

EXTENDED REPORT

Fine mapping and conditional analysis identify a new mutation in the autoimmunity susceptibility gene *BLK* that leads to reduced half-life of the *BLK* protein

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ABSTRACT

Objectives To perform fine mapping of the autoimmunity susceptibility gene *BLK* and identify functional variants involved in systemic lupus erythematosus (SLE).

Methods Genotyping of 1163 European SLE patients and 1482 controls and imputation were performed covering the *BLK* gene with 158 single-nucleotide polymorphisms. Logistic regression analysis was done using PLINK and conditional analyses using GENABEL's test score. Transfections of *BLK* constructs on HEK293 cells containing the novel mutation or the wild type form were analysed for their effect on protein half-life using a protein stability assay, cycloheximide and western blot. ChIP-qPCR for detection of nuclear factor κ B (NF κ B) binding.

Results Fine mapping of *BLK* identified two independent genetic effects with functional consequences: one represented by two tightly linked associated haplotype blocks significantly enriched for NF κ B-binding sites and numerous putative regulatory variants whose risk alleles correlated with low *BLK* mRNA levels. Binding of NF κ Bp50 and p65 to an associated 1.2 Kb haplotype segment was confirmed. A second independent genetic effect was represented by an Ala71Thr, low-frequency missense substitution with an OR=2.31 (95% CI 1.38 to 3.86). The 71Thr decreased *BLK* protein half-life.

Conclusions These results show that rare and common regulatory variants in *BLK* are involved in disease susceptibility and both, albeit independently, lead to reduced levels of *BLK* protein.

INTRODUCTION

The *BLK* gene located on chromosome 8p23-p22 encodes a tyrosine kinase of the SRC family of proto-oncogenes. A genome-wide association study identified a single-nucleotide polymorphism (SNP) rs13277113 in the 5' upstream region associated with systemic lupus erythematosus (SLE),¹ a chronic autoimmune disease with complex inheritance. To date, multiple studies have confirmed the association of *BLK* with SLE in European and Asian populations as well as with other autoimmune

disorders.^{2–10} *BLK* protein has 505 amino acids with SH3 (58–118), SH2 (124–220) and protein kinase domains (241–494). Although *BLK* is expressed in various tissues such as pancreatic β cells, thymus, hair follicles and salivary ducts,^{11 12} it is preferentially expressed in B lymphoid cells and has a role in B cell receptor signalling and B cell development.¹³

The *BLK*-rs13277113 SNP is part of a group of common variants across several genes that have been associated with SLE through genome-wide association study.¹⁴ Together, they account for 15% of the disease's familial aggregation and few have been demonstrated to be functional.¹⁴ The SLE-risk allele rs13277113-A correlated with decreased expression of *BLK* mRNA¹ but the mechanism by which this or another SNP in linkage disequilibrium (LD) with it affects gene expression has not been characterised yet.

To address which and if common and/or low frequency functional variants are involved in SLE susceptibility at the *BLK* locus, we performed fine mapping by genotyping tag SNPs aided by imputation.

METHODS

Patients and controls

After quality control of the data, the study sample consisted of 1163 patients with SLE and 1482 ethnicity-matched healthy control subjects from the European multicentre collaboration network BIOLUPUS (supported by the European Science Foundation), comprising individuals from Argentina (60 patients and 109 controls), Belgium (70 patients and 59 controls), Germany (284 patients and 176 controls), Hungary (38 patients and 35 controls), Italy (264 patients and 320 controls), Portugal (163 patients and 165 controls), Spain (206 patients and 227 controls) and Sweden (78 patients and 391 controls). A completely new and independent set of 1103 healthy Spanish controls was also used. All patients fulfilled at least four of the American College of Rheumatology 1982 criteria for the classification of SLE.¹⁵ Subjects with an individual genotyping rate lower than 90% or duplicated and/or related



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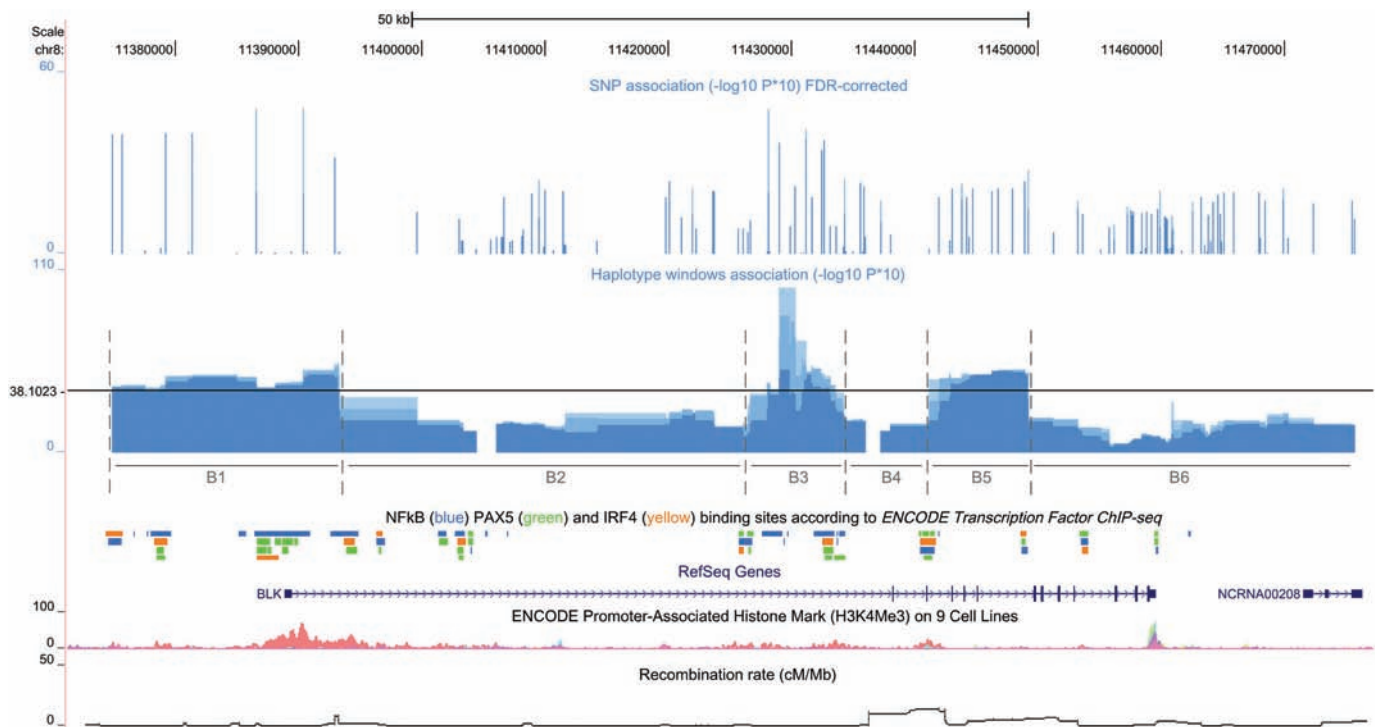


