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***POGLUT1*, the putative effector gene driven by rs2293370 in primary biliary cholangitis susceptibility locus chromosome 3q13.33**

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Primary biliary cholangitis (PBC) is a chronic and cholestatic autoimmune liver disease caused by the destruction of intrahepatic small bile ducts. Our previous genome-wide association study (GWAS) identified six susceptibility loci for PBC. Here, in order to further elucidate the genetic architecture of PBC, a GWAS was performed on an additional independent sample set, then a genome-wide meta-analysis with our previous GWAS was performed based on a whole-genome single nucleotide polymorphism (SNP) imputation analysis of a total of 4,045 Japanese individuals (2,060 cases and 1,985 healthy controls). A susceptibility locus on chromosome 3q13.33 (including *ARHGAP31*, *TMEM39A*, *POGLUT1*, *TIMMDC1*, and *CD80*) was previously identified both in the European and Chinese populations and was replicated in the Japanese population (OR = 0.7241, $P = 3.5 \times 10^{-9}$). Subsequent *in silico* and *in vitro* functional analyses identified rs2293370, previously reported as the top-hit SNP in this locus in the European population, as the primary functional SNP. Moreover, e-QTL analysis indicated that the effector gene of rs2293370 was *Protein O-Glucosyltransferase 1 (POGLUT1)* ($P = 3.4 \times 10^{-8}$). This is the first study to demonstrate that *POGLUT1* and not *CD80* is the effector gene regulated by the primary functional SNP rs2293370, and that increased expression of *POGLUT1* might be involved in the pathogenesis of PBC.

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Primary biliary cholangitis (PBC) is a chronic and progressive cholestatic liver disease characterized by chronic non-suppurative destructive cholangitis (CNSDC), ductopenia, interface hepatitis, fibrosis, and biliary cirrhosis^{1,2}. The destruction of small bile ducts is considered to be mediated by autoimmune responses against biliary epithelial cells (BEC), including CD4⁺ T cells, CD8⁺ T cells, B cells, and natural killer (NK) cells²⁻⁴. The higher monozygotic/dizygotic (MZ/DZ) ratio and the higher estimated relative sibling risk (λ s) in PBC patients as compared to unaffected individuals indicates the involvement of strong genetic factors in the development of PBC^{5,6}. Previous genome-wide association studies (GWASs), ImmunoChip analyses, and subsequent meta-analyses in populations of European descent identified human leukocyte antigen (*HLA*) and 30 non-*HLA* susceptibility regions (nearest candidate genes from the top-hit SNPs in each locus: *IL12RB2/DENND1B/C11orf53*, *YPPEL5/LBH*, *IL1RL1/IL1RL2*, *STAT4/NAB1*, *SLC19A3/CCL20*, *PLCL2*, *TIMMDC1/TMEM39A*, *IL-12A/IL12A-AS1/IQCJ/SCHIP1*, *DGKQ*, *NFKB1/MANBA*, *IL7R/CAPSL*, *NUDT12/C5orf30*, *IL12B*, *OLIG3/TNFAIP3*, *ELMO1*, *IRF5/TNPO3*, *RPS6KA4*, *DDX6/CXCR5*, *TNFRSF1A*, *ATXN2/BRAP*, *DLEU1/BCMS*, *RAD51B*, *EXOC3L4*, *RMI2/CLEC16A*, *IRF8/FOXF1*, *ZBP2/GSDMB/IKZF3*, *MAPT*, *TYK2*, *SPIB*, and *SYNGR1/PDGFB/RPL3*) in PBC⁷⁻¹⁴. Additionally, Asian-specific susceptibility regions for PBC, including *CD58*, *CD28/CTLA4*, *IL21-AS1*, *TNFSF15/TNFSF8*, *IL16*, *IL21R*, *CSNK2N2/CCDC113*, and *AATID3A*, were reported in the Japanese and Chinese populations by means of GWAS and subsequent genome-wide meta-analysis with genome-wide SNP imputation (already identified PBC susceptibility loci including this study are shown in Table 1)¹⁵⁻¹⁷. Thus, the evidence reported to date indicates presence of shared and non-shared genetic susceptibility profiles behind the pathogenesis of PBC in European and Asian populations.

Thousands of genetic variations associated with susceptibility to human complex diseases have been identified by GWASs¹⁸. Among genes located near the “top-hit SNP” in each susceptibility locus, candidate genes with well-known functions are often selected as the “disease susceptibility genes”. The majority of SNPs that regulate gene expression are actually found in the vicinity of genes within 100 kb of the transcription start site (TSS)¹⁹. However, trans-acting expression quantitative trait loci (e-QTL) variations, whose target transcripts are separated by arbitrary distances, are believed to explain a substantial proportion of the heritable variation in gene expression²⁰. For example, although *FTO* was reported as a susceptibility gene for obesity, the effector genes whose expression levels were influenced by the significantly associated SNPs were not *FTO* but *Iroquois Homeobox 3* (*IRX3*) and *IRX5*²¹. In PBC, a locus on chromosome 17q12-21 (*ORMDL3-GSDMB-ZBP2-IKZF3*) has been reported as a shared susceptibility locus in different populations. Although the top-hit SNP was located in the *IKAROS family zinc finger 3* (*IKZF3*), in which the function of the protein product is related to the proliferation and differentiation of B cells, the effector gene in this locus was identified as *ORMDL sphingolipid biosynthesis regulator 3* (*ORMDL3*), whose protein product regulates endoplasmic reticulum (ER)-mediated Ca²⁺ homeostasis and facilitates the unfolded-protein response (UPR)^{22,23}. Therefore, understanding the contribution of susceptibility loci to the onset of diseases requires identification of the effector genes that are regulated by the primary functional variation located in the disease susceptibility loci.

