Study of the common genetic background for rheumatoid arthritis and systemic lupus erythematosus

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ABSTRACT

Background Evidence is beginning to emerge that there may be susceptibility loci for rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE) that are common to both diseases.

Objective To investigate single nucleotide polymorphisms that have been reported to be associated with SLE in a UK cohort of patients with RA and controls.

Methods 3962 patients with RA and 9275 controls were included in the study. Eleven SNPs mapping to confirmed SLE loci were investigated. These mapped to the TNFSF4, BANK1, TNIPO1, PTTG1, UHRF1BP1, ATG5, JAZF1, BLK, KIAA1542, ITGAM and UBE2L3 loci. Genotype frequencies were compared between patients with RA and controls using the trend test.

Results The SNPs mapping to the BLK and UBE2L3 loci showed significant evidence for association with RA. Two other SNPs, mapping to ATG5 and KIAA1542, showed nominal evidence for association with RA (p=0.02 and p=0.02, respectively) but these were not significant after applying a Bonferroni correction. Additionally, a significant global enrichment in carriage of SLE alleles in patients with RA compared with controls (p=9.1×10−7) was found. Meta-analysis of this and previous studies confirmed the association of the BLK and UBE2L3 gene with RA at genome-wide significance levels (p=5×10−8). Together, the authors estimate that the SLE and RA overlapping loci, excluding HLA-DRBI alleles, identified so far explain −5.8% of the genetic susceptibility to RA as a whole.

Conclusion The findings confirm the association of the BLK and UBE2L3 loci with RA, thus adding to the list of loci showing overlap between RA and SLE.

INTRODUCTION

Rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE) are both autoimmune rheumatological diseases thought to have a substantial genetic contribution to susceptibility.1,2 Recent genome-wide association studies (GWAS) in both diseases have disclosed a number of genetic loci that are commonly associated. Examples include the human leucocyte antigen (HLA) locus, the R620W (rs2476601) polymorphism within the PTPN22 gene and association with the chromosome 6q23/NTFAIP3 locus.3,4 The high degree of familial aggregation that has been shown for RA and SLE further supports the presence of common genetic risk factors for both diseases.5,6

Recent GWAS in SLE have identified a number of novel associations, some of which have not been previously investigated in RA.4,7–10 We have reported previously on the overlap between type 1 diabetes and RA susceptibility loci and there are now numerous examples of overlap between diverse autoimmune diseases.11–14 We, therefore, hypothesised that the underlying autoimmunity of SLE and RA may be underpinned by additional overlap in the genetic susceptibility loci. The aim of this work was to investigate whether single nucleotide polymorphism (SNP) markers that had been reported to be associated with SLE were also associated with RA in a UK population of patients with RA and controls.

METHODS

Samples

Three thousand nine hundred and sixty-two patients with RA and 9275 controls were included in the study. The patients with RA were recruited as described previously15 and all satisfied the 1987 American College of Rheumatology criteria for RA modified for genetic studies.16,17 The clinical characteristics of the cohort have been described previously18–20 and proxy SNPs investigation from a recent large-scale replication study of SLE-associated loci,10 and proxy SNPs were included where assays could not be designed for the original SNP tested.

Of the 21 SLE loci identified to date, we have previously reported association with PTPN22, STAT4 and the 6q23/NTFAIP3 locus.18–20 The association of HLA-DRB1 alleles with RA has been extensively studied in the past. Different SNP’s mapping to the FCGR2A gene (rs12746613; r²=0.19 with the SLE SNP rs1801274) and PRDM1 (rs548234, r²=0.07 with the SLE SNP rs2245214) have been reported to be associated with RA in meta-analysis including the samples tested in the current cohort.21 SNPs mapping to the remaining 15 loci were selected for investigation. However, four SNPs mapping to IRF5, IRAK1, PXK and IL10 either failed assay
design or failed genotyping, resulting in 11 SNP markers being available for analysis (rs10489265 in TNFSF4, rs10516487 in BANK1, rs10036748 in TNIP1, rs2431697 in PTTG1, rs11755393 in UHRF1BP1, rs5658431 in ATG5, rs8644745 in JAZF1, rs2736340 in BLK, rs4963128 in KIAA1542, rs9888739 in ITGAM and rs5754217 in UBE2L3).

