Analysis of *IL2/IL21* Gene Variants in Cholestatic Liver Diseases Reveals an Association with Primary Sclerosing Cholangitis

Johannes Stallhofer[a]   Gerald Ulrich Denk[a]   Jürgen Glas[a, c]
Rüdiger Paul Laubender[b]   Burkhard Göke[a]   Christian Rust[a]
Stephan Brand[a]   Thomas Pusl[a, d]

[a]Department of Medicine II and [b]Institute of Medical Informatics, Biometry and Epidemiology, University Hospital Munich-Grosshadern, [c]Department of Preventive Dentistry and Periodontology, Ludwig Maximilian University, Munich, and [d]First Medical Clinic, Klinikum Augsburg, Augsburg, Germany

Abstract

Background/Aims: The chromosome 4q27 region harboring *IL2* and *IL21* is an established risk locus for ulcerative colitis (UC) and various other autoimmune diseases. Considering the strong coincidence of primary sclerosing cholangitis (PSC) with UC and the increased frequency of other autoimmune disorders in patients with primary biliary cirrhosis (PBC), we investigated whether genetic variation in the *IL2/IL21* region may also modulate the susceptibility to these two rare cholestatic liver diseases. ***Methods:*** Four strongly UC-associated single nucleotide polymorphisms (SNPs) within the *KIAA1109/TENR/IL2/IL21* linkage disequilibrium block were genotyped in 124 PBC and 41 PSC patients. Control allele frequencies from 1,487 healthy, unrelated Caucasians were available from a previous UC association study. ***Results:*** The minor alleles of all four markers were associated with a decreased susceptibility to PSC (rs13151961: p = 0.013, odds ratio (OR) 0.34; rs13119723: p = 0.023, OR 0.40; rs6822844: p = 0.031, OR 0.41; rs6840978: p = 0.043, OR 0.46). Moreover, a haplotype consisting of the four minor alleles also had a protective effect on PSC susceptibility (p = 0.0084, OR 0.28). A haplotype of the four major alleles was independently associated with PSC when excluding the patients with concomitant inflammatory bowel disease (p = 0.033, OR 4.18). ***Conclusion:*** The *IL2/IL21* region may be one of the highly suggestive but so far rarely identified shared susceptibility loci for PSC and UC.

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Introduction

Primary biliary cirrhosis (PBC) and primary sclerosing cholangitis (PSC) are chronic cholestatic liver diseases characterized by an immune-mediated destruction of the biliary system, resulting in biliary fibrosis, cirrhosis, and finally chronic liver failure [1, 2]. PBC is deemed to be a model autoimmune disease due to its striking female predominance and the existence of a disease-specific au-

Stephan Brand, MD
Department of Medicine II, Klinikum Grosshadern, Ludwig Maximilian University
DE–81377 Munich (Germany)
Tel. +49 89 7095 2295, Fax +49 89 7095 5291
E-Mail stephan.brand@med.uni-muenchen.de

toantibody directed against the E2 subunit of the mitochondrial pyruvate dehydrogenase complex [2]. In contrast, PSC may rather be caused by a dysregulated immune response to bacterial or viral antigens entering the portal circulation due to increased permeability of the colonic mucosa – or by activated T lymphocytes undergoing enterohepatic circulation [1]. Consistent with that, there is a strong association of PSC with inflammatory bowel disease (IBD). In western countries, between 53 and 98% of PSC patients have concomitant IBD, primarily ulcerative colitis (UC) [3, 4]. Conversely, the prevalence of PSC among patients with UC ranges from 2 to 7.6% [3, 4].