The present study aimed to further elucidate the genetic architecture of PBC in the Japanese population. To this end, we performed a GWAS and subsequent genome-wide meta-analysis based on a whole-genome SNP imputation analysis with previous GWAS¹⁶. The PBC susceptibility locus chromosome 3q13.33 (including *ARHGAP31*, *TMEM39A*, *POGLUT1*, *TIMMDC1*, and *CD80*) has been identified by GWAS as a PBC susceptibility

Chromosome	Location	Mapped gene(s)	Top-hit SNP	MAF ^a	OR ^b	P	Population	Ref.
1	1p13.1	<i>CD58</i>	rs2300747	0.39	1.29	2.E-12	Chinese	¹⁷
	1p31.3	<i>IL12RB2/DENND1B/C1orf53</i>	rs72678531	0.16	1.61	2.E-38	European	¹²
2	2p23.1	<i>YPEL5/LBH</i>	rs4952108	0.19	1.28	5.E-08	European	¹⁴
	2q12.1	<i>IL1RL1/IL1RL2</i>	rs12712133	0.44	1.14	5.E-09	European	¹⁴
	2q32.2	<i>STAT4/NAB1</i>	rs3024921, etc.	0.05	0.72	9.E-25	European	¹²
			rs10168266	0.32	1.31	4.E-14	Chinese	¹⁷
	2q33.2	<i>CD28/CTLA4</i>	rs4675369	0.42	1.31	1.E-13	Chinese	¹⁷
	2q36.3	<i>SLC19A3/CCL20</i>	rs4973341	0.33	1.22	2.E-10	European	¹⁴
3	3p24.3	<i>PLCL2</i>	rs1372072	0.37	1.20	2.E-08	European	¹⁰
	3q13.33	<i>TIMMDC1/TMEM39A</i>	rs2293370	0.16	1.39	7.E-16	European	¹²
			rs3732421	0.34	1.35	3.E-13	Chinese	¹⁷
			rs57271503	0.34	0.72	3.E-09	Japanese	This study
	3q25.33	<i>IL-12A/IL12A-AS1/IQCJ/SCHIP1</i>	rs2366643, etc.	0.38	0.62	3.E-35	European	¹²
		rs582537	0.29	1.33	2.E-11	Chinese	¹⁷	
4	4p16.3	<i>DGKQ</i>	rs11724804	0.44	1.22	9.E-12	European	¹⁴
	4q24	<i>NFKB1/MANBA</i>	rs7665090	0.49	1.26	8.E-14	European	¹²
			rs1598856	0.49	1.26	2.E-10	Chinese	¹⁷
			rs17033015	0.47	1.35	9.E-10	Japanese	This study
	4q27	<i>IL21-AS1</i>	rs925550	0.35	1.31	4.E-13	Chinese	¹⁷
5	5p13.2	<i>IL7R/CAPSL</i>	rs6871748	0.28	1.30	2.E-13	European	¹²
			rs12697352	0.19	0.68	2.E-09	Japanese	This study
	5q21.1	<i>NUDT12/C5orf30</i>	rs526231	0.32	1.15	1.E-08	European	¹⁴
	5q33.3	<i>IL12B</i>	rs2546890	0.50	1.15	1E-10	European	¹⁴
6	6q23.3	<i>OLIG3/TNFAIP3</i>	rs6933404	0.17	1.18	1E-10	European	¹⁴
7	7p14.1	<i>ELMO1</i>	rs6974491	0.16	1.25	4.E-08	European	¹⁰
	7q32.1	<i>IRF5/TNPO3</i>	rs10488631	0.10	1.59	5.E-23	European	¹⁴
9	9q32	<i>TNFSF15/TNFSF8</i>	rs4979467	0.37	1.53	1.E-29	Chinese	¹⁷
			rs4979462	0.32	0.60	2.E-26	Japanese	This study
11	11q13.1	<i>RPS6KA4</i>	rs538147	0.39	1.23	2.E-10	European	¹⁰
	11q23.3	<i>DDX6/CXCR5</i>	rs80065107	0.19	1.39	7.E-16	European	¹²
			rs77871618	0.16	1.40	3.E-13	Chinese	¹⁷
12	12p13.31	<i>TNFRSF1A</i>	rs1800693	0.43	0.74	7.E-19	European	¹²
			rs4149576	0.14	1.37	4.E-09	Chinese	¹⁷
	12q24.12	<i>ATXN2/BRAP</i>	rs11065987	0.37	1.19	3.E-08	European	¹⁴
13	13q14.2	<i>DLEU1/BCMS</i>	rs9591325	0.05	1.63	1.E-10	European	¹⁴
14	14q24.1	<i>RAD51B</i>	rs911263	0.33	1.29	2.E-11	European	¹⁰
	14q32.32	<i>EXOC3L4</i>	rs2297067	0.22	1.39	6.E-19	European	¹⁴
15	15q25.1	<i>IL16</i>	rs11556218	0.19	1.29	9.E-09	Chinese	¹⁷
16	16p12.1	<i>IL21R</i>	rs2189521	0.30	1.41	4.E-16	Chinese	¹⁷
	16p13.13	<i>RMI2/CLEC16A</i>	rs1646019, etc.	0.30	1.38	2.E-23	European	¹²
	16q21	<i>CSNK2N2/CCDC113</i>	rs2550374	0.48	1.23	2.E-08	Chinese	¹⁷
	16q24.1	<i>IRF8/FOXF1</i>	rs11117432	0.23	1.31	5.E-11	European	¹⁰
17	17q21.1	<i>ZBP2/GSDMB/IKZF3</i>	rs8067378	0.47	1.26	6.E-14	European	¹²
			rs9635726	0.41	1.37	2.E-16	Chinese	¹⁷
			rs4795395	0.35	1.42	4.E-12	Japanese	This study
	17q21.31	<i>MAPT</i>	rs17564829	0.23	1.25	2.E-09	European	¹²
19	19p13.2	<i>TYK2</i>	rs34536443	0.03	1.95	1.E-12	European	¹²
	19p13.3	<i>ARID3A</i>	rs10415976	0.47	1.30	4.E-12	Chinese	¹⁷
	19q13.33	<i>SPIB</i>	rs3745516	0.21	1.39	1.E-20	European	¹⁴
22	22q13.1	<i>SYNGR1/PDGFB/RPL3</i>	rs2267407	0.24	1.29	1.E-13	European	¹²
			rs137603	0.13	1.37	3.E-08	Chinese	¹⁷