Genotyping was undertaken using a Sequenom platform with iPLEX chemistry according to manufacturer's instructions (http://www.sequenom.com). Quality control analysis was undertaken such that only SNPs and samples that passed a 90% quality control threshold were subject to further statistical analysis. Control allele frequencies were tested to ensure that they conformed to Hardy–Weinberg expectations, and SNPs that deviated significantly from this were removed from further analysis.

Analysis

First, genotype frequencies were compared between RA cases and controls using the χ² trend test implemented in PLINK software23 to determine whether individual SLE susceptibility loci were also associated with RA. Where data were available for SLE variants in independent RA samples, data from this study were added to the data already available and reanalysed to determine the best estimate of the effect size. p Values <0.0045 were regarded as significant after correcting for multiple testing (11 tests) applying the Bonferroni correction.

Second, pathway analysis was carried out using Ingenuity Pathway Analysis 8.6 (Ingenuity Systems, http://www.ingenuity.com) in order to explore whether SNPs uniquely associated with either RA or SLE identified characteristic pathways. Bioinformatic analysis, using the Ingenuity Pathways Analysis library, identified the pathways that were most supported by the dataset. Molecules from the dataset that were associated with a canonical pathway in Ingenuity’s knowledge base were considered for the analysis. Fisher’s exact test was used to calculate a p value determining the probability that the association between the genes in the dataset and the canonical pathway is explained by chance alone.

Third, analysis of carriage of SLE alleles in patients with RA was carried out using STATA version 9.2 to determine if there is an overall enrichment of SLE susceptibility variants in RA cases. A SLE loci carriage score was calculated by summing the number of SLE risk (coded as 1) and protection (coded as −1) alleles carried by each individual, and differences in the mean score between RA cases and controls was tested using the Wilcoxon rank-sum test.

Finally, in order to explore how much of the genetic susceptibility to RA could be accounted for by variants identified to date, the sibling recurrence risk ratio (λs) was calculated using the formula:

\[
\lambda_s = \frac{1 + pq(\gamma - 1)^2}{2(p + q\gamma)}
\]

where q is the risk allele frequency, p=1−q and γ is the genotype relative risk under the additive model.

RESULTS

For the BANK1, JAZF1 and BLK SNPs, data were available from a previous GWAS in a UK population including 2000 RA cases and 3000 controls.24 In addition, part of the cohort used in our study had been previously genotyped for UBE2L3.24 Therefore, non-overlapping samples from these studies were added to the current cohort for the analysis of the three markers. Control allele frequencies for all SNPs tested conformed to Hardy–Weinberg expectations (table 1). Four SNPs, rs6568431 mapping to the ATG5 locus, rs2736340 close to BLK, rs4963128 mapping to the KIAA1542 locus and rs5754217 in UBE2L3 showed nominal evidence for association (p<0.05).

After applying a Bonferroni correction for the number of SNPs tested, only the SNPs mapping to BLK and UBE2L3 retained statistically significant evidence for association. It should be noted that control allele frequencies were similar and the direction of association was the same at all four loci with that observed in the SLE studies, although effect sizes were smaller. Therefore, although non-significant after applying a Bonferroni correction, ATG5 and KIAA1542 remain interesting candidates for further investigation. Repeating the association analysis in the anti-CCP positive and negative subgroups of RA cases did not substantially alter the observed effect sizes (data not shown). A test of heterogeneity of odds ratios (ORs) showed that effect sizes were similar among all RA, anti-CCP positive RA and anti-CCP negative RA subgroups for all analysed SNPs (p>0.05).

A meta-analysis including our UK cohort and the US cohort in which association of BLK with RA was described for the first time showed a strong association between the rs2736340 SNP in the BLK locus and RA (p=5.6×10−11, OR=1.14 95% CI 1.10 to 1.19). We also performed a pooled analysis for UBE2L3, expanding the validation cohort from the meta-analysis of Stahl et al24 with the UK non-overlapping samples genotyped in our study.