Figure 1 Systemic lupus erythematosus-associated single-nucleotide polymorphisms (SNPs) and haplotype blocks and genomic features of the *BLK* locus. From top to bottom: $-\log_{10}$ of the p value corrected by false discovery rate for 158 SNPs. Below, the association for haplotype windows of two, three and four SNPs is displayed; the horizontal black line marks the threshold for Bonferroni correction ($p=0.05/323$ windows tested). Only SNP windows contained within block B1 (5' upstream, exon 1 – UTR – and beginning of intron 1), B3 (end of intron 1) and B5 (exons 4, 5 and 6) were associated after correction. The exon/intron structure of *BLK* is displayed next and then NFkBp65 (blue), IRF4 (yellow) and PAX5 (green) Chip-Seq identified binding sites and promoter-associated histone marks (H3K4Me3) according to ENCODE project. Recombination rate (cM/Mb) is displayed at the bottom.

samples were excluded. We removed individuals with <90% of European ancestry, as estimated with STRUCTURE v2.3.3 and 350 ancestry informative markers.

Tag SNP selection

From the LD structure of the *BLK* locus in the HapMap CEU population (data release 27; available at <http://hapmap.ncbi.nlm.nih.gov/>), tag SNPs selection capturing more than 90% of common variation at the gene locus (minor allele frequency of greater than or equal to 10%) including 20 kb upstream and downstream of the gene, at a r^2 threshold of greater than or equal to 0.8, were selected using the tagger algorithm implemented in Haploview, V.4.1.¹⁶ After quality control of the data, 27 tag SNPs were used for genotyping and to guide the imputation.

Genotyping

All samples were genotyped at the Feinstein Institute for Medical Research (Manhasset, New York, USA) using a GoldenGate Custom Genotyping Assay and a BeadXpress Reader from Illumina (San Diego, California, USA). Two SNPs (rs1478895 and rs2248932) were genotyped by TaqMan 5'-exonuclease assay (ABI, Foster City, California, USA). SNP rs55758736 was genotyped by RFLP and sequencing for verification in 178 individuals. An Illumina custom BeadArray was used for genotyping this SNP in 1103 healthy controls.

Imputation

We used IMPUTE2¹⁷ across a 250 kb genomic region (chr8:11,288,930-11,559,517) of the *BLK* locus. As reference panels we used haplotypes from all HapMap Consortium^{18 19}

populations together (phase 3, release 2) and haplotypes of the CEU population from the pilot phase of 1000 Genomes Project²⁰ (downloaded from http://mathgen.stats.ox.ac.uk/impute/impute_v2.html#filtered_1kg_hm3_haps on May 13th, 2011). HapMap haplotypes duplicated with 1000 Genomes data were removed. Default parameters were used and the Ne argument set to 15 000. Only imputed genotypes with a probability equal to or greater than 0.9, a minor allelic frequency (MAF) equal to or greater than 0.005, following Hardy–Weinberg equilibrium ($p>0.001$), and a genotyping rate equal to or greater than 0.95 were retained for association.

Statistical analysis

Genetic association analysis was done using PLINK v1.07²¹ and GenABEL v1.6-5.²² All SNPs with a genotype call rate <95% or not in Hardy–Weinberg equilibrium ($p<0.001$) were excluded. For single-marker tests, we performed a Cochran–Mantel–Haenszel (CMH) meta-analysis, using the country of origin as the stratification variable, and a Breslow–Day test to assess homogeneity of the ORs. p Values were adjusted using false discovery rate. We also performed an omnibus haplotype test for all windows of 2, 3 and 4 SNPs across the gene. In this test, the alternate hypothesis of each haplotype having a unique effect is compared with the null hypothesis ($df=\text{number of haplotypes}-1$).²¹ Omnibus as well as haplotype-specific tests for haplotype blocks were conducted by testing each haplotype against all others pooled together (1 df). A Bonferroni correction using the number of windows tested was applied ($p<0.05/323$ windows tested).

