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Published in:
PLoS ONE

DOI:
10.1371/journal.pone.0084450

2013

Citation for published version (APA):
Association of \textit{STAT4} Polymorphism with Severe Renal Insufficiency in Lupus Nephritis

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Abstract
Lupus nephritis is a cause of significant morbidity in systemic lupus erythematosus (SLE) and its genetic background has not been completely clarified. The aim of this investigation was to analyze single nucleotide polymorphisms (SNPs) for association with lupus nephritis, its severe form proliferative nephritis and renal outcome, in two Swedish cohorts. Cohort I (n = 567 SLE cases, n = 512 controls) was previously genotyped for 5676 SNPs and cohort II (n = 145 SLE cases, n = 619 controls) was genotyped for SNPs in \textit{STAT4}, \textit{IRF5}, \textit{TNIP1} and \textit{BLK}. Case-control and case-only association analyses for patients with lupus nephritis, proliferative nephritis, and severe renal insufficiency were performed. In the case-control analysis of cohort I, four highly linked SNPs in \textit{STAT4} were associated with lupus nephritis with genome wide significance with p = 3.7 x 10\textsuperscript{-10}, OR 2.20 for the best SNP rs11889341. Strong signals of association between \textit{IRF5} and an HLA-DR3 SNP marker were also detected in the lupus nephritis case versus healthy control analysis (p < 0.0001). An additional six genes showed an association with lupus nephritis with p < 0.001 (\textit{TNIP1}, CARD11, \textit{ITGAM}, BLK and IRAK1). In the case-only meta-analysis of the two cohorts, the \textit{STAT4} SNP rs7582994 was associated with severe renal insufficiency with p = 1.6 x 10\textsuperscript{-3} and OR 2.22. We conclude that genetic variations in \textit{STAT4} predispose to lupus nephritis and a worse outcome with severe renal insufficiency.


Editor: Florian Kronenberg, Innsbruck Medical University, Austria

Received April 11, 2013; Accepted November 15, 2013; Published December 27, 2013

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Funding: This study was supported by the Swedish Research Council for Medicine, the Knut and Alice Wallenberg Foundation, the Swedish Rheumatism Foundation, the King Gustav V 80-year Foundation, the Ragnar Söderberg Foundation, Combin, the County Council of Östergötland, Swedish Society for Medical Research, the Ingrid Asp Research Foundation, The Swedish Heart-Lung Foundation, Stockholm County Council and Karolinska Institutet (ALF), The Foundation in memory of Clas Groschinsky and the Swedish Society of Medicine. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

Introduction
Lupus nephritis (LN) constitutes one of the main clinical challenges in patients with systemic lupus erythematosus (SLE) and is a cause of significant morbidity and mortality. LN occurs in 15–55\% of patients with SLE with the higher incidence in Asian and African populations [1]. Proliferative glomerulonephritis, classes III/IV, is considered to be the most severe form of nephritis and requires aggressive immunosuppressive treatment [2]. Despite improved treatment regimens, approximately 10\% of all LN patients develop end-stage renal disease (ESRD) [1]. Several non-HLA susceptibility genes for SLE have been identified through candidate gene and genome wide association studies (GWAS). Among these, polymorphisms in signal transducer and activator of transcription 4 (\textit{STAT4}), interferon regulatory factor 5 (\textit{IRF5}), the family with sequence similarity 167 member A-B lymphoid tyrosine kinase (\textit{FAM167A-BLK}) locus, TNFAIP3 interacting protein 1 (\textit{TNIP1}) and integrin-\textit{\alpha}4-integrin-\textit{\alpha}C (\textit{ITGAM-ITGAX}) display high signals of association that have been convincingly replicated [3-6].

