A Refined Study of FCRL Genes from a Genome-Wide Association Study for Graves’ Disease

Shuang-Xia Zhao1,2,*, Wei Liu1,*, Ming Zhan1, Zhi-Yi Song1, Shao-Ying Yang1, Li-Qiong Xue1, Chun-Ming Pan1, Zhao-Hui Gu1,3, Bing-Li Liu1, Hai-Ning Wang1, Liming Liang4, Jun Liang5, Xiao-Mei Zhang6, Guo-Yue Yuan7, Chang-Gui Li8, Ming-Dao Chen9, Jia-Lun Chen2, Guan-Qi Gao9,*, Huai-Dong Song1,2, The China Consortium for the Genetics of Autoimmune Thyroid Disease1

1 State Key Laboratory of Medical Genomics, Molecular Medicine Center, Ruijin Hospital Affiliated to Shanghai Jiao Tong University (SJTU) School of Medicine, Shanghai, China; 2 Department of Endocrinology, Shanghai Institute of Endocrinology and Metabolism, Ruijin Hospital Affiliated to SJTU School of Medicine, Shanghai, China; 3 Shanghai Center for Systems Biomedicine, SJTU, Shanghai, China; 4 Department of Epidemiology and Biostatistics, Harvard School of Public Health, Boston, Massachusetts, United States of America; 5 Department of Endocrinology, The Central Hospital of Xuzhou Affiliated to Xuzhou Medical College, Xuzhou, Jiangsu Province, China; 6 Department of Endocrinology, The First Hospital Affiliated to Bengbu Medical College, Bengbu, Anhui Province, China, 7 Department of Endocrinology, The Hospital Affiliated to Jiangsu University, Zhenjiang, Jiangsu Province, China; 8 Department of Endocrinology, Gout Laboratory, Medical School Hospital of Qingdao University, Qingdao, Shandong Province, China; 9 Department of Endocrinology, Linyi People’s Hospital, Linyi, Shandong Province, China

Abstract

To pinpoint the exact location of the etiological variant/s present at 1q21.1 harboring FCRL1-S and CD5L genes, we carried out a refined association study in the entire FCRL region in 1,536 patients with Graves’ disease (GD) and 1,516 sex-matched controls by imputation analysis, logistic regression, and cis-eQTL analysis. Among 516 SNPs with P<0.05 in the initial GWAS scan, the strongest signals associated with GD and correlated to FCRL3 expression were located at a cluster of SNPs including rs7528684 and rs3761959. And the allele-specific effects for rs3761959 and rs7528684 on FCRL3 expression level revealed that the risk alleles A of rs3761959 and C of rs7528684 were correlated with the elevated expression level of FCRL3 whether in PBMCs or its subsets, especially in CD19+ B cells and CD8+ T subsets. Next, the combined analysis with 5,300 GD cases and 4,916 control individuals confirmed FCRL3 was a susceptibility gene of GD in Chinese Han populations, and rs7528684 and rs7528684 met the genome-wide association significance level ($P_{\text{combined}} = 2.27 \times 10^{-12}$ and 7.11 $\times 10^{-11}$, respectively). Moreover, the haplotypes with the risk allele A of rs3761959 and risk allele C of rs7528684 were associated with GD risk. Finally, our epigenetic analysis suggested the disease-associated C allele of rs7528684 increased affinity for NF-kB transcription factor. Above data indicated that FCRL3 gene and its proxy SNP rs7528684 may be involved in the pathogenesis of GD by excessive inhibiting B cell receptor signaling and the impairment of suppressing function of Tregs.

Citation: Zhao S-X, Liu W, Zhan M, Song Z-Y, Yang S-Y, et al. (2013) A Refined Study of FCRL Genes from a Genome-Wide Association Study for Graves’ Disease. PLOS ONE 8(3): e57758. doi:10.1371/journal.pone.0057758

Editor: Massimo Pietropaolo, University of Michigan, United States of America

Received: October 20, 2012; Accepted: January 24, 2013; Published: March 7, 2013

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Funding: This work was supported in part by the National Natural Science Foundation of China (30971595, 30971383, 81100553, 81200568, 81270863, and 31171127), National Basic Research Program of China (973) (2010CB529204 and 2012CB517604), Shanghai Science and Technology Committee (10JC1410400), Program for Graves’ Disease Innovative Research Team of Shanghai Municipal Education Commission, and Natural Science Foundation of Jiangsu Province, China (BK2009208 and SBK201221245). 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.