Conditional analysis was done by logistic regression using GenABEL's score test. By specifying the country of origin as

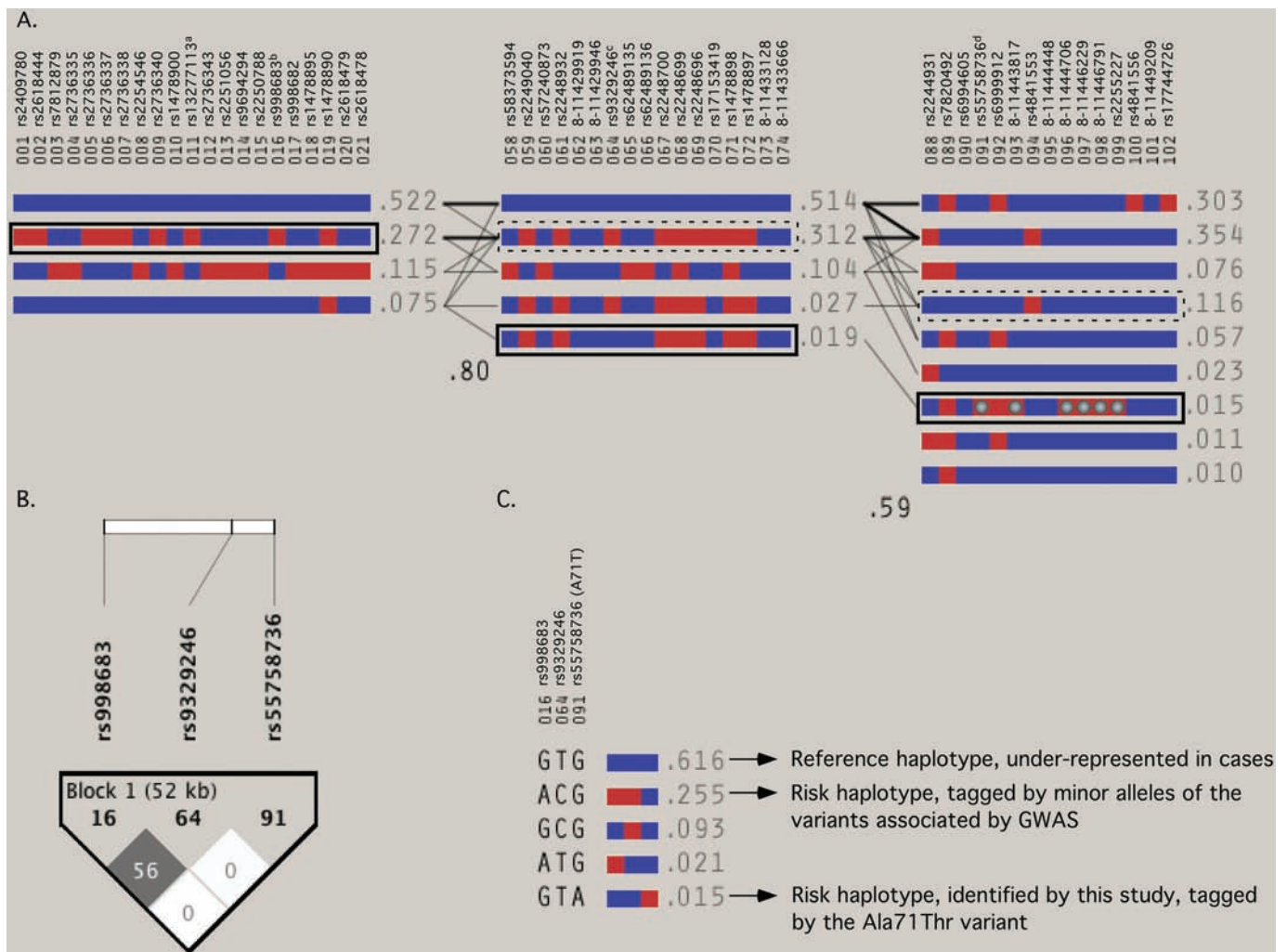


Figure 2 Structure of associated BLK haplotypes. (A) Haplotypes formed by single-nucleotide polymorphisms (SNPs) in each associated block B1, B3 and B5 as estimated with expectation maximisation algorithm (Haploview v.4.1). Blue and red squares represent major and minor alleles, respectively. To the right of each haplotype, its population frequency (cases and controls) and connections between blocks (thin lines if $> 1\%$, thick lines if $> 10\%$) are displayed. In crossing areas are the values of the multiallelic D' which represent the level of recombination between two blocks. See table 1 for haplotype-specific ORs and p values. Haplotypes associated with increased risk of developing systemic lupus erythematosus are enclosed within rectangles (solid line if $p < 1 \times 10^{-3}$; dashed line if $p < 0.05$). B1 contains a risk haplotype tagged by rs998683-A(b) (strongest hit in this study) and its proxies including the rs13277113-A allele(a) previously described.¹ Blocks B1 and B3 are highly correlated. B3 contains SNP rs9329246(c), which is shared by the two strongest four-SNP windows of the whole BLK locus. B5 contains the independent risk haplotype tagged by the mutant allele of the rs55758736/Ala71Thr non-synonymous SNP(d) and a set of highly correlated allelic variants (grey circles). The independence of B5 risk haplotype is further supported by (B) the linkage disequilibrium plot displaying r^2 values between the representative variants of each block and (C) the relationship between their alleles.

the *strata* argument, we performed a structured test of association for all SNPs. In a stepwise manner, the SNP with higher p value was identified in each step and then used as covariate for the next association step until no SNP remained associated. GenABEL package was run using R version 2.9.2.