However, while recent genome-wide association studies have revealed several overlapping susceptibility loci (reviewed in [5]) for a variety of immune-mediated diseases including PBC [6], the search for common genetic risk factors for UC and PSC provided results that were well behind expectations. Only 2 of 15 established UC loci tested, namely G protein-coupled bile acid receptor 1 (*GPBAR1*; 2q35) and macrophage-stimulating 1 (*MST1*; 3p21), showed moderate association with PSC in a Scandinavian cohort [7]. Apart from *glypican 6* (*GPC6*; 13q31), which is not implicated in UC, the first genome-wide association study in PSC failed to detect susceptibility loci outside the HLA complex on chromosome 6p21, whose role in PSC susceptibility has already been extensively studied [7].

Given the limited data on shared susceptibility loci for UC and PSC, we aimed to evaluate the role of four genetic polymorphisms in the *IL2/IL21* region (rs13151961, rs13119723, rs6822844 and rs6840978) in our cohort of PSC patients on a candidate gene basis. These polymorphisms are strongly associated with UC [8–11], but were not included in the above-mentioned genome-wide analysis [7] and were not part of the 15 UC loci previously analyzed in PSC [7].

The association of the *IL2/IL21* region on chromosome 4q27 with celiac disease [12], type 1 diabetes [13–15], rheumatoid arthritis [14, 16, 17], psoriatic arthritis [18], juvenile idiopathic arthritis [19, 20], systemic lupus erythematosus [17, 21], Sjögren's syndrome [17] and Grave's disease [15] suggests this region as a general autoimmune risk locus and makes it also an interesting candidate locus for PBC. The frequency of classic autoimmune diseases is increased in both PSC patients and PBC patients and their first-degree relatives [22, 23].

In order to examine a potential association with PBC or PSC, we determined allele frequencies and haplotype frequencies of the four aforementioned *IL2/IL21*-polymorphisms in two well-characterized patient cohorts and compared them with a large group of healthy control subjects.

Methods

Patients and Control Subjects
The study included 124 PBC and 41 PSC patients of European Caucasian descent. All patients were recruited at Grosshadern University Hospital, Munich, Germany. PBC was diagnosed using standard criteria: presence of anti-mitochondrial antibodies (AMA) in serum, elevation of cholestatic liver enzymes and/or disease-specific hepatic histopathology [24]. The diagnosis of PSC was based on biochemical changes consistent with chronic cholestasis in coincidence with characteristic intrahepatic and/or extrahepatic alterations of the bile ducts shown by endoscopic retrograde or magnetic resonance cholangiopancreatography [25]. Detailed clinical data for all patients were obtained by analysis of patient charts.

Genotyping results of 1,487 healthy unrelated European Caucasian controls for the herein tested SNPs in the *IL2/IL21* region were available from a previous study investigating their role in UC [10]. The epidemiological characteristics of the three study groups are given in table 1. Written informed consent was obtained from all participants. Ethical approval was given by the Ethics Committee of the Medical Faculty of Ludwig Maximilian University, Munich. The study adhered to the Ethical Principles for Medical Research Involving Human Subjects of the Helsinki Declaration. All data were stored in a coded, anonymized database.

SNP Selection and Genotyping
A roughly 440 kb-long region of pronounced linkage disequilibrium on chromosome 4q27 comprising the four genes *KIAA1109, TENR, IL2,* and *IL21* has initially been identified as the strongest susceptibility locus for celiac disease outside the HLA complex by a genome-wide association scan [12]. The four SNPs rs13151961 (A>G), rs13119723 (A>G), rs6822844 (G>T), and rs6840978 (C>T) were the strongest disease associated polymorphisms within this gene cluster in the initial celiac disease scan and all showed highly significant association with UC in two independent studies [8, 10]. Therefore, we chose these four SNPs to determine whether genetic variation in the chromosome 4q27 region is also implicated in the susceptibility to PBC or PSC.

Venous EDTA blood samples were obtained from all patients and genomic DNA was isolated from peripheral blood leukocytes by using the DNA Blood Mini Kit (Qiagen, Hilden, Germany). Genotyping was performed by melting curve analysis in a Light-Cycler® 480 instrument (Roche Diagnostics, Mannheim, Germany) as described previously [10] and is specified in the online suppl. appendix 1 (www.karger.com/doi/10.1159/000321619). The overall genotyping success rate was 99.0% for controls, 99.4% for PBC and 100% for PSC patients.

