chemotaxis and proliferation of mononuclear cells and/or granulocytes. These findings are consistent with a number of in vitro and in vivo studies reporting that anti- β 2GPI antibodies increased monocyte adhesion to EC.^{9 11 12} Moreover, placental biopsies from APS patients had a higher concentration of inflammatory cells particularly macrophages²³ and an association has been found between neutrophil recruitment and foetal loss in APS.²⁴

CX3CL1 (fractalkine) and its receptor CX3CR1 are expressed in atherosclerotic lesions of humans and mice²⁵ and in CX3CL1deficient mice there is a major reduction of atherosclerosis.²⁶ Roughly one third of PAPS patients have atherosclerosis and a direct association of aPL with the pathogenesis of accelerated atherosclerosis in APS patients has been reported.^{27 28} aPLs are thought to accelerate this process by activating EC. β_2 GPI has also been demonstrated in high concentration in atherosclerotic plaque.²⁹ Other cytokine and adhesion molecules found to be upregulated by anti- β_2 GPI antibody could also have a role in the development of atherosclerosis. Monocytes have been shown to strongly express IL-18 in atheromatous lesions *in situ*³⁰ and EC expression of IL-18R was increased 4.3-fold in our study. Gerdes *et al.*³¹ suggested an IL-18 mediated paracrine proinflammatory pathway involving monocytes ECs and smooth muscle cells in association with atherogenesis.

Expression of oxLDL receptor OLR1 was upregulated over fourfold in our study (table 2). OLR1 expressed on vascular EC is involved in binding, internalisation and degradation of oxLDL and might therefore play a significant role in atherogenesis.³² ³³ Anti- β_2 GPI antibodies bind to β_2 GPI-oxLDL complexes and have been shown in vitro to enhance uptake into monocytes/macrophages potentially accelerating the lesion formation.³⁴ GJA4 (connexin 37), a gap junction protein, was downregulated by anti- β_2 GPI antibodies and polymorphisms in this protein have been associated with the development of arteriosclerotic plaques in human subjects.³⁵

We have confirmed by gene microarray profiling anti- β_2 GPI mediated upregulation of molecules, previously reported to be upregulated at the protein level, including TF, E-selectin, ICAM, and VCAM-1.⁹ ¹¹ ¹² ³⁶⁻³⁸ It is tempting to speculate that a combination of increased adhesion molecules, pro-inflammatory cytokines and chemokines in addition to increased TF expression could strongly support development of thrombosis and contribute to the advancement of atherosclerotic lesions in response to anti- β_2 GPI antibodies.

A number of pro-angiogenic cytokines/chemokines such as IL-8 and fibroblast growth factor, which were upregulated by anti- β_2 GPI antibodies in the present study, might contribute to the hyperplasia associated with PAPS. APS is associated with EC proliferation and fibrosis characterised by intimal hyperplasia within the lumen of micro-capillaries typically within the kidney or skin.³⁹ It is also associated with deposition of aPL in the subendothelial layers.⁴⁰ Histologic examination of renal

Table 3 Anti- $\beta_2 GPI$ antibody downregulation of gene expression in HUVEC

Gene	Reduction (-fold)	Accession no.	Gene description		
Adhesion molec	ules/receptors				
GJA4	2.9	NM_002060	Gap junction protein α4 37 kDa (connexin 37)		
OCLN Cytokine/ chemokine	2.1	U53823	Occludin		
BDNF	2.1	NM_001709	Brain-derived neurotrophic factor		
Metabolism GFOD1	2.0	NM_018988	Glucose-fructose oxidoreductase domain containing 1		
Miscellaneous 13CDNA73	2.2	NM_023037	Hypothetical protein CG003		
Transcription fac	ctors/signalling				
MEOX2	3.1	NM_005924	Mesenchyme homeo bo> 2		
MAF	3.0	NM_005360	v-maf Musculoaponeurotic fibrosarcoma oncogene homolog (avian)		
BMP4	2.8	D30751	Bone morphogenetic protein 4		
TXB1	2.8	AF012130	T-box 1		
ID2	2.3	NM_002166	Inhibitor of DNA binding 2		
DACH1	2.2	NM_004392	Dachshund homolog 1 (Drosophila)		
RUNX1T1	2.2	NM_004349	Runt-related transcription		
MAFB	2.0	NM_005461	v-maf Musculoaponeurotic fibrosarcoma oncogene		
ZNF365	2.0	NM 014951	homolog B Zinc finger protein 365		