Table 1 Association results for SLE risk variants genotyped in UK RA cases and controls

| Chr | Locus | SNP         | Major allele/ minor allele | MAF cases | MAF controls | HWE controls | Trend test p value | Corrected p value | Allelic OR (95% CI) |
|-----|-------|-------------|-----------------------------|-----------|--------------|--------------|-------------------|-------------------|--------------------|
| 1   | TNFSF4| rs10489265  | T/G                         | 0.25      | 0.24         | 0.56         | 0.11              | 1.05 (0.99 to 1.12) |
| 4   | BANK1 | rs10516487  | C/T                         | 0.31      | 0.31         | 0.66         | 0.52              | 0.98 (0.93 to 1.04) |
| 5   | TNIP1 | rs10036748  | C/T                         | 0.24      | 0.24         | 0.21         | 0.46              | 1.02 (0.96 to 1.09) |
| 5   | PTTG1 | rs2431697   | T/C                         | 0.42      | 0.42         | 0.62         | 0.06              | 0.95 (0.90 to 1.00) |
| 6   | UHRF1BP1| rs11755393 | A/G                         | 0.34      | 0.34         | 0.79         | 0.41              | 1.01 (0.95 to 1.07) |
| 7   | ATG5  | rs5658431   | C/A                         | 0.41      | 0.39         | 0.27         | 0.02              | 0.17 (0.10 to 1.13) |
| 7   | JAZF1 | rs8644745   | G/A                         | 0.49      | 0.49         | 0.98         | 0.20              | 1.03 (0.98 to 1.08) |
| 8    | BLK   | rs2736340   | C/T                         | 0.26      | 0.26         | 0.95         | 3.0×10⁴           | 5.0×10⁻³         | 1.11 (1.05 to 1.17) |
| 11   | KIAA1542| rs4963128  | G/A                         | 0.32      | 0.34         | 0.96         | 0.02              | 0.22              | 0.93 (0.88 to 0.99) |
| 16   | ITGAM | rs9888739   | C/T                         | 0.10      | 0.11         | 0.42         | 0.16              | 0.94 (0.85 to 1.03) |
| 22   | UBE2L3| rs5754217   | G/T                         | 0.21      | 0.19         | 0.37         | 2.4×10⁻³          | 0.026             | 1.11 (1.04 to 1.19) |

Linkage disequilibrium between the genotyped and reported variant (in brackets), when different: TNFSF4 (rs22059650): r²=0.95; TNIP1 (rs7708392): r²=0.90; PTTG1 (rs2431099); r²=0.60; JAZF1 (rs8491421): r²=1; ITGAM (rs11860650); r²=0.92.

Chr, chromosome; CI, confidence interval; HWE, Hardy–Weinberg equilibrium; MAF, minor allele frequency; OR, odds ratio; RA, rheumatoid arthritis; SLE, systemic lupus erythematosus; SNP, single nucleotide polymorphism.

Extended report

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and including data from GWAS. In this expanded analysis, the rs5754217 at the UBE2L3 locus now reaches genome-wide significance (p=2.8×10⁻¹⁰, OR=1.14 95% CI 1.09 to 1.19).

We next performed a pathway analysis including the loci that have shown evidence of association with both SLE and RA (HLA-DRB1, PTPN22, STAT4, TNFAIP3, FCGR2A, PRDM1, IRF5, PXK, BLK and UBE2L2). All the over-represented pathways are involved in the immune response, such as dendritic cell maturation, T helper (Th) cell differentiation or CTLA4 signalling in cytotoxic T lymphocytes (table 2). As is the case in the over-represented loci, genes exclusively associated with RA (AFF3, ANKRD55/IL6ST, C5orf13, CCL21, CCR6, CD2/CD58, CD28, CD40, CTLA4, IL2/IL21, IL2RA, IL2RB, KIF5A, PRKCQ, PTPRC, RBPJ, REL, SPRED2, TACAP, TRAF1/C5 and TRAF6) are part of immune response pathways, with pathways related to Th cell activation being most over-represented. However, when analysing genes associated only with SLE (ATG5, BANK1, ITGAM, JAZF1, PHRF1, PTGCI, TNFSF4, TNIP1 and UHRF1BP1), a different pattern emerged. Four significantly over-represented pathways were identified but each included only one gene and only one of them was immune response related (table 2).

The number of SLE-associated SNPs showing at least nominal evidence for association with RA was higher than would be expected by chance alone. We explored, therefore, the extent of the total burden of SLE susceptibility alleles in RA. For this analysis we included previously generated genotype data for the markers: rs7574865 in STAT4, rs2476601 in PTPN22 and rs5029937 in TNFAIP3; and from this study: rs10489265 in TNFSF4, rs10516487 in BANK1, rs10036748 in TNIP1, rs2431697 in PTGCI, rs11755395 in UHRF1BP1, rs6568431 in ATG5, rs864745 in JAZF1, rs2756340 in BLK, rs4963128 in KIAA1542, rs9888739 in ITGAM and rs5754217 in UBE2L3. We found that the mean number of SLE risk alleles carried by patients with RA was significantly higher than that found in controls (2.9 vs 2.5, p=9.1×10⁻⁷).