Statistical Analysis
Before statistical analysis, conformance with the Hardy-Weinberg equilibrium was computed for all markers. The genotype frequencies predicted by allele frequencies were compared to the observed genotypes. Therefore, an exact test integrated in Haplo-

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Table 1. Clinical characteristics of the study population

	PBC (n = 124)	PSC (n = 41)	Controls (n = 1,487)
Male, n (%)	3 (2.4)	28 (68.3)	928 (62.4)
Female, n (%)	121 (97.6)	13 (31.7)	559 (37.6)
Concomitant IBD, n (%)	2 (1.6)	23 (56.1)	
Ulcerative colitis, n (%)	1 (0.8)	21 (51.2)	
Crohn's disease, n (%)	1 (0.8)	1 (2.4)	
Indeterminate colitis, n (%)	0	1 (2.4)	
AIH overlap syndrome, n (%)	10 (8.1)	3 (7.3)	
Mean age ± SD (range), years	63.9 ± 12.1 (19–89)	40.4 ± 13.5 (21–92)	46.0 ± 10.7 (18–71)
Mean age at diagnosis ± SD (range), years	48.9 ± 9.6 (19–70)	31.7 ± 14.9 (13–86)	
Mean age at diagnosis of concomitant IBD ± SD (range), years	48.0 ± 22.6 (32–64)	23.2 ± 15.3 (10–82)	
Liver transplantation, n (%)	15 (12.1)	4 (9.8)	
Cholangiocarcinoma, n (%)	0	1 (2.4)	
Hepatocellular carcinoma, n (%)	2 (1.6)	0	

view 4.2 [26] was applied to the combined dataset of all three cohorts. Haploview provided r^2 linkage disequilibrium (LD) statistics for the four tested polymorphisms and was further used for the evaluation of haplotype counts and frequencies. It analyzes haplotype association by χ^2 testing and performs permutations to correct for multiple testing. Since in the PSC cohort, some haplotype counts were 5 or less, we show Fisher's exact test p values in brackets in table 3. For single marker association analysis, case and control allele counts – or genotypes where indicated – were compared with Fisher's exact test. Blaker's exact test [27] was used where denoted by P_{BL}. A two-tailed p < 0.05 was considered statistically significant. Odds ratios (ORs) were calculated with a 95% confidence interval (CI) and statistical power of the odds ratios was defined with SNP_tools [28]. Fisher's exact test was performed with SPSS 15.0 software (SPSS Inc., Chicago, Ill., USA). Blaker's exact test was computed by R (version 2.11.1) software (R Development Core Team, Vienna, Austria). Student's t test was applied for quantitative variables and was calculated with Microsoft Excel (Microsoft Corp., Redmond, Wash., USA).

Results

Patient Characteristics

The main clinical characteristics of the PBC and PSC patients are shown in table 1. One hundred and twenty-one (97.6 %) of the 124 PBC patients were female reflecting the known substantial female preponderance of this disease. Ten (8.1%) of the PBC patients had an autoimmune hepatitis (AIH) overlap syndrome. The mean age at diagnosis of PBC was 48.9 ± 9.6 SD years. Histological staging was available for 64 of the 124 PBC patients. Of these, 23 (35.9%) showed advanced disease (stage III–IV), whereas 41 (64.1%) were in stage I or II. Fifteen of the 124

PBC patients (12.1%) had already undergone liver transplantation. This percentage was similar in the PSC group (4 of 41 patients; 9.8%). Malignancies were seen in both groups: 1 PSC patient had been diagnosed for cholangiocarcinoma, and 2 PBC patients exhibited hepatocellular carcinoma.