biopsies from 16 patients with PAPs showed small vessel vasoocclusive lesions associated with myofibroblastic intimal cellular proliferation and thrombosis, five patients showed endothelialised channels indicating recanalising thrombosis and EC proliferation.⁴¹

 β_2 GPI has been reported to bind to cells in a number of different ways. For example, it can bind to anionic membrane molecules such as heparan sulphate and it has also been reported to bind as a ligand to the annexin II receptor.^{10 42} Intriguingly, an indirect mechanism for EC stimulation by anti- β_2 GPI antibody could exist. Annexin II is also a high affinity receptor for Tenascin C, a component of the extracellular matrix that functions as an adhesion molecule, shown in this study to be upregulated by anti- β_2 GPI antibody.⁴³

One possibility that has to be considered, however, is that our regulated genes might include some or many genes not regulated by anti- β_2 GPI antibody directly but rather indirectly by autocrine cytokine/chemokine production produced by EC cells shortly after anti- β_2 GPI antibody exposure. We chose to study gene expression at 4 h after exposure to anti- β_2 GPI antibody in order to study the early gene expression profile. However, many cytokines/chemokines are induced rapidly and they could themselves then induce gene expression in EC by binding to high affinity receptors on the EC. This possibility should be addressed in future studies aimed at investigating the signal transduction mechanisms responsible for anti- β_2 GPI antibody mediated gene regulation in EC. The anti- β_2 GPI antibody induced gene panel described here is largely distinct to

those described in gene profiling studies on HUVEC with different cytokines or LPS.^{44–46} Nonetheless, a small subset of anti- β_2 GPI antibody-induced genes (for example; E-selectin, IL-8, VCAM-1, TNFAIP6, TNFAIP2, TNFAIP8, TNFAIP3), have been shown to be induced by cytokine and/or LPS-induced gene profiling of HUVEC.^{44–46} A study profiling monoclonal anti- β_2 GPI antibody mediated gene regulation in human monocytes found upregulation of a number of genes using cDNA arrays, such as, IL-1 β and TF, which were also identified in our study.¹⁶ However many more anti- β_2 GPI antibody regulated genes in HUVEC were found in the present study probably due to the much larger number of genes represented on the Affymetrix chips in comparison to the cDNA arrays used in the earlier study.¹⁶

An important question in relation to our findings is how they relate to the in vivo situation. A recent study, measuring a limited number of parameters of EC function, concluded that aPL were unable to support a full-blown endothelial perturbation in vivo.⁴⁷ There is evidence however from other studies for increased circulating levels of TF, IL-6, TNF α^{48} and VCAM-1⁴⁹ in APS patients. Our studies suggest increased levels of some cytokines might, at least in part, be EC derived and therefore evidence of endothelial perturbation in vivo.

In conclusion, global gene expression profiling using microarray technology has been used for the first time to examine the extent and diversity of PAPs patient-derived anti- β_2 GPI antibody mediated gene regulation in HUVEC. These studies have identified important anti- β_2 GPI antibody regulated EC genes that might contribute to the vasculopathy in PAPs. Further studies on signal transduction mechanisms responsible for anti- β_2 GPI antibody mediated gene regulation and the role of individual anti- β_2 GPI antibody gene targets in APS pathogenesis should provide opportunities for new therapeutic strategies by either inhibiting the expression of particular (pathogenic) genes or the activation of corresponding signalling pathways. Moreover, these findings could have wider implications for other autoimmune diseases, where anti- β_2 GPI antibodies have been described.

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