Genome sequence track analysis for epigenomic marks and transcription factor binding sites

Associated and non-associated SNPs within haplotype blocks were analysed for enrichment with eight epigenomic marks using GenomeRunner.²³ For SNPs within each haplotype block the same number of randomly selected nucleotides from the whole range of haplotype blocks within chr8:11374997-11475653 coordinates (NCBI36/hg18 genome assembly) was sampled over the course of 100 Monte-Carlo simulations. The average expected frequency of their association with a given genomic feature

(eg, nuclear factor κ B (NF κ B) binding site, epigenomic marks) was compared with the observed frequency using a χ^2 test. Specifically, SNPs within haplotype blocks were tested for enrichment against experimentally validated NF κ Bp65, IRF4 and PAX5 transcription factor binding sites annotated in the wgenocoderegtfbs clustered UCSC table of the genome browser.²⁴ Other tables included histone acetylation and methylation marks (Regulation/Broad histone tables for Gm12878 lymphoblastoid cell line). p Values were $-\log_{10}$ converted and a $-$ was included for under-represented p values. The values are shown as a heatmap plotted using Matlab (Natick, Massachusetts, USA) (online figure S2). p Values are presented in the online table S3.

We used SIFT²⁵ to predict the status of rs55758736. SIFT predicts whether an amino acid substitution affects protein function based on similarity to related sequences and physical properties of amino acids (<http://sift.jcvi.org/>).

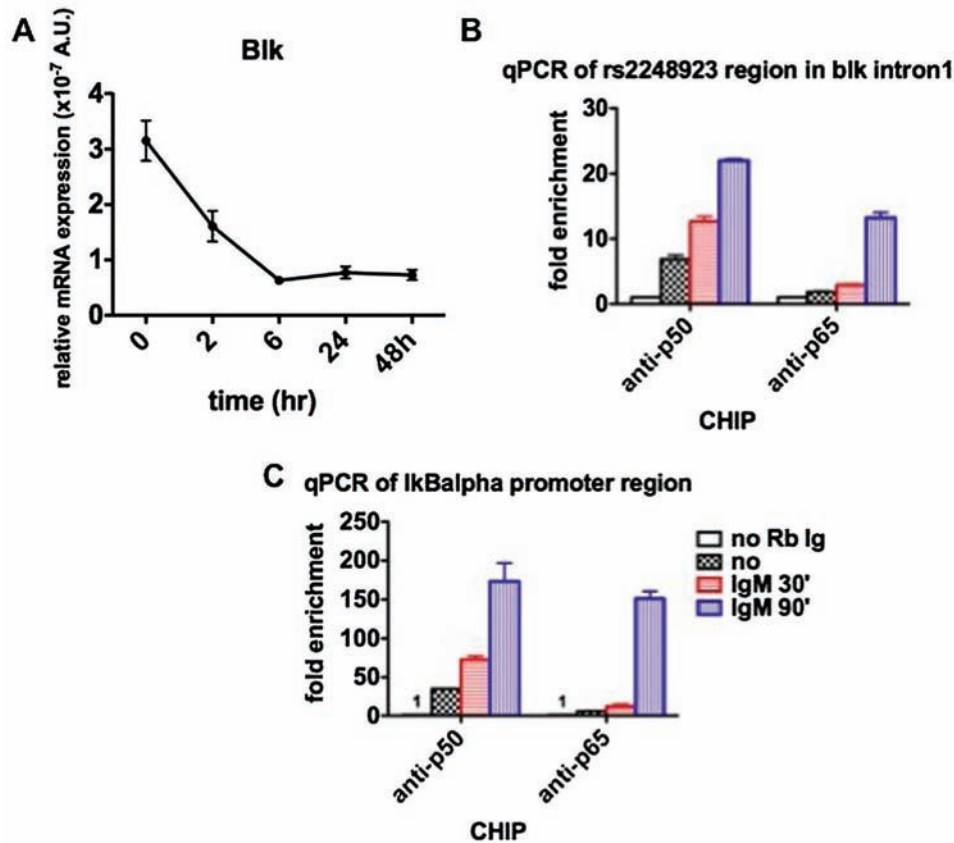


Figure 3 CHIP-qPCR showing binding of NF κ B p50 as well as NF κ Bp65 within the genomic segment contained in the 1.2 Kb haplotype window in Daudi cells. (A) mRNA expression of the BLK gene after Bcr stimulation. (B) qPCR of the portion containing SNP rs2248932 within the 1.2 kb genomic segment in intron 1 of human BLK. (C) qPCR of the IkBa gene used as positive control.

CHIP-qPCR for NF κ B p50 and p65 on the 1.2 Kb associated haplotype genomic segment

CHIP experiments were performed according to the manufacturer's recommendations (EZ-Magna CHIP A, Millipore, Billerica, California, USA). In brief, 4×10^6 Daudi cells were incubated with or without 10 mg/ml anti-immunoglobulin M (IgM) F(ab')₂ fragments (Jackson ImmunoResearch, West Grove, Pennsylvania, USA) for the indicated time. Cells were fixed with 1% formaldehyde and nuclei were isolated and sonicated within 300 ml of lysis buffer. An amount of 50 ml of chromatin-protein complexes were immunoprecipitated overnight at 4°C by mild agitation with 5 mg of pAb specific for p65 (Santa Cruz, California, USA) or p50 (Abcam, Cambridge, Massachusetts, USA) or normal rabbit IgG (Millipore) as negative control. After elution from the immunoprecipitated chromatin complexes followed by reverse-crosslink and cleanup, DNA samples were subjected to real-time PCR analysis using primers as follows: rs2248932 neighbouring region within Blk intron 1 primer set: forward – TGCATCAGCATCACTGGG; reverse – GGCACAATAGTTCTGAAACCTC. IkBa was used as control for NF κ B binding with the following primer set: forward – CACTTGCAGAGGGACAGGAT; reverse – GAGAACTCCCTGCGATGAG.