The genetic background of LN has been less well elucidated and there are hitherto no GWAS published in LN [7]. Studies in Caucasian populations have demonstrated associations between LN and several gene polymorphisms including \textit{STAT4}, \textit{ITGAM}, \textit{TNIP1}, \textit{FAM167A-BLK}, programmed cell death 1 (\textit{PDCD1}), tumour necrosis factor alpha-induced protein 3 (\textit{TNFAIP3}), tumour necrosis factor superfamily 4 (\textit{TNFSF4}), apolipoprotein H (\textit{APOH}, encoding beta-2-glycoprotein 1), interleukin-6 (\textit{IL-6}), monocyte chemoattractant protein 1 (\textit{MCP-1}), Fc\gamma receptor (\textit{FcyR}), XK, Kell blood group complex subunit-related family member 6 (\textit{XKR6}) and C-reactive protein (\textit{CRP}) genes, though with inconsistent results [8–19]. Few studies have addressed the potential association between susceptibility genes, type of LN and renal outcome. Taylor and co-workers found an association between the single nucleotide polymorphism (SNP) rs7574865 in \textit{STAT4} and severe nephritis, defined as histopathologic evidence of severe, progressive disease or ESRD [18]. An association between proliferative nephritis and SNPs in \textit{FcyR3A} and \textit{CRP} has also been demonstrated [10].
The aim of this study was to further elucidate the genetic component in LN using data on more than 5000 SNPs generated in our previous study on SLE [6]. In addition, the association between LN susceptibility genes and proliferative nephritis as well as the development of severe renal insufficiency was investigated.

Materials and Methods

Patients and controls

Cohort I consisted of 567 Swedish Caucasian patients with SLE and 512 controls. The patients originate from the rheumatology clinics in the Uppsala (n = 143) and Lund (n = 155) University Hospitals and the Karolinska University Hospital, Stockholm (n = 269), Sweden. The controls were individually matched for age, gender and area of residence and consisted of healthy blood donors from Uppsala (n = 132) and Lund (n = 91) while the controls from Stockholm (n = 289) were samples from the population-based Epidemiological Investigation of Rheumatoid Arthritis (EIRA) cohort [20]. Cohort II consisted of 145 Swedish SLE patients of Caucasian origin from Linköping University Hospital, and 619 healthy Swedish blood donor controls. Five hundred and fifty two cases and 499 controls in cohort I and 144 cases and all controls in cohort II were previously described in a study by Wang et al [19]. All patients fulfilled the 1982 ACR criteria for SLE [21]. Clinical data was extracted from the patient files.

Definition of lupus nephritis

Occurrence of LN was defined according to the ACR criteria and onset of nephritis was defined as the year of fulfilling ACR nephritis criteria. Renal biopsies were performed in 159 patients in cohort I, for which 152 histopathology results were available. In cohort II, 26 patients were subjects to renal biopsies, all with available histopathology results. LN according to the WHO classification system was verified in 160 patients (134 in cohort I and 26 in cohort II) [2], while in cohort I, 18 biopsies showed vascular changes including thrombotic microangiopathy (data not shown). Patients having WHO class III or IV at any time were defined as the proliferative nephritis group (Table 1).

Renal insufficiency outcome

The follow-up time from nephritis onset was until December 31° 2009 (median 14 years, range 0–46). The glomerular filtration rate (GFR) was calculated at follow up with the Modification of Diet in Renal Disease (MDRD) formula. Renal function was assessed in LN patients in both cohorts were significantly more often men, younger at disease onset and fulfilled more ACR criteria compared with the SLE patients without nephritis (Table 1). There was no difference in disease duration between patients with or without LN in cohort I whereas in cohort II, patients with LN had significantly longer disease duration compared with SLE patients without nephritis. The renal biopsies showed a proliferative nephritis in 92/152 (60.1%) in cohort I and 20/26 (76.9%) in cohort II [2]. A total of 31 patients, 28 (14.7%) in cohort I and 3 (8.6%) in cohort II had developed severe renal insufficiency at follow up (Table 1). In both cohorts, patients with severe renal insufficiency had a significantly longer disease duration compared with SLE patients without nephritis; in cohort I 28.0±11.0 versus 20.7±11.5 years (p = 7.6×10⁻⁴), and in cohort II 27.3±7.7 versus 13.7±10.3 years, (p = 0.03) (data not shown).