Finally, we calculated the sibling recurrence risk ratio (λs) for the confirmed RA and SLE overlapping loci (PTPN22, STAT4, TNFAIP3, FCGR2A, PRDM1, IRF5, PXK, BLK and UBE2L2). We estimate that, after excluding HLA-DRB1 alleles, these explain 5.8% of the genetic susceptibility to RA as a whole, while all the non-HLA confirmed RA loci identified to date are able to explain 10.7%.

**DISCUSSION**

The findings confirm the association of the BLK and UBE2L3 loci with RA thus adding to the list of loci showing overlap between RA and SLE, which currently include HLA-DRB1, PTPN22, STAT4, TNFAIP3, FCGR2A, PRDM1, IRF5 and PXK. In addition, two loci, ATG5 and KIAA1542, showed nominal association with RA and the associated allele was the same that was previously reported for SLE, although the associations did not remain statistically significant after Bonferroni correction was applied. However, the effect sizes conferred by BLK, ATG5 and KIAA1542 were significantly higher for SLE than for RA (test of heterogeneity of ORs p values=1×10⁻⁶, 3×10⁻³ and 4×10⁻³, respectively).

The finding of an association with BLK confirms a study in a US population where this locus was also associated with RA. Interestingly, the BLK locus has also shown association with RA in a Japanese population. BLK encodes a tyrosine kinase that is involved in the regulation of B-cell activation. B cells have a key role in the pathogenesis of both RA and SLE through the production of autoantibodies, antigen presentation to T cells, and cytokine production, and B-cell depletion has proved successful in the treatment of these diseases. UBE2L3 encodes an ubiquitin-conjugating enzyme involved in the regulation of interferon and TLR7/9 signalling pathways. Furthermore, this locus has been shown to be associated with coeliac disease. Therefore, BLK and UBE2L3 are promising candidate genes for both RA and SLE.

The lack of association in our population between RA markers mapping to ITGAM and BANK1 is in accordance with a previous study in a Spanish population. However, the Spanish study failed to detect association with BLK, probably owing to lack of power to detect modest effect sizes. In this regard, our study had >95% power to detect an association with similar effect sizes as those previously reported for SLE at the 5% significance level for all the loci tested.

All the shared SLE-RA loci and RA-only loci are involved in important pathways for autoimmunity and inflammation. On the other hand, the burden of immune pathways seems to be lower for genes associated with SLE only. However, pathway analysis results should be considered with caution since, for most of the disease-associated loci, the true causal variant and therefore the gene responsible for the association has not yet been identified. In addition, the exact role of several associated genes has not been elucidated and our knowledge of the relationships between molecules is limited.

The degree of genetic overlap between RA and SLE is substantial, but it is difficult to assess and likely to be an underestimate, based on several factors. First, we have only analysed associated loci at genome-wide significance levels; however, additional SLE loci not yet satisfying this criterion have been identified and there are probably more to be discovered. Second, large sample sizes were included in the studies undertaken in SLE leading to the identification of variants with small effects, for which studies in RA may be underpowered to detect. Third, as only the SNP identified in the primary study is tested in the other diseases, it may be that a different variant in the same gene/region is responsible for risk in the second disease.

There are already examples of loci common to two or more autoimmune diseases for which the associated SNP and/or allele is not the same in each disease. For example, the SNPs at TNFAIP3 region, associated with RA, SLE, type 1 diabetes, are different from those associated with coeliac disease and psoriasis. Another example is the R620W variant of the PTPN22 gene, which has been widely associated with many autoimmune diseases but not psoriasis, for which evidence of association of two different PTPN22 SNPs (rs1217414 and rs3789604) has been found and this has been independently replicated. In addition, with regard to the JAZF1 locus, the variant associated with prostate cancer differs from that associated with SLE, type 2 diabetes and height variation. For these reasons, the actual overlap between the two diseases may be higher than estimated in this study.