* E-mail: lygqgao@163.com (GQG); huaidong_s1966@163.com (HDS)

† These authors contributed equally to this work.

†† Membership of The China Consortium for the Genetics of Autoimmune Thyroid Disease is provided in the Acknowledgments

Introduction

Graves’ disease (GD), the most frequent form of autoimmune thyroid disease (AITD), is triggered by the combination of genetic susceptibility and environmental encounters. Using the candidate gene strategy, several susceptibility genes for GD have been validated in different ethnic populations and have been divided into two classes: one class is immune-related genes, such as HLA on 6p21 [1,2], CTLA-4 on 2q33 [3,4], CD40 on 20q12 [5,6], PTPN22 on 1p13 [7–9], as well as SCGB3A2 on 5q31 [10–12]; and the other class is thyroid-specific gene, such as TSHR on 14q31 [13,14].

FC receptor-like-3 (FCRL3, also known as CD307c) on 1q21.1 encodes a member of the immunoglobulin receptor superfamily and is one of several Fc receptor-like glycoproteins. The encoded protein of FCRL3 contains immunoreceptor-tyrosine activation motifs and immunoreceptor-tyrosine inhibitory motifs in its cytoplasmic domain and may play a role in regulation of the immune system. The 1p21–23 region, in which the FCRL family resides, has been identified as a candidate locus for multiple autoimmune disorders in both human and murine models [15]. Mutations in FCRL3 have been reported to be associated with a plethora of autoimmune diseases, such as rheumatoid arthritis, systemic lupus erythematosus, and AITD [16–18]. Recently, two genome-wide association studies (GWAS) from Wellcome Trust Case Control Consortium (WTCCC) and our group, both identified FCRL3 as a susceptibility gene of GD in individuals of European ancestry and Chinese Han populations, respectively.
After the WTCCC GWAS, a case-control association study investigating twelve tag SNPs within FCRL5 was performed in 2,304 UK Caucasian patients with GD and 2,688 geographically matched controls and the results suggested that the association of FCRL5 with GD is secondary to the effect of FCRL3 [21]. Nevertheless, a refined association study in the entire FCRL region is required to determine the exact location of the etiological variant’s present.

In this study, we refined the association in the 1q21.1 region harboring FCRL1-5 and CD5L, and confirmed FCRL3 was a susceptibility gene of GD in Chinese Han populations and the most significant signals associated with GD and correlated to FCRL3 expression were located at a cluster of SNPs including rs3761959 and rs7528684. Moreover, the haplotypes with the risk allele A of rs3761959 and the risk allele C of rs7528684 were associated with the predisposition of GD and can up-regulate the mRNA expression level of FCRL3, whether in peripheral blood mononuclear cells (PBMCs) or the subsets of PBMCs, especially in CD19+ B cells and CD8+ T subsets. Finally, the risk allele C of rs7528684 can increase the binding with NF-KB transcription factor, resulting in the pathogenesis of GD.

Materials and Methods

Subjects

All samples were recruited from Chinese Han population through collaboration with multiple hospitals in China. This study was approved by the ethics committee committee from Ruijin Hospital, the Central Hospital of Xuzhou, the first affiliated hospital of Bengbu Medical College, Medical School Hospital of Qingdao University, and Linyi People’s Hospital, respectively. All subjects in this study provided written informed consent using protocols approved by local ethics committee. As mentioned in our previous GWAS paper, 1,536 patients with GD and 1,516 sex-matched controls were recruited for the initial GWAS stage, and additional 3,994 patients with GD and 3,510 sex-matched controls were recruited for the replication study [4,10,20]. Diagnosis of GD was based on documented clinical and biochemical evidence of hyperthyroidism, diffuse goiter, and the presence of at least one of the following: positive TRAb tests, diffusely increased 131I uptake in thyroid gland, or exophthalmos [4,10,20]. All individuals classified as GD were interviewed and examined by experienced clinicians.

All the 1,516 controls in the GWAS stage were individuals with neither GD nor family history of GD, and without any other autoimmune disorders. Control subjects were matched for sex with cases and were over 35 years. Since GD or other AITD has a preponderance in the young female population, this age criteria could reduce the number of controls who might develop GD later on. To exclude clinical or sub-clinical AITD, the levels of sensitive TSH (sTSH) and TPOAb in control subjects were measured using chemiluminescence immunoassay (CLIA) in our laboratory. Of the 1,832 healthy controls whose levels of sensitive TSH and TPOAb were measured, 257 individuals with the levels of TPOAb ≥5.61 U/ml and 94 subjects with the levels of sensitive TSH ≥4.94 µU/ml or ≤0.35 µU/ml were excluded, the remaining 1,516 served as the control cohort in the GWAS stage [20].