Proliferative nephritis was the most frequent cause of developing severe renal insufficiency. Out of the 31 patients with severe renal insufficiency at follow up, 24 had undergone a previous renal biopsy where 12 (50%) of the patients had a proliferative nephritis. Conversely, of the 112 patients with proliferative nephritis, outcome data was available for 110. The 12 patients whose outcome was severe renal insufficiency constituted 11% of all patients with proliferative nephritis (data not shown).
<table>
<thead>
<tr>
<th></th>
<th>Cohort I(^a)</th>
<th>Cohort II(^b)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>All SLE patients</td>
<td>SLE with lupus nephritis</td>
</tr>
<tr>
<td>Number of patients (%)</td>
<td>567</td>
<td>195 (34.4)</td>
</tr>
<tr>
<td>Number of females (%)</td>
<td>501 (88.4)</td>
<td>159 (81.5)</td>
</tr>
<tr>
<td>Age at SLE diagnosis, years (mean, sd)</td>
<td>34.4±14.9</td>
<td>30.1±14.6</td>
</tr>
<tr>
<td>Disease duration, years (mean, sd)</td>
<td>21.1±11.6</td>
<td>21.7±10.9</td>
</tr>
<tr>
<td>Age at nephritis onset (mean, sd)</td>
<td>34.0±15.4</td>
<td></td>
</tr>
<tr>
<td>Number of ACR criteria (mean, sd)</td>
<td>5.7±1.4</td>
<td>6.3±1.5</td>
</tr>
<tr>
<td>Number of patients with proliferative nephritis(^d) (%)</td>
<td>92/152 (60.1)</td>
<td></td>
</tr>
<tr>
<td>Number of patients with severe renal insufficiency(^e) (%)</td>
<td>28/190 (14.7)</td>
<td></td>
</tr>
</tbody>
</table>

\(^a\)Uppsala, Stockholm and Lund, Sweden
\(^b\)Linköping, Sweden
\(^c\)Comparison between SLE with lupus nephritis and SLE without lupus nephritis. Frequencies compared with Chi square test and continuous variables with Mann-Whitney U-test.
\(^d\)WHO class III or IV on renal biopsy, according to the 1995 WHO classification system [2]. Biopsy data was not available from all patients.
\(^e\)Glo\(\text{merular filtration rate}<30 \text{ mL/min/1.73 m}^2\) [22].

doi:10.1371/journal.pone.0084450.t001
Case-control association with lupus nephritis

In cohort I, we performed a LN case versus healthy control association analysis. The strongest signals of association were detected for four highly linked SNPs in STAT4; rs11889341, rs7574865, rs7568275 and rs7582694 ($r^2 = 0.98$), with p-values reaching genome wide significance ($p < 5 \times 10^{-8}$) (Figure 1). The most significant SNP in STAT4 was rs11889341 with $p = 3.7 \times 10^{-9}$, odds ratio (OR) 2.20 (95% confidence interval (CI) 1.70–2.84). Strong signals of association with LN were also detected for two nearly perfectly linked SNPs in IRF5, (rs2070197 and rs10488631, $r^2 = 1.0$) and the HLA-DR3 marker SNP rs3155394, all $p < 1 \times 10^{-4}$. In addition, SNPs in the postmeiotic segregation increased 2 (PMS2), TNIP1, caspase recruitment domain family, member 11 (CARD11), ITGAM, BLK and interleukin-1 receptor-associated kinase 1 (IRAK1) genes were associated with LN with p-values $<0.001$ and OR between 1.53 and 2.21 (Table 2, Table S1 and Figure 1). Table 2 lists the best SNP in each of the nine genes that displayed an association with LN with $p < 0.001$ and for STAT4, IRF5, TNIP1 and BLK also the SNPs used for further meta-analysis, see below. A Q-Q plot of the results from the LN versus healthy controls association analysis shows p-values deviating from the expected distribution indicating the presence of true associations (Figure S1).