A high degree of overlap between SLE and RA susceptibility loci might be expected as the two diseases show some clinical overlap in joint involvement, autoantibody production, systemic features and response to treatments such as B-cell depletion (rituximab). Indeed, there was a proposal put forward for an overlap syndrome of ‘rhupus’ as some patients develop features of both diseases. For example, the frequency of anti-nuclear antibody, the hallmark of SLE, is higher in patients with RA than the general population. Unfortunately, antinuclear...
Extended report

Table 2  Over-represented (p<0.05) canonical pathways in which RA and SLE overlapping loci, RA only loci and SLE only loci are involved

| Canonical pathway | Type of pathway | p Value | Genes in pathway |
|-------------------|-----------------|---------|------------------|
| **SLE/RA overlap** |                 |         |                  |
| Dendritic cell maturation | Cellular immune response, cytokine signalling, pathogen-influenced signalling | 1.4×10^{-4} | STAT4, FCGR2A, HLA-DRB1 |
| T helper cell differentiation | Cellular immune response, cytokine signalling | 9.8×10^{-4} | STAT4, HLA-DRB1 |
| CTLA4 signalling in cytotoxic T lymphocytes | Cellular immune response | 5.2×10^{-5} | IL21, IL6ST, CD28, CD40, IL2RA |
| Role of NFAT in regulation of the immune response | Cellular immune response, humoral immune response, intracellular and second messenger signalling | 1.3×10^{-4} | TRAF6, CD28, PRKCD, CTLA4 |
| TNFR2 signalling | Apoptosis, cytokine signalling | 0.02 | TNFAIP3 |
| B-cell development | Cellular growth, proliferation and development, humoral immune response | 0.02 | HLA-DRB1 |
| Antigen presentation pathway | Cellular immune response, humoral immune response | 0.03 | HLA-DRB1 |
| Allograft rejection signalling | Cellular immune response, disease specific pathway | 0.03 | HLA-DRB1 |
| Autoimmune thyroid disease signalling | Cellular immune response, disease specific pathway, humoral immune response | 0.03 | HLA-DRB1 |
| Graft-versus-host disease signalling | Cellular immune response, disease specific pathway | 0.03 | HLA-DRB1 |
| TNFR1 signalling | Apoptosis, cytokine signalling | 0.03 | TNFAIP3 |
| Nur77 signalling in T lymphocytes | Apoptosis, cellular immune response, Nuclear receptor signalling | 0.04 | HLA-DRB1 |
| Calcium-induced T lymphocyte apoptosis | Apoptosis, cellular immune response | 0.04 | HLA-DRB1 |
| CD40 signalling | Cellular immune response, humoral immune response | 0.04 | TNFAIP3 |
| IL-10 signalling | Cellular immune response, cytokine signalling | 0.04 | FCGR2A |
| JAK/Stat signalling | Apoptosis, cellular growth, proliferation and development, intracellular and second messenger signalling | 9.3×10^{-4} | CD28, CD40, IL2RB |
| **RA only** |                 |         |                  |
| iCOS-iCOSL signalling in T helper cells | Cellular immune response | 9.8×10^{-4} | PTPRC, CD28, PRKCD, CD40, IL2RA, IL2RB |
| T helper cell differentiation | Cellular immune response, cytokine signalling | 5.2×10^{-4} | IL21, IL6ST, CD28, CD40, IL2RA |
| Altered T-cell and B-cell signalling in RA | Cellular immune response, disease-specific pathways | 6.6×10^{-4} | IL21, CD28, CD40, CCL21 |
| T-cell receptor signalling | Cellular immune response, disease-specific pathways | 1.3×10^{-4} | TRAF6, CD28, PRKCD, CTLA4 |
| IL-12 signalling and production in macrophages | Cellular immune response, cytokine signalling | 2.0×10^{-4} | TRAF6, PRKCD, CD40, REL |
| CD28 signalling in T helper cells | Cellular immune response | 2.7×10^{-4} | PTPRC, CD28, PRKCD, CTLA4 |
| CD40 signalling | Cellular immune response, humoral immune response | 1.0×10^{-4} | TRAF6, CD40, TRAF1 |
| Cross-talk between dendritic cells and natural killer cells | Cellular immune response | 3.7×10^{-4} | CD28, CD40, IL2RB |
| **B cell development** |                 |         |                  |
| Systemic lupus erythematosus signalling | Disease-specific pathways | 1.0×10^{-3} | PTPRC, CD28, CD40 |