Twenty-three PSC patients (56.1%) had concomitant IBD (UC, n = 21; Crohn's disease, n = 1; indeterminate colitis, n = 1). The mean age at diagnosis of IBD (23.2 ± 15.3 SD years) was significantly lower than the age at diagnosis of PSC (31.7 ± 14.9 SD years; p = 0.041). In 19 of 23 PSC patients with concomitant IBD (82.6%), the diagnosis of IBD preceded the onset of PSC or was made in the same year. Three PSC patients had a PSC-AIH overlap syndrome. As noted in an earlier study [29], the male predominance in PSC (overall men to women ratio approximately 3:2) was especially pronounced in the subgroup with IBD (78.3% male). In the subgroup with PSC alone, the sex ratio was more balanced (55.6% male).

SNPs in the KIAA1109-TENR-IL2-IL21 Gene Cluster Are Associated with PSC but Not PBC Susceptibility

The genotype frequencies of all four tested genetic polymorphisms were in accordance with the Hardy-Weinberg equilibrium. The minor alleles of the four SNPs rs13151961 (p = 0.013), rs13119723 (p = 0.023), rs6822844 (p = 0.031) and rs6840978 (p = 0.043) were associated with a decreased susceptibility to PSC in our patient cohort (table 2). For the most strongly PSC-associated SNP, rs13151961, the minor allele frequency was 0.061 in PSC patients, whereas it was 0.162 in controls.

Table 2. Chromosome 4q27 markers in PBC, PSC and healthy controls

Marker	Minor allele	PBC (n = 124)				PSC (n = 41)				Controls (n = 1,487)
		MAF	p value[a]	OR [95 % CI]	Power	MAF	p value[a]	OR [95 % CI]	Power	MAF
rs13151961	G	0.154	0.857	0.94 [0.66–1.35]	0.05	0.061	**0.013**	**0.34 [0.14–0.83]**	0.65	0.162
rs13119723	G	0.169	0.859	1.03 [0.73–1.45]	0.04	0.073	**0.023**	**0.40 [0.17–0.92]**	0.58	0.166
rs6822844	T	0.150	0.718	0.92 [0.64–1.32]	0.06	0.073	**0.031**	**0.41 [0.18–0.95]**	0.55	0.161
rs6840978	T	0.195	0.800	1.04 [0.75–1.45]	0.04	0.098	**0.043**	**0.46 [0.22–0.97]**	0.53	0.189

Minor allele frequencies (MAF), allelic test p values, odds ratios (OR, shown for the minor allele) with 95% CIs and power of odds ratio 95% CI. Significant associations are highlighted in bold.
[a] Two-tailed p values were calculated by Fisher's exact test analysis of allele counts.

Table 3. Chromosome 4q27 haplotypes in PBC, PSC and healthy controls

Haplotype block	Allelic order	PBC (n = 124)				PSC (n = 41)				Controls
		HF	p value[a]	OR [95% CI]	$P_{100,000}$[b]	HF	p value[a]	OR [95% CI]	$P_{100,000}$[b]	(n = 1,487)
1 2 3 4	AAGC	0.791	0.66	0.93 [0.68–1.29]	0.96	0.878	*0.089* (0.092)	1.77 [0.91–3.46]	0.28	0.802
	GGTT	0.148	0.77	0.95 [0.66–1.37]	0.97	0.049	**0.0084** (0.0048)	0.28 [0.10–0.77]	**0.035**	0.155
	AAGT	0.045	0.17	1.56 [0.82–2.96]	0.39	0.037	0.70 (0.73)	1.25 [0.39–4.04]	1	0.029
1 2	AA	0.836	0.99	1.00 [0.70–1.42]	1	0.927	**0.027** (0.023)	2.49 [1.08–5.75]	*0.054*	0.836
(KIAA1109)	GG	0.148	0.57	0.90 [0.62–1.30]	0.84	0.061	**0.014** (0.013)	0.34 [0.14–0.84]	**0.042**	0.161
2 3	AG	0.833	0.94	1.02 [0.72–1.44]	0.99	0.915	**0.046** (0.050)	2.18 [1.00–4.75]	*0.071*	0.831
(IL2)	GT	0.150	0.79	0.95 [0.66–1.37]	0.94	0.061	**0.018** (0.013)	0.35 [0.14–0.87]	**0.045**	0.157
3 4	GC	0.805	0.88	0.98 [0.70–1.35]	1	0.890	*0.063* (0.064)	1.92 [0.95–3.86]	0.23	0.809
(IL21)	TT	0.150	0.72	0.94 [0.64–1.35]	1	0.061	**0.016** (0.013)	0.34 [0.14–0.85]	**0.040**	0.159
	GT	0.045	0.22	1.49 [0.79–2.83]	0.40	0.037	0.75 (0.74)	1.20 [0.37–3.87]	1	0.031