Case-control association with proliferative nephritis and outcome

The nine genes that had shown an association with LN in cohort I with $p < 0.001$ were further studied. First association analysis of patients with proliferative nephritis (n = 92) versus healthy controls was performed. The STAT4, IRF5 and HLA-DR3 SNP proxy were all found to be associated with proliferative nephritis, with $p < 0.001$, OR between 2.17 and 2.44 (Table 2). Next the association between these genes and the outcome measure severe renal insufficiency was analyzed. Despite the low number of cases, LN patients who had developed severe renal insufficiency (n = 28) displayed signals of association with STAT4 with $p = 7.6 \times 10^{-6}$ and OR 3.61 (95% CI 2.09–6.23) (Table 2). When adjusting for age and gender, the effect measures (OR, 95% CI) were largely unchanged (Table 2) and conditioning on the matched pairs yielded analogous results (data not shown).

Case-only sub-phenotype analysis

Next a case-only association analysis was performed of the 13 SNPs in the nine genes that were associated with LN in cohort I. The risk allele frequencies were compared between patients with or without LN, proliferative nephritis and severe renal insufficiency, respectively. A nominal association was found with LN for SNPs in the PMS2 and TNIP1 genes ($p < 0.05$) while there were no associations with proliferative nephritis. Signals of association between STAT4 and the development of severe renal insufficiency were detected, with a p-value of 0.02, OR 1.91 (95% CI 1.11–3.28) for SNP rs11889341 (Table S2). However, correcting for the nine loci analysed, none of the associations remained significant. There was 64% power to detect an association between the STAT4 risk allele rs11889341 and severe renal insufficiency (Table S3).

Meta-analysis

To evaluate the robustness of our findings we used data from 145 patients with SLE from an additional Swedish cohort (cohort II) where detailed renal data were available (Table 1) and 619 healthy Swedish controls. The STAT4, IRF5, TNIP1 and BLK genes had been genotyped in cohort II. The SNPs genotyped in both cohort I and II, used for meta-analysis, were STAT4 rs7582694 ($r^2 = 0.98$ with rs11889341), IRF5 rs10488631 ($r^2 = 1.00$ with rs2070197), TNIP1 rs7708392 ($r^2 = 1.00$ with rs6889239) and BLK rs13277113 ($r^2 = 0.87$ with rs922483) (Table 2). In the LN case versus healthy controls (n = 1131) meta-analysis, the SNPs in STAT4 and IRF5 were associated with LN with genome wide significance ($p < 5 \times 10^{-8}$). An association between the STAT4 SNP rs7582694 and severe renal insufficiency...
Table 2. Case-control association analysis in cohort I. The best SNPs in genes associated with lupus nephritis with $p < 0.001$ are shown.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Chr</th>
<th>SNP</th>
<th>n = 195</th>
<th>n = 92</th>
<th>n = 28</th>
<th>n = 567</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>OR (95% CI)</td>
<td>OR (95% CI)</td>
<td>OR (95% CI)</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Padj</td>
<td>adj</td>
<td>Padj</td>
<td>adj</td>
</tr>
<tr>
<td>STAT4</td>
<td>2</td>
<td>rs11889341</td>
<td>3.7 x 10^{-3}</td>
<td>2.20 (1.70–2.84)</td>
<td>1.3 x 10^{-6}</td>
<td>2.10 (1.56–2.84)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>rs7582694</td>
<td>1.5 x 10^{-8}</td>
<td>2.12 (1.64–2.74)</td>
<td>3.2 x 10^{-6}</td>
<td>2.04 (1.51–2.76)</td>
</tr>
<tr>
<td>IRF5</td>
<td>7</td>
<td>rs2070197</td>
<td>1.0 x 10^{-5}</td>
<td>2.00 (1.48–2.71)</td>
<td>1.4 x 10^{-5}</td>
<td>2.14 (1.52–3.01)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>rs10488631</td>
<td>1.1 x 10^{-5}</td>
<td>1.99 (1.47–2.69)</td>
<td>1.6 x 10^{-5}</td>
<td>2.13 (1.51–3.00)</td>
</tr>
<tr>
<td>HLA-</td>
<td>DRA</td>
<td>6</td>
<td>rs135394</td>
<td>1.3 x 10^{-5}</td>
<td>1.95 (1.45–2.62)</td>
<td>4.2 x 10^{-5}</td>
</tr>
<tr>
<td>PMS2</td>
<td>7</td>
<td>rs1860460</td>
<td>1.6 x 10^{-6}</td>
<td>1.67 (1.26–2.17)</td>
<td>3.6 x 10^{-6}</td>
<td>1.79 (1.30–2.46)</td>
</tr>
<tr>
<td>TNP1</td>
<td>5</td>
<td>rs6892339</td>
<td>1.8 x 10^{-4}</td>
<td>1.62 (1.26–2.07)</td>
<td>2.6 x 10^{-4}</td>
<td>1.70 (1.28–2.26)</td>
</tr>
<tr>
<td>CARD1</td>
<td>7</td>
<td>rs7183473</td>
<td>3.0 x 10^{-4}</td>
<td>1.60 (1.25–2.05)</td>
<td>3.7 x 10^{-4}</td>
<td>1.68 (1.26–2.21)</td>
</tr>
<tr>
<td>ITGAM</td>
<td>16</td>
<td>rs1143679</td>
<td>5.9 x 10^{-4}</td>
<td>1.82 (1.30–2.56)</td>
<td>6.7 x 10^{-4}</td>
<td>1.70 (1.16–2.49)</td>
</tr>
<tr>
<td>BLK</td>
<td>8</td>
<td>rs922483</td>
<td>8.3 x 10^{-4}</td>
<td>1.53 (1.19–1.95)</td>
<td>1.9 x 10^{-3}</td>
<td>1.55 (1.18–2.05)</td>
</tr>
<tr>
<td>IRAK1</td>
<td>23</td>
<td>rs1059702</td>
<td>1.7 x 10^{-3}</td>
<td>1.78 (1.28–2.46)</td>
<td>3.0 x 10^{-4}</td>
<td>2.7 (1.23–5.36)</td>
</tr>
</tbody>
</table>