Table 1. Non-*HLA* PBC susceptibility loci in European, Chinese, and Japanese populations. ^aMAF (minor allele frequency) in 1000 genome project in each population. ^bOR (odds ratio).

locus in European and Chinese populations; consequently, this genome-wide meta-analysis involved replicating chromosome 3q13.33 in the Japanese population. Here, we show *in silico* and *in vitro* functional analyses and identify the effector gene and the primary functional SNP in the PBC susceptibility locus chromosome 3q13.33.

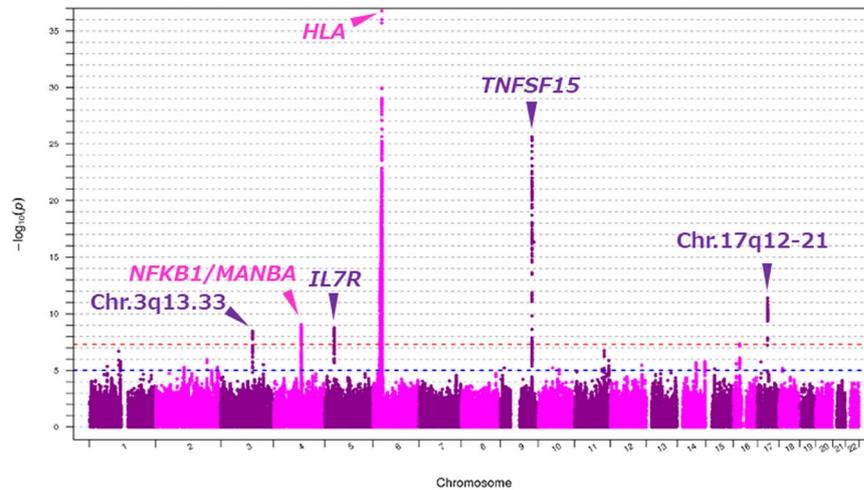


Figure 1. Genome-wide Manhattan plot of the GWAS meta-analysis between two data sets from the ASI and Japonica platforms. Negative log₁₀ P-values of qualified SNPs are plotted against their genomic positions. The genome-wide significance line (red) is shown at 7.30 ($-\log_{10} P [5e-8]$). The genome-wide suggestive line (blue) is shown at 5 ($-\log_{10} P [1e-5]$).

Results

GWAS and genome-wide meta-analysis. We genotyped an independent set of 1,148 samples (668 PBC cases and 480 healthy controls) using the Affymetrix Japonica V1 Array²⁴. Thirty-four samples were excluded by Dish QC (<0.82) or overall call rate for a total of 20,000 SNPs (<0.97) and 13 samples were excluded because of cryptic relatives. A further 13 samples were located far from the JPT cluster drawn using the first and second components after PCA and were removed from further analysis (Supplementary Fig. 1A). We re-genotype called about 2,897 samples (1,392 PBC cases and 1,505 healthy controls) collected in the previous study¹⁶. Eighteen samples were excluded by Dish QC (<0.82) or overall call rate for a total of 20,000 SNPs (<0.97) and 15 samples were excluded because of cryptic relatives. Seventeen samples were located far from the HapMap JPT cluster drawn using the first and second components after PCA and were removed from further analysis (Supplementary Fig. 1B).