Haplotype frequencies (HF), p values, odds ratios (OR) with 95% CIs and power of odds ratio 95% CI. 1 = rs13151961; 2 = rs13119723; 3 = rs6822844; 4 = rs6840978. Significant associations are highlighted in bold and suggestive ones in italics. For each block, all haplotypes with an overall frequency >1% were examined. [a] Individual two-tailed p values from χ^2 test analysis of haplotype counts (for PSC, Fisher's exact test p values in brackets). [b] Permutated p values (100,000 permutations).

The odds ratios for the minor allele ranged from 0.34 for rs13151961 to 0.46 for rs6840978. The demonstrated odds ratios of <1.0 suggest protective effects of the minor alleles on PSC susceptibility similar to the association observed for other immune-mediated diseases [8–12, 14, 16, 17, 20]. In line with that, homozygosity for the major allele was positively associated with development of PSC when examining rs13151961 (p = 0.014, OR 3.03, 95% CI 1.18–7.76), rs13119723 (p = 0.036, OR 2.53, 95% CI 1.06–6.06) or rs6822844 (p = 0.037, OR 2.45, 95% CI 1.02–5.86).

In contrast, we did not find any significant association with PBC concerning allele or genotype frequencies (see table 2 for allele frequencies).

Haplotypes Formed by the SNPs within the KIAA1109-TENR-IL2-IL21 Linkage Disequilibrium Block Are Associated with Susceptibility to PSC

The four SNPs in the *KIAA1109-TENR-IL2-IL21* gene cluster are in accentuated linkage disequilibrium to each other (fig. 1). The aforementioned association of the single markers with PSC prompted us to evaluate, whether single haplotypes formed by the SNPs are also associated with susceptibility to PSC or PBC. First, the four SNPs were configured in a single haplotype block. Three haplotypes exhibiting an overall frequency >0.01 were observed (table 3). As expected, a haplotype consisting of the four minor alleles was significantly associated with a

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decreased susceptibility to PSC (p = 0.0084, OR 0.28, 95% CI 0.10–0.77). A similar haplotype including these four alleles has also a protective effect on UC [10].

In order to better represent the different candidate genes within the chromosome 4q27 region, we analyzed three further haplotypes. One encompassed rs13151961 and rs13119723 within *KIAA1109*, the two SNPs with the strongest linkage disequilibrium. One included rs13119723 and rs6822844, which distantly surround *IL2*, and the third one comprised rs6822844 and rs6840978 next to *IL21* (fig. 1). All haplotypes formed by the corresponding minor alleles were observed with a significantly lower frequency in PSC patients compared to the healthy controls (table 3). In case of the *IL2* and *KIAA1109* haplotypes, the assembled major alleles showed a significant positive association with PSC vice versa.

In contrast, we did not detect PBC-associated haplotypes (table 3).