The best SNP in each gene is shown and for STAT4, IRF5, TNP1 and BLK also the SNPs used for meta-analysis, marked in bold; STAT4 rs11889341, rs7582694 $r^2 = 0.98$, IRF5 rs2070197, rs10488631 $r^2 = 1.00$, TNP1 rs7708392, rs6892339 $r^2 = 1.00$ and BLK rs922483, rs1377113 $r^2 = 0.87$ calculated in 512 Swedish controls. OR; odds ratio, CI; confidence interval, NA: not available.

1. Uppsala, Stockholm and Lund, Sweden, $n = 567$ SLE cases, $n = 512$ controls
2. WHO class III or IV on renal biopsy, according to the 1995 WHO classification system [2].
3. Glomerular filtration rate < 30 mL/min/1.73 m² [22].
4. rs3135394 has an $r^2 = 0.87$ with the HLA-DRA (DRB1*0701) allele [6].
5. Unadjusted $p$-value and OR for differences in allele frequencies between patients and controls.
6. Adjusted $p$-value and OR from logistic regression analysis including age and gender as covariates. Number of cases and controls; lupus nephritis, $n = 194$, proliferative nephritis, $n = 91$, severe renal insufficiency, $n = 28$, SLE, $n = 566$, controls, $n = 504$. 

The best SNP in each gene is shown and for STAT4, IRF5, TNP1 and BLK also the SNPs used for meta-analysis, marked in bold; STAT4 rs11889341, rs7582694 $r^2 = 0.98$, IRF5 rs2070197, rs10488631 $r^2 = 1.00$, TNP1 rs7708392, rs6892339 $r^2 = 1.00$ and BLK rs922483, rs1377113 $r^2 = 0.87$ calculated in 512 Swedish controls. OR; odds ratio, CI; confidence interval, NA: not available.

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2. WHO class III or IV on renal biopsy, according to the 1995 WHO classification system [2].
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doi:10.1371/journal.pone.0084450.t002
### Table 3: Case-control meta-analysis of cohort \(^1\) and cohort \(^2\) in a total of 712 SLE cases and 1131 controls.