A quantile-quantile plot of the distribution of test statistics for the comparison of allele frequencies in the PBC cases and healthy controls provided an inflation factor lambda value of 1.097 for all tested SNPs for the 1,148 entries in the current dataset and a value 1.061 for the 2,897 entries in the previous dataset (Supplementary Fig. 2). Genotype imputation and the association study were separately performed for the two datasets. The process of data cleaning and meta-analysis is summarized in Supplementary Fig. 3.

Figure 1 shows a genome-wide view of the single-point association data based on allele frequencies after meta-analysis. The loci *HLA*, *TNFSF15*, *IL7R*, *NFKB1/MANBA*, and chromosome 17q12-21 showed significant associations with PBC, as reported in the previous GWAS performed on a Japanese population¹⁶. In addition to these regions, meta-analysis to combine the two datasets showed a significant association in chromosome 3q13.33 (Top hit SNP: rs57271503, OR = 0.7241, $P = 3.5 \times 10^{-9}$, Fig. 2), although this locus appears as evidence of no association with PBC from studies using each platform (Japonica and ASI, Supplementary Fig. 4).

Identification of rs2293370 as the primary functional SNP in chromosome 3q13.33. Among the 29 SNPs whose P values were less than 1.0×10^{-6} upon genome-wide meta-analysis, SNPs located in the 3'-untranslated region (UTR) and synonymous substitutions were selected as potential candidates for primary functional variation in the chromosome 3q13.33 region (Table 2 and Fig. 2). Five of the 29 SNPs [rs57271503 and rs3830649 in the 3'UTR of *CD80*, rs2305249 in exon 11 of *ARHGAP31* (P567P), rs1131265 in exon 3 of *TIMMDC1* (V146V), and rs3732421 in the 3'UTR of *TMEM39A*] are located in the 3'UTR or synonymous substitutions but are unrelated to their own gene expression as determined by e-QTL analysis²⁵ (Supplementary Fig. 5) and thus were excluded from further analysis.

Two of the remaining 24 SNPs had RegulomeDB scores higher than 3 and these scores were supported by their location in DNase hyper-sensitivity clusters and the binding of transcription factor. Consequently, these two SNPs were selected as potential candidates²⁶ (Table 2; rs2293370 in intron 2 of *TIMMDC1* and rs56008261 in intron 8 of *ARHGAP31*). Both SNPs were located in DNase I hyper-sensitivity clusters and in H3K27Ac markers in at least one cell type identified by the UCSC genome browser²⁷.

We performed electrophoretic mobility shift assays (EMSAs) to evaluate the effect of candidate SNPs that potentially regulate the binding affinity of transcription factors. A difference in mobility shift between the major allele and the minor allele was detected for rs2293370 in HepG2 (Fig. 3A) and Jurkat (Supplementary Fig. 6A) cells. The shifted band was abrogated by incubation with a 200× concentration of a non-labeled probe (competitor probe) (Fig. 3B and Supplementary Fig. 6B). In contrast, there was no difference in mobility shift for rs56008261 between the major allele and the minor allele (Fig. 3A and Supplementary Fig. 6A).

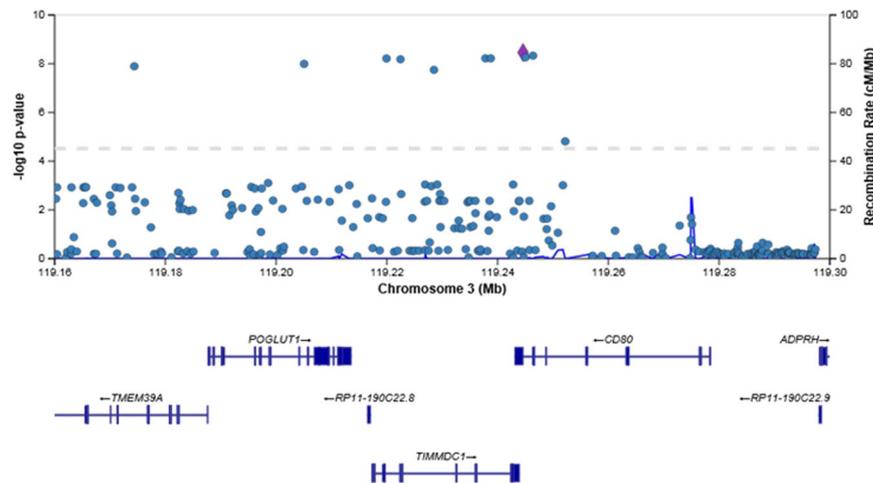


Figure 2. Regional plot of association results and recombination rates for the region surrounding *POGLUT1* (chromosome 3: 119,160,000–119,300,300). Each dot shows the P-value of each SNP after meta-analysis. The purple diamond represents the SNP with the minimum P-value in the region. Genetic recombination rates are shown with a blue line.

Additionally, in order to deny the possibility of the existence of other variations with independent genetic contributions in chromosome 3q13.33, conditional logistic regression analysis was performed. When the rs2293370 was conditioned on, significant associations of other SNPs in chromosome 3q13.33 totally disappeared (Supplementary Fig. 7).

These results indicated that rs2293370 is the primary functional SNP in chromosome 3q13.33.