KIAA1109-TENR-IL2-IL21 Variants Are Associated with PSC Independently of Concomitant IBD

The herein studied genetic variants are associated with UC, and there is also some evidence for an association with Crohn's disease [8–11]. PSC-IBD is considered a distinct IBD phenotype on its own [3]. The colitis associated with PSC is usually mild and is characterized by a more severe right-sided disease, rectal sparing and backwash ileitis [30]. However, since 23 of our 41 PSC patients (56.1%) had concomitant IBD, we aimed to investigate whether the observed association with PSC is independent of a co-affection with IBD. Therefore, the haplotypes depicted in table 3 and all four single markers were tested for association with the 18 PSC cases without IBD. Despite the limited sample size, the haplotype containing the four major alleles of rs13151961, rs13119723, rs6822844 and rs6840978 showed significant association with PSC (P_{BL} = 0.033, OR 4.18, 95% CI 1.12–24.51). Of the further haplotypes, the one encompassing rs6822844 and rs6840978 next to *IL21* was associated with PSC without IBD when combining the two major alleles (P_{BL} = 0.033, OR 4.02, 95% CI 1.08–23.53).

With regard to the single markers, rs6840978 did not lose significance when excluding the patients with accompanying IBD (P_{BL} = 0.034, OR 0.25, 95% CI 0.04–0.94; OR shown for the minor allele). Homozygosity for the major allele of rs6840978 was a risk factor for PSC without IBD (P_{BL} = 0.045, OR 4.11, 95 % CI 1.05–25.13).
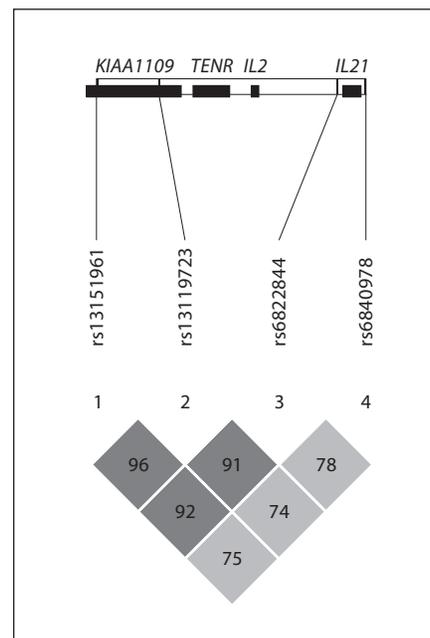

Fig. 1. Overview over the chromosome 4q27 region. The 439-kb section between rs13151961 and rs6840978 is shown, with genes and LD statistics (r^2) calculated from the combined dataset of controls, PBC, and PSC patients using Haploview 4.2.

Discussion

Here, we demonstrate for the first time that the established UC risk locus on chromosome 4q27 [8–11] is associated with susceptibility to PSC.

The contribution of genetic factors to the pathogenesis of PSC is highlighted by a nearly 100-fold higher prevalence of this disorder in first-degree relatives of PSC patients compared with the general population [31]. According to a recent Swedish study [32], the hazard ratio for UC among first-degree relatives of PSC patients is also raised. Even relatives of PSC patients without IBD have a more than seven times increased risk of developing UC, which strongly suggests the existence of shared genetic susceptibility genes for PSC and UC [32].

However, to date, only two other loci have been described which confer susceptibility to both of these epidemiologically tightly linked diseases. Of 15 known UC loci tested so far, only *GPBAR1* and *MST1* showed association with overall PSC susceptibility even in a group where the proportion of concomitant IBD was 81% [7]. Of these two, only one *(GPBAR1)* was further associated with PSC without IBD in the corresponding subgroup of 77 PSC patients without IBD [7].

Interestingly, the same polymorphisms in the *KIAA1109-TENR-IL2-IL21* linkage disequilibrium block investigated are also associated with a variety of other immune-mediated diseases. Especially rs6822844 has been extensively studied. It has been associated with celiac disease [12], UC [8–11], rheumatoid arthritis [14, 16], type 1 diabetes [14], psoriatic arthritis [18], juvenile idiopathic arthritis [19, 20], systemic lupus erythematosus [17] and Sjögren's syndrome [17].