Genotyping and Quality Control

GWAS was performed by Illumina Human660-Quad BeadChips [20]. Genotype clustering was conducted using Illumina GenomeStudio V2011.1 software based on the 660W-Quad_v1_H manifest files. This software, which is used to convert the fluorescence intensities into SNP genotypes, was different from the software used in the previously published GWAS paper [20].

The mean call rate across all samples was 99.8%. Quality filtering was performed on SNPs and samples before analysis to ensure robust association tests. Cryptic relationships between genotyped individuals were examined using pairwise identity-by-descent (IBD) estimation by PLINK software [20]. To maintain the maximum number of available samples, all the pairwise relationships were evaluated and the person who formed the node that related to the most other nodes in the family trees was first excluded. This process was iterated several times until the remaining samples were not related to one another.

Of the 653,214 markers assayed, 3,185 that were from the Y or mitochondrial chromosomes or were CNV-related were excluded. Next, 168,062 markers with Hardy-Weinberg equilibrium $P \leq 10^{-6}$, with genotype call rates below 90%, or with a minor allele frequency (MAF) < 0.01 were discarded, leaving 403,947 SNPs for subsequent analysis. After removing samples with low call rates (< 98%, n = 23), gender inconsistencies (n = 6), and cryptic relatedness (n = 113), 2,910 samples were available for further association analysis.

In the replication cohort, six SNPs on 1q21.1 were genotyped using TaqMan SNP Genotyping Assays in Fluidigm EP1 platform [20], and one SNP (rs7528684) was genotyped using ABI 7900HT platform. Of the seven SNPs genotyped, none of SNPs was removed for further association analysis. Ultimately, 3,653 GD patients and 3,303 controls with a 100% call rate were analyzed in the replication cohorts.

Statistical Analysis

After quality control [20], we used the genotypes of 67 SNPs on 1q21.1 in 1,442 patients with GD and 1,468 controls for association analysis using the Cochran-Armitage trend test by PLINK [22]. The forward and two locus logistic regression analysis were performed using R statistics packages. The linkage disequilibrium (LD) block was analyzed by Haplovew software version 4.2.

The genotype imputation was performed using IMPUTE2 software [23] and the updated 1000G phase 1 integrated variant set [Mar 2012] were used as a reference. Of the imputed SNPs, we analyzed only those that could be imputed with a relatively high confidence (estimated probability > 0.9), had a MAF > 1%, a genotype call rate > 98%, and a Hardy-Weinberg equilibrium $P$-value $> 10^{-6}$. To take into account the uncertainty of imputed SNPs, the association analysis of the imputed SNPs was carried out utilizing the SNPTEST v2 software [24].

We inspected three eQTL databases from European Caucasian population. One was developed by Dixon et al, and contained 405 children of British descent organized into 206 sibships including 297 sib pairs and 11 half-sib pairs [25]. Another database assessed the transcriptome of circulating monocytes from 1,490 German individuals [26]. The third database was the cell type-specific eQTLs relevant to immunity and inflammation in paired samples of primary monocytes and B cells, purified by positive selection directly from 283 healthy British individuals [27].

For the replication stage, the Cochran-Armitage test for trend was used to examine the associations. Association analysis in the combined samples was performed by Cochran-Mantel-Haenzel stratification analysis [22]. We examined heterogeneity among studies using the Breslow-Day test [22,23]. The genome-wide significance level was set at $5 \times 10^{-8}$, in keeping with the current consensus of the field.
Figure 1. Regional plots of association results, logistic regression analysis, and cis-eQTL analysis at 1q21.1 and expression analysis of FCRL3. Panel A shows the GD association of 67 genotyped and 972 imputed SNPs in the GWAS samples. The color of each genotyped SNP spot reflects its $r^2$ with the top SNP within each association locus shown as a large red diamond, and smaller values changing from red to white. Genetic recombination rates are shown in cyan. Genetic recombination rates, estimated using the 1000 Genomes pilot 1 CHB and JPT samples, are showing
Real-time RT-PCR