Cloning and expression of BLK constructs with the Ala71Thr substitution

BLK sequence was PCR amplified using cDNA from a BJAB cell line and primers f-BLK: 5'-CACCAtggggctgtaagtagc-3 and r-BLK 5'-gggctgcagctgactgccc-3. The start codon in the forward primer is underlined. The open reading frame was

cloned in pcDNA3.1D/V5-His (Invitrogen, Life Technologies, Grand Island, New York, USA) and confirmed by sequencing. The protein tagged with the V5 epitope at the C terminal was produced by deletion of the stop codons. The BLK 71Thr isoform was produced by mutagenesis PCR with pfu-Ultra II fusion HS polymerase (Stratagene, Agilent Technologies, Santa Barbara, California, USA) and the primers BLKm71f: 5'-TATGACTACACCaTATGAATGATCGGGACCT-3 and BLKm71r: 5'-ATCATTCATAGtGGTGTAGTCATACAGAG-3. Expression of the constructs was assayed by western blot with anti-V5 antibody (online figure S4).

Protein stability assay

Embryonic kidney HEK293T cells grown in RPMI 1640 medium supplemented with 10% fetal calf serum were seeded on six-well plates and transfected with 4 μ g of expression plasmids V5-tagged BLK isoforms using Lipofectamine 2000. At 22 h cells were harvested and distributed in six wells of 12-well plates. After 2 h cells were treated with 20 μ g/ml cycloheximide in dimethyl sulphoxide (DMSO) or DMSO alone (time 0) for various times. Cellular extracts were prepared in lysis buffer: 1% NP40, 150 mM NaCl, 10 mM Tris (pH 7.5), 2 mM sodium orthovanadate, 1 mM EDTA, 10% glycerol, 1 mM phenylmethylsulfonyl fluoride and protease and phosphatases inhibitor cocktails (Roche). A fifth of the extract was resolved on SDS-PAGE and immunoblotting carried out using standard protocols with anti-V5 antibodies (Invitrogen), β -tubulin (Sigma-Aldrich) and antimouse IgG-HRP (Zymed, San Francisco, California, USA). Quantification of the bands was done using ImageJ.

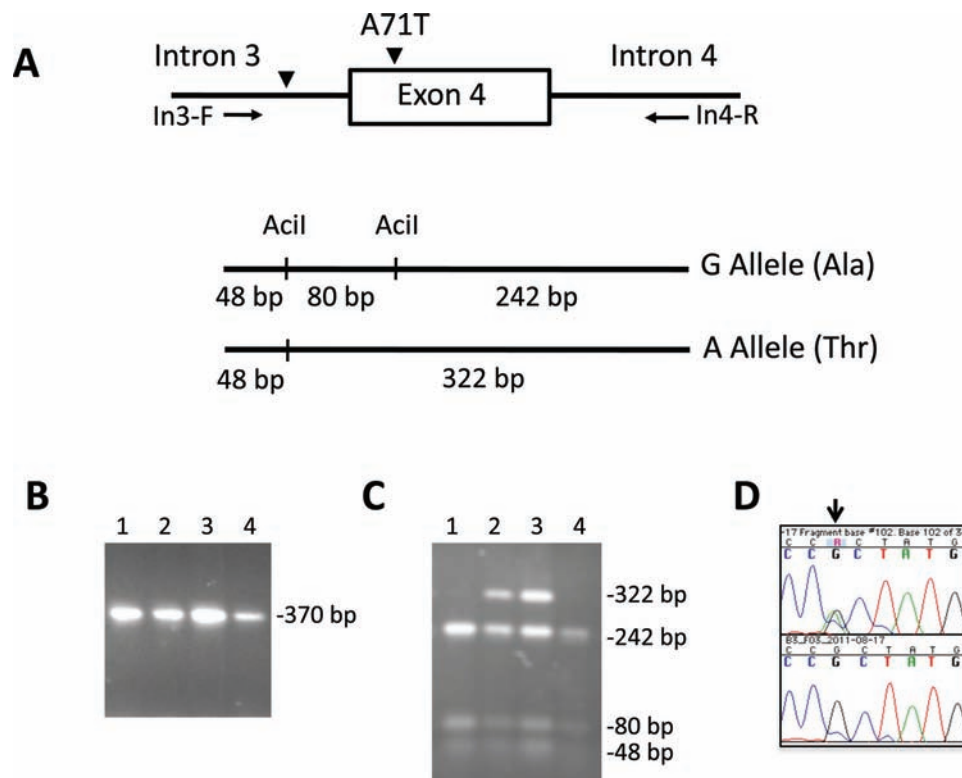


Figure 4 Genotyping of the Ala71Thr substitution in exon 4 of BLK. (A) Schematic diagrams showing the procedure for genotyping the single-nucleotide polymorphism (SNP) rs55758736 in exon 4 of BLK. Genomic DNA was amplified with primers flanking exon 4 (In3-F: 5'AGAAGCCTGTCCTCCTTGGTAGC 3' and In4-R: 5'GGAAGATTTGGAGAGGAAGACA 3') and the PCR products were digested with the restriction enzyme *Acil*. The A allele disrupts the restriction site generating only two fragments of 48 and 322 bp while the G allele produces three fragments of 48, 80 and 242 bp. (B) PCR products of four subjects showing a unique band of 370 bp and (C) the subsequent *Acil* digestion of the amplification products. Subjects 2 and 3 are heterozygotes (G/A) and subjects 1 and 4 are homozygotes for the wild type allele (G/G). (D) Sequence chromatographs showing one subject heterozygous for the BLK mutation (above) and one subject homozygous for the wild type allele (below).