Molecular features of disease susceptibility influenced by rs2293370. We performed luciferase reporter assays in HepG2 and Jurkat cells to determine the differences in transcription efficiency between the C (major allele, PBC-susceptibility) and T (minor allele, PBC-protective) alleles of rs2293370. Concordant with the result of EMSA, the luciferase activity of cells 24 h after transfection with a reporter construct containing the C allele of rs2293370 was significantly higher than that of cells containing the T allele for both cell lines (Fig. 3C,D and Supplementary Fig. 6C).

Next, we performed *in silico* prediction of transcription factor binding using the TRANSFAC database²⁸ to identify the transcription factor responsible for the mobility shift associated with the C allele of rs2293370. The C allele of rs2293370, but not the T allele, was predicted to be involved in a binding motif of Runt-related transcription factors (Supplementary Fig. 8). Although the DMRT and Myb families also showed similar patterns, they are not expressed in HepG2 or Jurkat cells²⁹. Of the Runt-related transcription factors, Runt-related transcription factor (RUNX1) -1, but not RUNX-2 and RUNX-3, was confirmed to be expressed in both HepG2 and Jurkat cells²⁹ (Supplementary Fig. 9). Consistent with the *in silico* prediction of transcription factor binding, the mobility shift associated with the C allele of rs2293370 was reduced by pre-incubation with an anti-RUNX1 antibody prior to electrophoresis (Fig. 3E).

These results indicated that the PBC susceptibility allele of rs2293370 enhances transcription via binding with RUNX1.

The mRNA expression level of *POGLUT1* is influenced by rs2293370. We used the GTEx portal database²⁵ to assess the influence of rs2293370 on endogenous gene expression by comparing the expression levels of all genes in the human genome for the different genotypes of rs2293370 in every organ whose expression level of *POGLUT1* was above the threshold for detection. Individuals carrying the C allele (i.e., the PBC-susceptible allele) of rs2293370 showed a significantly higher level of expression of *POGLUT1* in several organs (Fig. 4; statistical significance level: $P < 0.05/47$ organs = 0.00106). Other genes located in chromosome 3q13.33 (*ARHGAP31*, *TMEM39A*, *POGLUT1*, *TIMMDC1*, and *CD80*) showed no significant association between rs2293370 genotypes and gene expression (Supplementary Fig. 10).

Discussion

In the present study we identified chromosome 3q13.33, which includes the genes *ARHGAP31*, *TMEM39A*, *POGLUT1*, *TIMMDC1*, and *CD80*, as a PBC susceptibility locus in the Japanese population by genome-wide meta-analysis based on whole-genome SNP imputation analysis of two distinct data sets of Japanese PBC-GWAS. The role of chromosome 3q13.33 had previously been identified in European and Chinese populations. Consequently, rs2293370, which is located in intron 2 of *TIMMDC1*, was identified as the primary functional SNP for disease susceptibility to PBC in chromosome 3q13.33 by *in silico* and *in vitro* functional analyses. In addition, the disease protective allele of rs2293370 was shown to disrupt a RUNX1 binding site and was associated with significantly decreased *POGLUT1* mRNA expression levels in tissues compared with individuals without this allele.

rs number	SNP location (Chr.3)	GWAS/imputation	Allele 1	Allele 2	P value	OR	Regulome DB score	UCSC (Regulatory Motifs)	Location
rs57271503	119244593	imputation	G	A	3.48E-09	0.724	No data	×	CD80 3'UTR
rs9855065	119130141	imputation	G	A	3.57E-09	0.725	No data	Δ	ARHGAP31 intron 11
rs3830649	119246385	imputation	G	del	4.66E-09	0.727	No data	×	CD80 3'UTR
rs2305249	119128398	imputation	G	A	5.07E-09	0.727	6	×	ARHGAP31 Exon 11 (P567P)
rs13092998	119245044	GWAS (Japonica)	G	T	5.45E-09	0.728	No data	×	CD80 intron 6
rs62264485	119237798	imputation	C	A	6.00E-09	0.728	6	Δ	TIMMDC1 intron 6
rs35264490	119238753	imputation	A	del	6.00E-09	0.728	No data	Δ	TIMMDC1 intron 6
rs2293370	119219934	GWAS (ASI, Japonica)	G	A	6.08E-09	0.728	3a	Δ	TIMMDC1 intron 2
rs1463138	119128634	imputation	T	C	6.34E-09	0.751	6	×	ARHGAP31 intron 11
rs1131265	119222456	imputation	G	C	6.57E-09	0.729	No data	×	TIMMDC1 Exon 3 (V146V)
rs1463139	119128628	imputation	A	G	6.70E-09	0.749	No data	×	ARHGAP31 intron 11
rs3732421	119150089	imputation	A	G	9.93E-09	0.732	5	×	TMEM39A 3'UTR
rs7650774	119205050	imputation	T	C	1.01E-08	0.731	No data	×	POGLUT1 intron 6
rs12636784	119174383	imputation	A	G	1.27E-08	0.733	6	×	TMEM39A intron 3
rs4687853	119130360	imputation	A	G	1.47E-08	0.754	6	×	ARHGAP31 intron 11
rs9843355	119228508	imputation	G	A	1.79E-08	0.735	6	×	TIMMDC1 intron 4
rs1530687	119114515	imputation	G	A	6.26E-08	0.767	5	Δ	ARHGAP31 intron 8
rs9831023	119111762	GWAS (ASI, Japonica)	T	C	6.98E-08	0.768	5	×	ARHGAP31 intron 7
rs9884090	119116150	imputation	G	A	9.34E-08	0.753	5	×	ARHGAP31 intron 8
rs1000198	119113820	imputation	A	C	1.34E-07	0.771	6	×	ARHGAP31 intron 8
rs11922594	119125822	imputation	T	C	1.50E-07	0.771	5	×	ARHGAP31 intron 10
rs6773050	119123814	GWAS(ASI)	C	T	1.62E-07	0.774	6	×	ARHGAP31 intron 10
rs12494314	119122820	imputation	T	C	1.90E-07	0.758	No data	×	ARHGAP31 intron 10
rs4279094	119114693	GWAS(ASI)	A	G	2.12E-07	0.774	4	×	ARHGAP31 intron 8
rs9846036	119116064	imputation	A	C	2.12E-07	0.774	5	×	ARHGAP31 intron 8
rs56008261	119114927	GWAS(Japonica)	T	C	2.61E-07	0.776	1b	O	ARHGAP31 intron 8
rs6776377	119115556	imputation	T	C	2.81E-07	0.776	5	×	ARHGAP31 intron 8
rs6787836	119115567	imputation	A	G	5.85E-07	0.782	5	×	ARHGAP31 intron 8
rs11715698	119118497	imputation	A	G	6.61E-07	0.788	5	×	ARHGAP31 intron 9