| Role of macrophages, fibroblasts and endothelial cells in rheumatoid arthritis | Disease-specific pathways | 1.2×10^{-3} | TRAF6, IL6ST, PRKCD, TRAF1 |
| NF- B signalling | Cellular immune response, cytokine signalling, humoral immune response, organinal growth and development | 1.3×10^{-3} | TRAF6, PRKCD, CD40 |
| April -mediated signalling | Apoptosis | 1.5×10^{-3} | TRAF6, TRAF1 |
| Dendritic cell maturation | Cellular immune response, cytokine signalling, pathogen-influenced signalling | 1.6×10^{-3} | TRAF6, CD40, CD58 |
| B-cell activating factor signalling | Cellular growth, proliferation and development, humoral immune response | 1.7×10^{-3} | TRAF6, TRAF1 |
| Allograft rejection signalling | Cellular immune response, disease-specific pathways | 1.8×10^{-3} | CD28, CD40 |
| Autoimmune thyroid disease signalling | Cellular immune response, disease-specific pathways, humoral immune response | 1.9×10^{-3} | CD28, CD40 |
| Primary immunodeficiency signalling | Cellular immune response, disease-specific pathways, humoral immune response | 2.3×10^{-3} | PTPRC, CD40 |
| IL-2 signalling | Cellular immune response, cytokine signalling | 3.1×10^{-3} | IL2RA, IL2RB |
| Lymphotoxin receptor signalling | Apoptosis | 3.2×10^{-3} | TRAF6, TRAF1 |
| Activation of IRF by cytosolic pattern recognition receptors | Cellular immune response | 4.1×10^{-3} | TRAF6, CD40 |
| Small cell lung cancer signalling | Cancer, disease-specific pathways | 5.5×10^{-3} | TRAF6, TRAF1 |
| Communication between innate and adaptive immune cells | Cellular immune response | 5.8×10^{-3} | CD28, CD40 |
| **IL-6 signalling** |                 |         |                  |
| CTLA4 signalling in cytotoxic T lymphocytes | Cellular immune response, cytokine signalling | 8.1×10^{-3} | TRAF6, IL6ST |
| Type I diabetes mellitus signalling | Apoptosis, disease-specific pathways, | 0.01 | TRAF6, CD28 |
| PKC signalling in T lymphocytes | Cellular immune response | 0.01 | CD28, PRKCD |
| Hepatic fibrosis/hepatic stellate cell activation | Disease-specific pathways | 0.02 | CD40, CCL21 |
| Hepatic cholestasis | Disease-specific pathways | 0.02 | TRAF6, PRKCD |
| B cell receptor signalling | Humoral immune response | 0.02 | TRAF6, PRKCD |
| IL-6 signalling | Cellular immune response, cytokine signalling | 0.03 | TRAF6, IL6ST |
| Acute phase response signalling | Cytokine signalling | 0.03 | TRAF6, PRKCD |
| Role of NFAT in regulation of the immune response | Cellular immune response, humoral immune response, intracellular and second messenger signalling | 0.03 | CD28, PRKCD |
| Role of NFAT in cardiac hypertrophy | Cardiovascular signalling, disease-specific pathways | 0.03 | IL6ST, PRKCD |

Continued

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Table 2 Continued

| Canonical pathway | Type of pathway | p Value | Genes in pathway |
|-------------------|-----------------|---------|------------------|
| TNFR2 signalling  | Apoptosis, cytokine signalling | 0.04 | Traf1 |
| 4-1BB signalling in T lymphocytes | Cellular immune response | 0.04 | Traf1 |
| SLE only          | Mitotic roles of polo-like kinase | 0.035 | Pttg1 |
|                   | Angiopoietin signalling | 0.041 | Tnip1 |
|                   | Ubiquinone biosynthesis | 0.045 | Uhf1bp1 |
|                   | Caveolar-mediated endocytosis signalling | 0.046 | Itgam |

NFAT, nuclear factor of activated T cells; RA, rheumatoid arthritis; SLE, systemic lupus erythematosus.

antibody data were not available for the RA samples tested here so we were not able to explore whether the associations seen were greater in the antinuclear antibody-positive subgroup.

In conclusion, this study has shown that a high degree of overlap exists between RA and SLE and raises the possibility that shared phenotypic characteristics may be a result of shared genetic susceptibility loci implicated in overlapping inflammatory pathways.

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