RESULTS

Fine mapping and conditional analysis of BLK reveals two independent effects

A total of 158 SNPs with MAF>0.005 were tested for association in 1163 European patients with SLE and 1482 age- and country-of-origin-matched controls. A meta-analysis demonstrated that the strongest association signal was in the *BLK* promoter region (rs998683, $P_{CMH-corrected}=1.05\times 10^{-4}$ and OR 1.38 (1.21 to 1.58)) (online table S1). However, even after correction for multiple testing, multiple association signals across the gene remained significant. To refine the *BLK* association, we tested sliding windows, which narrowed it down to three blocks (denominated B1, B3 and B5 in figure 1). The best model of association was observed for a 1.2 kb haplotype window between SNPs rs2248932 and rs9329246 located at the end of *BLK*'s first intron ($p=1.58\times 10^{-10}$, omnibus haplotype test).

The first block (B1) covered *BLK* 5' upstream region, exon 1 (untranslated-UTR) and beginning of intron 1, which correspond to the promoter. This block comprised a set of highly correlated SNPs including all variants previously associated with SLE (rs2409780, rs2618444, rs2736336, rs2736337, rs2736338, rs2736340, rs13277113) and our strongest hit (rs998683) (figure 2A and online figure S1). Haplotype-specific analysis demonstrated a common, risk haplotype tagged by the minor alleles of these SNPs, including the rs13277113-A variant (omnibus test p value= 1.61×10^{-5} , OR=1.32 (1.16 to 1.49)) (table 1).

The second block (B3) was at the end of intron 1 (figure 1) and displayed moderate LD with B1 (figure 2A). Consistent with

this observation, a risk haplotype correlated with the promoter risk haplotype and with similar haplotype frequency was over-represented in cases, although only with nominal association ($p=0.013$) (table 1).

In addition, an independent and low-frequency-haplotype within B3 (1.1% in controls) was strongly associated and had a large effect size ($p=5.16\times 10^{-7}$, OR=2.75 (1.80 to 4.19)) (table 1). This haplotype correlated completely with a risk haplotype observed on the third associated block B5 ($p=1.57\times 10^{-4}$, OR=2.48 (1.54 to 4.00)), which covered the protein-coding exons 4, 5 and 6 (figure 1). The minor alleles of six low-frequency variants occurred in this haplotype: rs55758736, a non-synonymous SNP in exon 4 resulting in an alanine to threonine substitution at amino acid position 71 (Ala71Thr; GCT>aCT); chr8:11443817 (intron 4); chr8:11444706 (intron 5), chr8:11446229 (intron 5); and chr8:8-11446791 and rs2255227 (intron 6) (figure 2A).

Conditional analysis using multivariate logistic regression demonstrated that the association of SNPs in B3 disappeared after adjusting by the strongest hit located in B1 (rs998683) suggesting that the B3 and the B1 association was not independent (online table S2).

In contrast, the low-frequency associated SNPs located in B5 remained associated after adjustment to rs998683 supporting two independent effects in *BLK*. Further, we observed that SNP rs55758736 had an $r^2\approx 0$ with SNPs tagging B1 and B3 (figure 2B,C and online table S2), although this may be an underestimation due to the low frequency of the SNP.

Table 1 Haplotype analysis of the *BLK*-associated blocks

Block (SNPs)/Start-End (Size)	No. SNPs	Omnibus test	Haplotype	Frequency Cases	Frequency Controls	OR (95% CI)	P-value
B1 (rs2409780-rs2618478) 11374997-11393411 (18.4 kb)	21	1.75E-04	TACGGTAGCTGTAGGGGCCGA	0.079	0.073	ns	0.4517
			CCCGTCCGTTATAGGAGCCGA	0.299	0.245	1.32 (1.16-1.49)	1.61E-05
			TACGGTAGCTGTAGGGGCCGA	0.504	0.559	0.81 (0.73-0.91)	7.56E-05
			TATAGTAACCGCCAGAGCAA	0.011	0.014	ns	0.3503
			TATAGTAACCGCCAGAGCAC	0.108	0.109	ns	0.9182
B3 (rs58373594-8-11433666) 11428036-11433666 (5.6 kb)	17	3.85E-07	ATCGCATAGAGTAAAG	0.489	0.541	0.80 (0.72-0.89)	2.70E-04
			TTGGCATCAATAGAAG	0.113	0.113	ns	0.9928
			AACACACAGGACAGTAG	0.045	0.045	ns	0.9493
			AACACACAGGACGGTAG	0.323	0.290	1.13 (1.01-1.27)	0.013
			AACACATAGGACAGTAG	0.030	0.011	2.75 (1.80-4.19)	5.16E-07
Strongest window (rs2248932-rs9329246) / 11429059-11430289 (1.2 kb)	4	1.58E-10					
B5 (rs2244931-rs17744726) 11441178-11449232 (8.1 kb)	15	2.56E-04	CAAGAGTACCGTTTA	0.291	0.328	0.84 (0.75-0.95)	3.94E-03
			CGAGGGCACCCTATG	0.134	0.110	1.26 (1.06-1.49)	0.011
			GAAGAGTACCGTATG	0.014	0.010	ns	0.2331
			CAAGAGTACCGTATG	0.061	0.067	ns	0.3859
			GGAGGGCACCCTATG	0.370	0.362	ns	0.5478
			GAAGGGTACCGTATG	0.077	0.078	ns	0.8688
			CAAGGGTACCGTATG	0.012	0.010	ns	0.6186
			GGAGGGTACCGTATG	0.019	0.024	ns	0.236
			CAAAAATATTCATG	0.023	0.010	2.48 (1.54-4.00)	1.57E-04