Table 2. 29 SNPs associated with susceptibility to PBC in the Japanese population in chromosome 3q13.33 by high-density association mapping.

The contribution of *POGLUT1* to the pathogenesis of PBC has not been reported to date. Endoplasmic reticulum (ER)-localized protein O-glucosyltransferase 1, which is encoded by *POGLUT1*, adds glucose moieties to serine residues of the epidermal growth factor (EGF)-like domains of Notch family proteins^{30,31}. Notch signaling is an evolutionarily conserved cascade that includes four receptors (Notch 1–4) and five ligands [Jagged 1, Jagged 2, Delta-like ligand 1 (DLL1), DLL3 and DLL4]. Therefore, it might be possible that genetic polymorphisms affecting the expression levels of *POGLUT1* influence the Notch signaling pathway by altering Notch glycosylation. The generation and development of diverse blood cell lineages and peripheral immune responses are regulated by this Notch signaling cascade, especially in hematopoiesis during T cell lineage commitment and maturation in the thymus, and during marginal zone B (MZB) cell development in the spleen³². Recently, dendritic cell (DC) homeostasis and the development of several lymphocyte subsets belonging to the innate immune system have been reported to be regulated by Notch³². Therefore, inappropriate immune responses against self-antigens could occur due to impaired regulation of Notch signaling. In experimental autoimmune encephalomyelitis (EAE) and non-obese diabetic (NOD) mice, which are mouse models for multiple sclerosis and type 1 diabetes (T1D), respectively, disease progression was impeded by the administration of blocking antibodies against Notch receptors or DLL4³². Therefore, higher endogenous levels of *POGLUT1* caused by the PBC-susceptible allele of rs2293370 may induce excessive Notch signaling and inappropriate immune responses against self-antigens. Very importantly, Notch signaling is also involved in the development or formation of intrahepatic bile ducts. Mutations in *JAG1* or *Notch2* are known causes of Alagille syndrome, an autosomal dominant disease characterized by congenital cholangiopathy with jaundice and bile duct paucity^{33–35}. *POGLUT1* was shown to regulate the number of bile ducts around portal veins in a *JAG1*-dependent manner using *JAG1*^{+/-} and *POGLUT1*^{+/-} mice³⁶. These results indicate that *POGLUT1* might be involved in the mechanism of bile duct loss in PBC. However, a limitation of this study was that endogenous *POGLUT1* expression levels in PBC patients were not examined in this study. Additional studies are warranted to improve our understanding of the relationship between PBC pathogenesis and *POGLUT1*.

A more than 100-kb stretch of the genome is located in chromosome 3q13.33 that includes *ARHGAP31*, *TMEM39A*, *POGLUT1*, *TIMMDC1*, and *CD80*. In addition to the present study on the Japanese population, this