<table>
<thead>
<tr>
<th>Gene</th>
<th>SNP</th>
<th>P [^{\ast}]</th>
<th>95% CI</th>
<th>OR</th>
<th>P [^{\ast}] adj</th>
<th>95% CI adj</th>
<th>OR adj</th>
<th>95% CI adj</th>
<th>OR adj (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>STAT4</td>
<td>rs7582694</td>
<td>2.4 \times 10^{-7}</td>
<td>1.99</td>
<td>1.59–2.4</td>
<td>1.28</td>
<td>0.13</td>
<td>0.13–1.33</td>
<td>0.13</td>
<td>0.13–1.33</td>
</tr>
<tr>
<td>STAT4</td>
<td>rs7089392</td>
<td>1.2 \times 10^{-8}</td>
<td>1.59</td>
<td>1.24–2.0</td>
<td>1.50</td>
<td>0.01</td>
<td>1.50–2.0</td>
<td>1.50</td>
<td>1.50–2.0</td>
</tr>
<tr>
<td>BLK</td>
<td>rs7568275</td>
<td>1.0 \times 10^{-8}</td>
<td>0.99</td>
<td>1.16–0.83</td>
<td>0.21</td>
<td>0.15</td>
<td>0.15–0.21</td>
<td>0.15</td>
<td>0.15–0.21</td>
</tr>
</tbody>
</table>

### Discussion

Here we demonstrate that polymorphisms in the \textit{STAT4} gene are associated with LN with genome wide significance in a LN case-versus-healthy controls analysis of Swedish SLE patients. Furthermore an association between the \textit{STAT4} SNP rs7582694 and severe renal insufficiency was present in our case-only meta-analysis of two independent SLE cohorts. Although we were not able to detect a significant association with \textit{STAT4} in our case-only analysis of LN versus non-LN SLE patients, possibly due to a lack of power, our results support previous observations that \textit{STAT4} is particularly strongly associated with a more severe SLE phenotype with renal engagement [18]. In the study by Taylor and co-workers [18] an association between the \textit{STAT4} SNP rs7574865, in strong LD (\(r^2>0.99\)) with the SNP rs7582694 here studied, and LN was found in a case-control and case-only analysis. Here we extend the knowledge and present for the first time the association between \textit{STAT4} and the severe form of proliferative nephritis in a case-control analysis. We also demonstrate for the first time in our case-only analysis, an association between \textit{STAT4} and a worse outcome in terms of severe renal insufficiency defined as a GFR <30 mL/min/1.73 m\(^2\) at follow up.

The highly linked SNPs rs11889341, rs7574865, rs7568275 and rs7582694 (\(r^2 = 0.98\)) in \textit{STAT4}, which showed an association with LN in our case-control study, are all located in the large third intron. While there are no common coding \textit{STAT4} SNPs in LD with these intronic SNPs, their possible functional role has been investigated. Allelic expression analysis have observed an overexpression of the \textit{STAT4} risk allele (rs6179673, \(r^2=0.95\) to rs7582694) in human cells of mesenchymal origin but not in transformed B-cells, indicating that these intronic SNPs may regulate gene expression in different tissues [16]. There are several possible mechanisms by which \textit{STAT4} may contribute to the development of LN. The main \textit{STAT4} activating cytokines are interleukin 12 (IL-12) and IL-23 leading to Th1 and Th17 differentiation with IFN-\(\gamma\) and IL-17 production, which are key players in a pro-inflammatory immune response [24]. These

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\[^{1}\] Upplands, Stockholm, Lund, n = 67 cases, n = 512 controls.
\[^{2}\] Linköping, n = 145 cases, n = 619 controls.
\[^{3}\] \(n=31,\) SLE, n = 71, controls, n = 512.
\[^{4}\] \(n=31,\) SLE, n = 71, controls, n = 512.