Blood samples (10 ml) were collected from 95 unrelated healthy Chinese Han volunteers for gene expression analysis in PBMCs. Samples with more blood volume (100 ml) were donated by these 95 individuals for gene expression assay in distinct subpopulations of PBMCs. The expression levels of 1,490 individuals. Panel C shows the cis-eQTL analysis of 516 SNPs with $P<0.05$ in the initial GWAS scan from three different cis-eQTL databases. Panel C shows plot of linkage disequilibrium (LD) structures at 1q21.1 and correlation of SNPs to transcript abundances of FCRL3 and FCRL5 at 1q21.1 in transcriptome data from about 400 lymphoblastoid cell lines. The LD structures of 1,039 SNPs at 1q21.1 were analyzed by Haploview software version 4.2 based on our imputed data. The LD color scheme is stratified according to the logarithm of the odds (LOD) score and $D^\prime$: LOD $<2$ (white for $D^\prime<1$ and blue for $D^\prime=1$) or LOD $>2$ (shades of pink/red for $D^\prime<1$ and bright red for $D^\prime=1$). Two different red crosses indicate the association results of SNPs to the expression level of FCRL3. Three different blue signs indicate the correlation results of SNPs to the expression level of FCRL5. Panel D shows the correlation of 10 SNPs to transcript abundances of FCRL3 in the transcriptome of circulating monocytes from 1,490 individuals. Panel E shows the correlation of SNPs to the expression of FCRL5 in both-cis dataset of the cell type-specific cis-eQTL database. The expression levels of FCRL3 in B cell and monocyte were shown in red and blue color, respectively. FCRL3 expression detected by different probe was shown in two different crosses. Panel F shows the correlation of SNPs to the expression of FCRL3 and FCRL5 in B-cis dataset of the cell type-specific cis-eQTL database. The expression of FCRL3 was shown in different red signs and that of FCRL5 was shown in blue. Panel G shows the relative mRNA expression levels of FCRL3 for different genotypes of rs3761959 and rs7528684 in PBMCs from 95 individuals (GG and TT, n = 29; GA and TC, n = 47; and GG and CC, n = 19). Panel H shows the relative mRNA expression levels of FCRL3 for different genotypes of rs3761959 and rs7528684 in the subset of PBMCs from above 95 individuals: *, $P<0.05$; **, $P<0.01$; ***, $P<0.001$.

doi:10.1371/journal.pone.0057758.g001

Results

The association and cis-gene expression (cis-eQTL) analysis in the initial GWAS scan cohort.

Our previous two-staged GWAS illustrated that FCRL3 was a predisposing gene of GD on 1q21.1 harboring FCRL1-5 and CD5L genes [20]. To pinpoint the exact location of the etiological variant/s present, we carried out the imputation analysis in the initial scan cohorts with 1,031 SNPs (except 7 SNPs with high LD within a 124 SNPs with $P<0.0001$ using R statistics packages and the results displayed that rs761959 was an independent variant in the original scan cohort. Next, the two locus logistic regression analysis was performed to confirm the independent variant. As shown in Figure 1B, rs761959 selected as the best SNP on 1q21.1, was put individually into the regression models, and all other markers were sequentially added to see if a second locus could improve the model. The two locus regression results in the original scan manifested that none of 1,031 SNPs (except 7 SNPs with high LD with rs761959, $r^2>=0.99$, Figure S1A) improved the model with rs761959 at the $P<0.001$ level (Figure 1B). Conversely, the majority of SNPs, except for 50 SNPs with significant $P$ value with the GD risk ($P=<2.30\times10^{-6}$; Figure S1B) and within a high LD region ($\gamma>0.70$; Figure S1A), were improved by adding rs761959 (Figure 1B). The logistic regression analysis could not pinpoint which SNP was the independent variant among a cluster of SNPs in a high LD block.

To further determine the most significant variant correlated with the FCRL1-5 expression within 1q21.1 region, we carried out the cis-eQTL analysis for the 516 SNPs with $P<0.05$ in the GWAS scan cohort (Figure 1A, Table S1). From the cis-eQTL analysis using transcriptome data from about 400 lymphoblastoid cell lines [25], we found that the expression level of FCRL3 was associated with a cluster of SNPs, with the strongest signal at rs7528684 ($P=3.38\times10^{-11}$ for probeset 231093_at; Figure 1C). Other three SNPs (rs2210913, rs3761959, and rs945635), which were all in high LD with rs7528684 ($r^2=1$ in our data, Figure S1A), also exhibited the significant correlation with FCRL3 expression ($P<1.00\times10^{-10}$ for probeset 231093_at; Figure 1C). Furthermore, the four SNPs also showed the eQTL effect on the expression of FCRL5 ($P<5.77\times10^{-8}$ for probeset 224405_at; Figure 1C). Nonetheless, among a cluster of SNPs with the association with FCRL5 expression, the strongest signal was located at rs6679793 ($P=5.90\times10^{-18}$ for probeset 224405_at; Figure 1C), which was not in high LD with any SNP associated with the FCRL3 expression and was weakly associated with GD in the original GWAS scan, in FCRL5 ($\gamma<0.12$, $P_{GWAS}=0.0252$; Figure 1A, Figure S2, and Table S1).