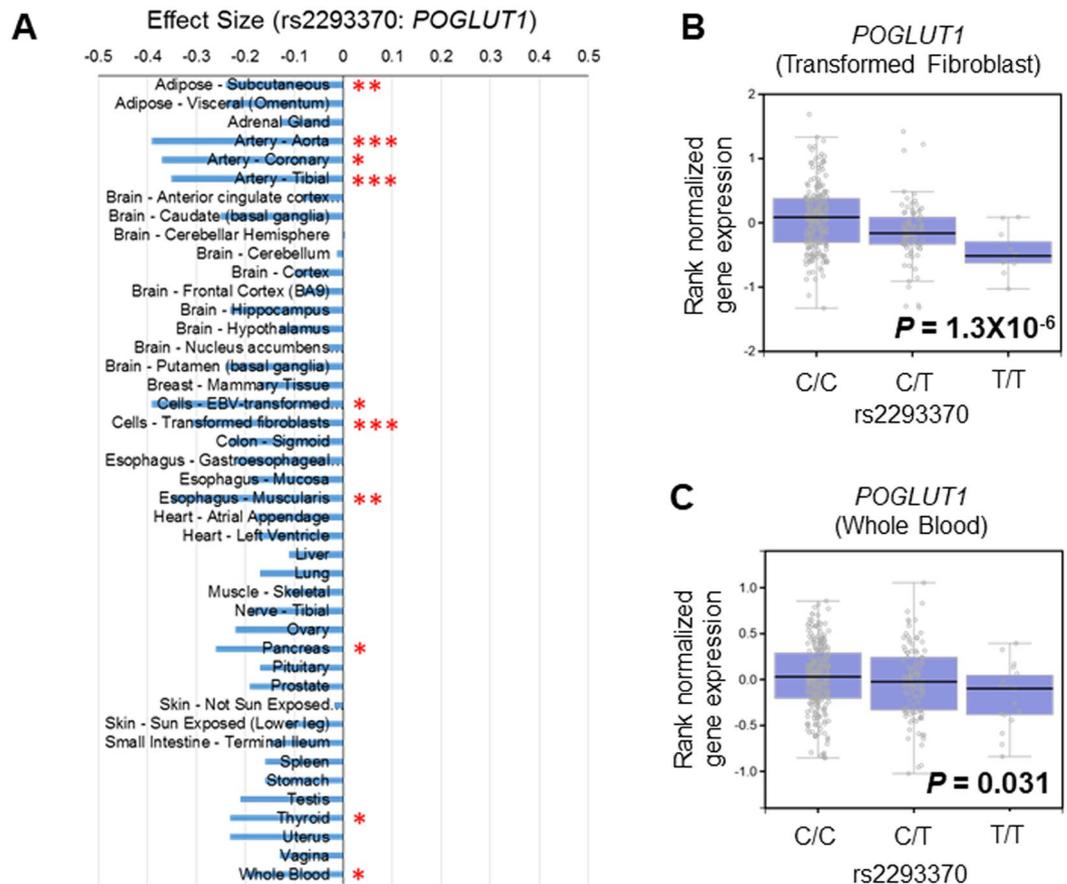


Figure 4. rs2293370 genotypes are associated with differences in endogenous *POGLUT1* expression levels. (A) The relationship between rs2293370 genotype and the endogenous expression of *POGLUT1* was compared in all tissues registered in the GTEX database. The effect sizes of the rs2293370 minor allele (T allele; disease protective) in every organ are shown. Statistical significance levels before Bonferroni multiple comparison correction were $P = 0.00116$. * $P_c < 0.05$, ** $P_c < 0.005$, and *** $P_c < 0.0005$, after Bonferroni multiple comparison correction. (B and C) Box plots showing the association between endogenous *POGLUT1* expression and rs2293370 genotypes in (B) Transformed Fibroblast and (C) Whole Blood.

to T cell receptor (TCR). *CD80* had been assumed as a candidate effector gene in previous GWASs, whereas our approach identified *POGLUT1* as the target transcript for disease susceptibility in this locus comprehensively without stereotypes. Of the PBC susceptibility genes identified in the Japanese population, we previously identified the primary functional SNPs of *TNFSF15*, *PRKCB*, and chromosome 17q12-21, and their effector genes^{16,22,41}, as well as chromosome 3q13.33 in the present study. Similar post-GWAS approaches for susceptibility genes are needed to further clarify the molecular mechanisms of disease development.

Materials and Methods

Subjects. DNA samples for GWAS using the Japonica array platform were collected from 1,148 individuals (668 PBC cases and 480 healthy controls). The demographics of the PBC cases and controls are shown in Supplementary Table 1.

Written informed consent was obtained from all participants. The protocol of this study was approved by the committee on research ethics and genetically modified organisms of the Graduate School of Medicine, The University of Tokyo, by the ethics committees of Nagasaki Medical Center, and by the ethics committees of Tohoku Medical Megabank Organization, Tohoku University. All experiments were performed in accordance with relevant guidelines and regulations.

Genotyping, quality control, and genotype imputation. Genotyping was performed using the Japonica V1 array (1,148 Japanese individuals in the present study; Affymetrix Japan). Genotype calling was performed with the apt-probeset-genotype program in Affymetrix Power Tools ver. 1.18.2 (Thermo Fisher Scientific Inc., Waltham, MA). Sample quality control was conducted by following the manufacturer's recommendation (dish QC > 0.82 and sample call rate > 97%). Clustering of each SNP was evaluated by the P_s classification function in the SNPcluster package (version 1.5.2, Thermo Fisher Scientific Inc.). SNPs that were assigned "recommended" by the P_s classification function were used for downstream analyses. SNPs that satisfied the following criteria were used for genotype imputation: a call rate > 99.0%, a Hardy-Weinberg Equilibrium (HWE) p -value > 0.0001, and a minor allele frequency (MAF) > 0.5%. Pre-phasing was conducted with EAGLE v2.3.2⁴²

with default settings. Genotype imputation was conducted with IMPUTE4 v1.0⁴³ using a phased reference panel of 2,049 Japanese individuals from a prospective, general population cohort study performed by the Tohoku Medical Megabank Organization (ToMMo)^{44,45}. These procedures were conducted using default settings. Cryptic relatives were excluded using PRIMUS⁴⁶ with default settings. In addition, principal component analysis (PCA) was performed using East Asian samples from the International 1000 Genome Project (104 JPT, 103 CHB, 93 CHS, 91 CDX, and 99 KHV samples) in addition to the case and control samples. PCA identified outliers to be excluded using the Smirnov–Grubbs test with a Bonferroni corrected p-value < 0.05. We had previously analyzed the data (2,897 Japanese individuals) using the Axiom Genome-Wide ASI 1 Array¹⁶ and re-analyzed the data using the above-mentioned procedures.