The first column indicates the block for which the haplotype analysis corresponds to. For each block, the first and the last SNP, the starting and ending positions, as well as the size in kilobases (kb) are also presented. The Omnibus *P* value indicates the overall significance of the association of the block. Only haplotypes with frequencies equal to or greater than 0.01 were tested. For the haplotype-specific analyses, the odds ratio (OR) with 95% confidence interval (95% CI) and *P*-values were determined for each haplotype tested against all of the others pooled together. In block B3, the SNPs comprising the strongest associated window are underlined and the omnibus test for this window is presented. All analyses were performed using PLINK software, version 1.07. ns: non-significant

Analysis of epigenetic marks and transcription factor binding sites shows an over-representation of NFκB and IRF4 along the promoter region associated blocks

We first attempted the identification of functional regulatory variants across the promoter blocks B1 and B3. Bioinformatic analysis revealed that B1 was significantly enriched for H3K4me3 sites, a hallmark of active promoters (figure 1, online figure S2 and online table S3). Furthermore, SNPs in B1 and B3, when compared with randomly chosen nucleotides, were enriched for binding sites for the transcription factor NFκBp65 and IRF4 but not PAX5 (using data from ENCODE project Chip-Seq for lymphoblastoid cell lines), while SNPs in the non-associated blocks B2 and B4 were not (figure 1, online figure S2 and online table S3). However, we were unable to single out a unique variant to explain the correlation between low *BLK* gene expression and risk alleles of SNPs in B1 and B3 due to the strong LD. We hypothesised that multiple sites would therefore explain a coordinated regulatory effect on the expression of *BLK*. Nevertheless, the 1.2 Kb haplotype window with the strongest genetic association and within B3 contained SNP rs2248932 that overlapped with a DNase hypersensitive cluster and with a strong NFκB binding site (online figure S3 and online table S4). To confirm if NFκB binds to this segment of *BLK* we performed a ChIP-qPCR experiment in a human Daudi cell line (figure 3A–C). We observed that NFκBp50 binds somewhat earlier than NFκBp65 (30 min post-BcR stimulation). The IκBa promoter served as control (figure 3C). Simultaneously, expression of *BLK* is reduced after activation (figure 3A).

The 71Thr mutation leads to reduced half-life of BLK protein

The independent Ala71Thr substitution is located on the SH3 (Src homology 3) domain of the *BLK* protein, which is of importance

in protein–protein interactions. The SIFT algorithm^{25,26} predicted this substitution to be potentially damaging. As rs55758736 was identified through imputation, we verified the presence of the mutation in 178 selected samples of cases and controls. Of these, we genotyped all of those individuals predicted by imputation to have the mutation and a group of individuals predicted not to have it. Verification was done using PCR, RFLP and sequencing (figure 4) reaching 92% concordance. The mutation was observed in 2.17% of SLE patients and 0.92% of controls, all in the heterozygous state (OR=2.31; 95% CI 1.38 to 3.86 with the Pearson's goodness-of-fit χ^2 (df=1)). Adding 1103 new controls, the OR was adjusted to 1.79 (95% CI 1.15 to 2.51).

At the translational level, the substitution of alanine for threonine implies the formation of a putative phosphorylation site that could lead to the reduction of the half-life of the protein. We investigated if this was the case. Using constructs containing each allele of rs55758736 in transfection experiments we observed that, indeed, 71Thr had an accelerated degradation after treatment with the protein synthesis inhibitor cycloheximide as compared with the Ala71 allele (figure 5 A,B and figure S4).

DISCUSSION

We have herein shown that blocks of associated SNPs within the promoter regions of the *BLK* gene were significantly enriched for NFκB and IRF4 binding sites, potentially involved in regulating levels of *BLK* mRNA and the related reduction in *BLK* gene expression levels correlating with the risk haplotypes. Also, through conditional analysis we have identified a potentially deleterious, low-frequency mutation leading to reduced *BLK* protein half-life. Unlike the wild type allele, the threonine residue of the mutated variant is capable of being phosphorylated,