In all of these diseases, like in PSC, the minor allele frequency of rs6822844 is significantly decreased in cases suggesting protective effects of the minor allele on autoimmune disease susceptibility. On the other hand, the 'wild-type' major allele is a risk factor for the development of autoimmunity.

Insulin-dependent diabetes 3 *(IDD3),* the corresponding locus in mice, also harbors the four genes *KIAA1109, TENR, IL2* and *IL21*. It is the strongest non-MHC linked susceptibility locus for type 1 diabetes in the nonobese diabetic (NOD) mouse. Several detailed studies have addressed the functional impact of disease-associated alleles within this autoimmunity locus using the NOD mouse model [33–35]. Naturally occurring susceptibility alleles correlate with an approximately twofold reduction in IL-2 expression and hence impair the function of CD4+ CD25+ regulatory T cells, which are critical for maintaining immune homoeostasis [34]. In contrast, protective *IDD3* allelic variants promote the expansion and suppressive functions of CD4+Foxp3+ regulatory T cells and restrain the proliferation and IL-17 production of pro-inflammatory CD4+ T cells by boosting IL-2 expression [33]. IL-2 is essential for TGF-β to convert naive CD4+CD25- cells to CD25+Foxp3+ regulatory T cells [36] and via STAT5 constrains the generation of Th17 cells [37], which are implicated in the pathogenesis of autoimmune diseases.

Mice with a disrupted *IL2* gene develop an UC-like disease [38]. Defective IL-2 production has also been described for freshly isolated liver derived T lymphocytes from PSC patients. Compared with patients with PBC, AIH, or normal controls, significantly higher levels of tumor necrosis factor (TNF)-α and IL-1β but lower levels of IL-2, IL-10, and interferon-γ were found in the supernatants of mitogen-stimulated lymphocyte cultures [39]. Like IL-2 [40], IL-10 is considered an anti-inflammatory cytokine promoting immune tolerance [41].

Another study on the role of autoimmunity-related alleles in *IDD3*, the mouse homologue for human chromosome 4q27, indicates that a loss of locus parity between *IL2* and *IL21* decreases IL-2 mRNA stability and ensures high IL-21 production as a basis for autoimmunity [35]. IL-21 plays a key role in Th17 differentiation [42], leads to a down-regulation of FOXP3 expression in CD4+ T cells [43] and renders CD4+CD25– T cells resistant to regulatory T-cell-mediated suppression [44]. The opposing functions of IL-2 and IL-21 in tolerance and immunity underpin the disastrous effect of a dysregulated expression of these two cytokines.

Unlike in PSC, we could not detect any impact of the *KIAA1109-TENR-IL2-IL21* SNPs on susceptibility to PBC. This finding is in line with a recent genome-wide association study comprising these SNPs [6]. Taking into account that for rs13151961, our study would have had a 98% power to reveal a difference in minor allele frequency, like it was observed in PSC, it is unlikely that genetic variation in the *IL2/IL21* region plays a major role in the pathogenesis of PBC. However, a minor effect on PBC susceptibility cannot be excluded, since the power of our study to detect a lower difference in minor allele frequency of 5%, for instance, for rs13151961, was only 51%.

The aforementioned recent genome-wide analysis in PBC [6] could find an association with rs6838639 on chromosome 4q27 about 200 kb away from the *KIAA1109-TENR-IL2-IL21* linkage disequilibrium block in its discovery panel. This finding, however, could not be verified in two replication cohorts [6].

In contrast to *IL2* and *IL21, KIAA1109* is a predicted gene of largely unknown function [12]. *TENR* (testis nuclear RNA-binding) expression is restricted to testes making it an unlikely disease gene for PSC [12].

In conclusion, we here provide first evidence that the *KIAA1109-TENR-IL2-IL21* linkage disequilibrium block represents a shared susceptibility locus for UC and PSC. *IL2* and *IL21* are the likely disease genes. Further replication studies in larger cohorts are required to confirm this disease locus.

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