---

**Table 3.** Case-control meta-analysis of cohort \(^1\) and cohort \(^2\) in a total of 712 SLE cases and 1131 controls.
STAT4 also signals via the type I IFN receptor. SLE patients carrying the STAT4 risk allele rs7574865 have increased sensitivity to IFN-γ signaling, measured as an increased expression of IFN-γ regulated genes [28]. An increased activation of IFN stimulated genes (ISG) will promote the autoimmune process by activating number of cells in the immune system as reviewed by Rönnblom et al. in [29]. One such ISG is TNSF13B that encodes B cell activating factor (BAFF)/B lymphocyte stimulator (BLyS), which promotes B cell differentiation and autoantibody production, including antibodies against double stranded DNA (anti-dsDNA) [30,31]. Several investigators have also detected high signals of association between STAT4 and anti-dsDNA autoantibodies [16,18,32,33]. Consequently, risk-variants of STAT4 via several different effects in the immune system, could promote a progressive autoimmune process in the kidney, which ultimately may lead to renal failure.

Polymorphisms in IRF5 display strong signals of association with LN in populations of different ethnicities [5,34–36]. No particular SLE phenotype has been associated with IRF5 in case-only analyses but an association with the presence of anti-dsDNA antibodies has been demonstrated [32]. A case-control analysis in an Asian population demonstrated an association between LN and IRF5; however, this could represent the strong association with SLE per se [37]. Here we found the association with LN to be of similar strength as the association with SLE. This is in concordance with other studies where IRF5 polymorphisms have been strongly associated with SLE regardless of disease phenotype [33,38].

The TNPI SNP rs7708392 has been associated with LN in case-control studies of Asian and Caucasian populations [19,39]. In our previous case-only analysis of an SLE patient cohort largely overlapping with this study, a nominally significant association with LN was shown, notwithstanding multiple testing correction [19]. In this study we extended the investigation and explored the association with proliferative nephritis and renal outcome. However, no associations with these sub-phenotypes were shown. The FAM167A-BLK locus intergenic SNP rs13277113 was recently associated with LN in a case-only analysis [8] whereas previous studies have failed to find an association between this SNP and LN [3,14]. In this study we did not detect any significant associations with BLK in our case-only analysis of LN, proliferative nephritis or renal outcome.

Cohort I was analysed for association with LN using a large set of SNPs. Interestingly, in the case-control analysis, the HLA-DR3 (DRB1*0301) SNP marker was not as strongly associated with LN as STAT4. While the HLA-DR3 allele confers a 2-3 fold increased risk of LN in Caucasian populations the role of the MHC in LN has been less well elucidated [7,40]. One study found an association between an HLA-DR3 SNP proxy and LN [33] whereas we detected similar minor allele frequencies for the HLA-DR3 (DRB1*0301) SNP proxy in LN, LN sub-phenotypes and all SLE cases (Table 2).

An association between the SNP rs1143679 in ITGAM and LN has previously been demonstrated in both case-control and case-only analyses in patients of European and Asian ancestry with SLE [11,14,41]. Here we replicate the results in the LN case versus control analysis in cohort I. The association between LN or SLE...
and SNPs in the PMS2 and CARD11 genes, both located on chromosome 7, has hitherto not been reported. The PMS2 gene encodes a DNA mismatch repair endonuclease and mutations have been associated with malignancies, in particular colorectal cancer [42]. Mutations in CARD11 have been associated with diffuse large B cell lymphomas [43], the dominating lymphoma subtype in SLE [44]. The polymorphisms detected here in association with LN and SLE are intriguing and warrant further investigations. Finally, we found an association between IRAK1 and LN in our case-control analysis while the case-only analysis displayed an unadjusted p-value of 0.05 for association with LN. Polymorphisms in IRAK1 have previously been associated with SLE but the possible association with LN remains to be established [45].