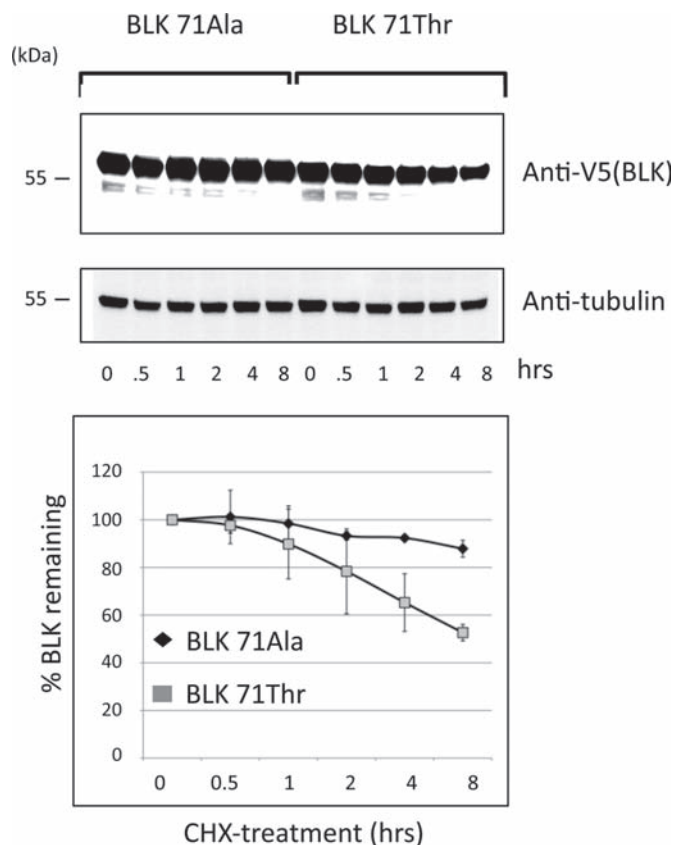


Figure 5 Reduced half-life of BLK protein in the presence of the 71Thr mutation. (A) Plasmids expressing each of the two BLK isoforms fused with V5 were transfected into HEK293T cells. Twenty-four hours after transfection, the cells were treated with 20 μ g/ml cycloheximide (CHX) for various times as indicated. The recombinant proteins were detected by western blot using anti-V5 antibody. Tubulin was used as loading control. (B) Quantification of the blots from three independent experiments; the SD at each time point is represented by bars. After 8 h of inhibition of protein synthesis, the level of BLK 71Thr was reduced to half while the wild type isoform Ala71 remained highly stable.

and there is evidence that while phosphorylation sites are important for activation of proteins in signal transduction pathways phosphorylation sites can act at the same time as signals for degradation by ubiquitin ligases.^{27 28}

Protein stability has been extensively studied in the cycling protein family. The abundance of cycling E is controlled by phosphorylation-triggered ubiquitin-dependent proteolysis.^{29 30} Phosphorylation of the Thr380 allows cyclin E to be recognised by Fbw7, an F box protein substrate of related E3 ubiquitin ligases.³¹ Mutation of this Thr380 to Ala prevents degradation of cyclin E.³² We are currently investigating if the reduction of the half-life of the BLK 71Thr protein is due to an active process of degradation mediated by phosphorylation or just the result of a general decrease in protein stability.

As the LD within the promoter blocks of *BLK* was very tight, it was not possible for us to define a single variant that could explain the correlation between low BLK levels and a polymorphism. Instead, we observed a clear correlation between associated blocks and transcription factor binding sites for NF κ B as experimentally determined by ChIP-Seq and contained in the ENCODE site. However, the database contains only NF κ Bp65 experiments. NF κ Bp65 is known to have a after BcR activation. Alternatively, NF κ Bp50 homodimers that lack a transactivating domain bind to the human *BLK* promoter, as has been shown

in mice.³³ Here, homodimers of NF κ B/p50 were shown to compete with *Pax5* and reduce *Blk* gene expression upon mature B cell activation and development to antibody-producing plasma cells,³³ opposite to what occurs during early B cell differentiation, when *Blk* expression plays an important role.³³ We also do not know the role of IRF4 in this context and a much more detailed analysis of the regulatory landscape of *BLK* is required to understand the correlation between the promoter risk haplotypes and lowered *BLK* gene expression. Also, due to the strong LD within the promoter haplotypes, it has also not been possible to discard the region proximal to the C8orf13 or FAM167A region lying 5' of *BLK*. In this context, the same associated SNPs correlate with increased levels of FAM167A gene expression.¹ The meaning of this is currently unknown and there is no knowledge that this gene would have any role in immunity in general. In this context, we chose not to include the FAM146A gene in our fine mapping, as ours and the actual evidence in other autoimmune diseases support *BLK* as the susceptibility gene in this locus.

We propose that subtle quantitative differences between risk and protective haplotypes occur during mature B cell stimulation leading to lower *BLK* levels, and that epigenetically several sites show a variegated effect of NF κ Bp50 homodimers on the promoter region of *BLK*. Nevertheless, our genetic analysis did show a potentially unique location within the highly associated 1.2 Kb haplotype window where a single binding site for NF κ Bp65 was shown to be particularly strong in the ENCODE data and confirmed here for NF κ Bp50 as well.

In summary, we identified two independent effects within the *BLK* locus one of which covers the promoter region of the gene where the associated haplotype blocks are enriched for transcription factor binding sites for NF κ B and IRF4, providing a potential mechanism for the correlation of the risk alleles and reduced levels of *BLK* expression. We also identified a novel mutation where the SLE-associated 71Thr leads to the reduced half-life of BLK protein.

What effect reduced BLK expression has on the function of human B lymphocytes is at present under investigation.

Contributors AMDV performed all the genetic analyses and wrote the initial draft of the manuscript; MGD and JDW performed the bioinformatic analyses; YYW performed the qPCR-CHIP; BMG did the genotyping for the Ala71Thr; CCL designed the protein degradation experiments on the Ala71Thr and the RFLP; MBQ performed the degradation experiments; JF, LT, EdR, MFGE, BAPE, SD'A, GDS, TW, BRL, EE, LK, CV, BMdaS and JM provided samples; MEAR directed the work; MEAR, ADG and CCL wrote the manuscript. AMDV, MEAR, CCL and MGD contributed equally to this work.

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