Association analysis and meta-analysis. Association analysis was performed with PLINK (version 1.9) in each dataset (i.e., 2,897 ASI array data and 1,148 Japonica array data). The following options were used for PLINK: a call rate > 97.0%, a HWE p-value > 0.000001, a minor allele frequency (MAF) > 0.1%, and a logistic regression model.

Meta-analysis was performed using PLINK with the meta-analysis option after excluding duplicates between the two datasets. The fixed-effects meta-analysis p-value was used.

Databases. The probability that a candidate functional variation might influence transcription regulation was evaluated using the RegulomeDB database (<http://www.regulomedb.org/index>)²⁶ and the UCSC genome browser (<http://genome.ucsc.edu/index.html>)²⁷. Transcription factor binding was predicted using TRANSFAC Professional (QIAGEN, Valencia CA; <http://www.gene-regulation.com/pub/databases.html>)²⁸. Gene expression levels in each cell line and the correlation between the genotypes of candidate SNPs and gene expression were examined using GeneCards (<http://www.genecards.org/>) and the GTEx portal database (<http://gtexportal.org/home/>), respectively^{25,29}. P values < 0.05, after adjustment for multiple testing (Bonferroni correction), were regarded as statistically significant.

Electrophoretic mobility shift assay (EMSA). EMSA was performed using a LightShift Chemiluminescent EMSA Kit (Thermo-Fisher Scientific) and biotin-labeled double-stranded oligonucleotide probes corresponding to each major and minor allele (Supplementary Table 2), according to the manufacturer's instructions. These oligonucleotide probes (10 fmol/μL) and a nuclear extract (2.5 μg/mL) of HepG2 or Jurkat cells (Nuclear Extract Kit; Active Motif, Carlsbad, CA) were incubated together for 30 min at 25 °C.

The super-shift assay was performed by incubating the biotin-labeled probe with the nuclear extracts for 30 min at 25 °C, before subsequently incubating these complexes with Anti-RUNX1/AML1 antibody - ChIP Grade (ab23980) (Abcam, Cambridge, UK) for 30 min at 25 °C.

Each assay was independently performed three times.

Luciferase reporter assay. Amplicons of part of the 2nd intron of *TIMMDC1*, which contain each allele of rs2293370, were obtained from human genomic DNA using specific PCR primers (Supplementary Table 3) and were then subcloned into the luciferase reporter pGL4.23 (luc2/minP) vector (Promega, Madison, WI). pGL4.23 constructs (500 ng) of each allele and 50 ng of the pGL4.74 (hRLuc/TK) vector as an internal control were transfected into Jurkat and HepG2 cells using Lipofectamine 3000 (Thermo-Fisher Scientific). The Dual-Luciferase Reporter Assay system (Promega) was used to measure luciferase activity. Differences in relative luciferase activity were compared between the major and minor alleles of each SNP using Student's *t*-test. P values < 0.05 were regarded as statistically significant. Each figure shows representative data from experiments performed independently three times. The data in the figures represent the mean ± standard deviation of triplicate assays in a single experiment.

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Author Contributions

Y.H. and K.U. wrote the main manuscript text and made the Tables and Figures. Y. Kawai, N. Nishida, K.K., M. Kawashima, Y.A., M. Nagasaki, M. Nakamura and K.T. contributed to materials of the research and reviewed the manuscript. H. Nakamura, Hiroshi Kouno, Hirotaka Kouno, H. Ota, K.S., T.N., T.Y., S. Katsushima, T. Komeda, K. Ario, A.N., M. Shimada, N.H., K. Yoshizawa, F.M., K.F., M. Kikuchi, N. Naeshiro, H. Takahashi, Y. Mano, H. Yamashita, K. Matsushita, S.T., I.Y., H. Nishimura, Y.S., K. Yamauchi, T. Komatsu, R.S., H. Sakai, E.M., M. Koda, Y.N., H. Kamitsukasa, T.S., M. Nakamura, N.M., H. Takikawa, A. Tanaka, H.O., M.Z., M.A., S. Kaneko, M. Honda, K. Arai, T.A.H., E.H., M.T., T.U., S.J., K.N., T.I., H. Shibata, A. Takaki, S.Y., M. Seike, S. Sakisaka, Y.T., M. Harada, M. Senju, O.Y., T. Kanda, Y.U., H.E., T.H., K. Murata, S. Shimoda, S.N., S.A., A.K., K. Migita, M.I., H. Yatsuhashi, Y. Maehara, S.U. and N.K. contributed to collecting DNA samples.

Additional Information

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