The strength of this study is the availability of renal biopsies from the majority of patients as well as the longterm follow-up data on renal outcome. Approximately two thirds of our LN patients with available biopsies were diagnosed with a proliferative nephritis, which is linked to a less favourable renal outcome [46]. In this study 11% of the patients with proliferative nephritis had progressed to severe renal failure at follow up. This is in concordance with previous reports where approximately 10% of all patients with LN develop ESRD [1]. Only half of our patients with severe renal insufficiency where a previous biopsy was available had progressed from a proliferative nephritis. We therefore conclude that the two groups proliferative nephritis and severe renal insufficiency are not completely overlapping and that the case-only association between STAT4 and severe renal insufficiency cannot be explained by an association with proliferative nephritis.

Renal biopsies had not been performed in 36/195 (18%) of the LN patients and 7 histopathology results could not be retrieved in cohort I, while in cohort II 9/35 (26%) of the LN patients had not undergone a biopsy. There are various reasons for not performing a renal biopsy, including a bleeding diathesis, uncontrolled hypertension, patients’ or physicians’ choice or for practical reasons. It is also possible that patients presenting with a clinically milder nephritis are less likely to undergo a biopsy. LN patients without biopsies were excluded from the case-only analysis of proliferative nephritis versus non-proliferative nephritis and the results presented are based on available data. However, the lack of complete biopsy data from all our LN patients has decreased the power to detect genetic associations with the sub-group proliferative nephritis.

A further weakness of our study is the low power to detect significant differences in the LN or renal outcome case-only analyses. The power to detect a possible association between STAT4 and LN in our case-only analysis of cohort I was only 22% and for TNIP1 62% (Table S2). We had 62% power to detect an association between the STAT4 risk allele rs7582694 and severe renal insufficiency in our case-only analysis of cohort I. However, the addition of cohort II increased the strength of the association between STAT4 and severe renal insufficiency. Unfortunately, detailed clinical data on renal biopsies and outcome is not readily available from all centres, which has limited the inclusion of additional cohorts in this study.

One can hypothesize that there is a genetic contribution to the type of nephritis an individual will develop as well as to outcome, as here demonstrated. Males with SLE are more likely to develop LN. We found no differences in genotypes between the genders and correcting the case-control analyses for age and gender did not affect the OR for association. We therefore conclude that in the case-control analyses, the genetic associations here presented are with LN, proliferative nephritis and severe renal insufficiency per se, regardless of age and gender. LN patients with severe renal insufficiency have a longer disease duration compared with patients without such adverse outcome. We found no differences in disease duration between the genotypes for STAT4, IRF5, TNIP1 and BLK. While adjusting for disease duration and gender, the association between STAT4 and severe renal insufficiency did not remain significant after Bonferroni correction. However, we conclude that in this study, the STAT4 risk allele is associated with an adverse renal outcome and not with disease duration or gender. There are many reasons for an unfavourable outcome, including renal atherosclerosis, but certain susceptibility genes may contribute to a worse prognosis. Interestingly, the STAT4 risk allele has been shown to be a risk factor for stroke and anti-phospholipid antibodies in patients with SLE [47].

In conclusion, this LN case versus healthy control study has demonstrated an association between STAT4 and LN with genome wide significance. In the case-only meta-analysis the STAT4 risk allele displayed signals of association with a poor renal outcome with severe renal insufficiency. Future studies will try to define the precise role for this STAT4 genetic variant in LN pathogenesis.

Supporting Information

Figure S1

Table S1 Risk allele frequencies in cohort I

Table S2 Case-only association analysis in cohort I

Table S3 Power calculations in case-only analysis of cohort I

Table S4 Disease duration by genotype

Table S5 Genotype by gender

Acknowledgments

We thank Rezvan Kiani Dehkordi for assistance in DNA sample collection. Genotyping was performed at the SNP&SEQ technology platform in Uppsala (http://www.genotyping.se). We thank Torbjörn Öst, Ann-Christin Wiman, Sofia Nordman and Annika Ahlford for assistance with genotyping.

Author Contributions

Conceived and designed the experiments: KB JKS LR ACS IG GN. Performed the experiments: KB JKS. Analyzed the data: KB JKS GN. Contributed reagents/materials/analysis tools: KB AZ AJ CS ES AAB MLE IG. Wrote the paper: KB JKS GN.

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