Additionally, we inspected a cis-eQTL database assessing the transcriptome of circulating monocytes from 1,490 individuals [26] and found rs7528684 was correlated with FCRL3 expression level ($P=1.41\times10^{-8}$; Figure 1D). Also, two SNPs (rs6681272 and rs7522061), which were in high LD with rs7528684 and rs761959 ($r^2=0.99$, Figure S1A), displayed the high correlation with FCRL3 ($P=1.89\times10^{-8}$ and $1.65\times10^{-8}$; Figure 1D).
![Table 1. The association results of seven SNPs on 1q23.1 in the combined populations.](image-url)

| SNP       | Gene region | Allele/ Genotype | N (%) | OR (95% CI) | P     | N (%) | OR (95% CI) | P     | N (%) | OR (95% CI) | P     |
|-----------|-------------|------------------|-------|-------------|-------|-------|-------------|-------|-------|-------------|-------|
| rs10908583| C           | 1,451 (53.2)     | 1,422 (52.6) | 1.00 (ref)  |      | 1,433 (50.3) | 1,462 (53.9) | 1.00 (ref)  |      | 3,648 (53.9) | 3,777 (53.8) | 1.00 (ref)  |
|           | T           | 1,383 (46.8)     | 1,322 (47.4) | 1.22 (1.13–1.33) | 0.0003 | 1,383 (49.7) | 1,403 (46.1) | 1.22 (1.13–1.33) | 0.0003 | 3,648 (46.1) | 3,933 (46.2) | 1.13 (1.06–1.21) |
|           | CCG         | 385 (12.6)       | 312 (11.0)   | 0.94 (0.86–1.02) | 0.22  | 385 (12.6) | 312 (11.0)   | 0.94 (0.86–1.02) | 0.22  | 770 (12.0) | 724 (11.2) | 1.00 (ref)  |
|           | CTC         | 900 (30.1)       | 720 (25.4)   | 1.16 (1.07–1.25) | 0.0003 | 900 (30.1) | 720 (25.4)   | 1.16 (1.07–1.25) | 0.0003 | 1,800 (30.0) | 1,440 (24.0) | 1.04 (1.00–1.08) |
|           | G           | 1,422 (53.5)     | 1,451 (53.2) | 1.00 (ref)  |      | 1,462 (53.9) | 1,422 (53.5) | 1.00 (ref)  |      | 3,777 (53.8) | 3,648 (53.9) | 1.00 (ref)  |
| rs2210911 | A           | 3,057 (46.1)     | 2,658 (42.7) | 1.12 (1.05–1.19) | 0.0003 | 3,057 (46.1) | 2,658 (42.7) | 1.12 (1.05–1.19) | 0.0003 | 6,114 (47.1) | 5,316 (46.5) | 1.05 (1.01–1.09) |
|           | AAG         | 707 (10.9)       | 627 (10.2)   | 0.98 (0.88–1.09) | 0.56  | 707 (10.9) | 627 (10.2)   | 0.98 (0.88–1.09) | 0.56  | 1,414 (2.3) | 1,254 (2.3) | 1.00 (ref)  |
|           | AG          | 1,422 (53.5)     | 1,451 (53.2) | 1.00 (ref)  |      | 1,462 (53.9) | 1,422 (53.5) | 1.00 (ref)  |      | 3,777 (53.8) | 3,648 (53.9) | 1.00 (ref)  |
| rs2260040 | A           | 2,388 (82.6)     | 2,552 (86.9) | 1.00 (ref)  |      | 2,438 (82.8) | 2,552 (86.9) | 1.00 (ref)  |      | 4,926 (83.1) | 4,954 (83.1) | 1.00 (ref)  |
|           | AA          | 673 (22.1)       | 603 (20.7)   | 0.91 (0.82–1.02) | 0.15  | 673 (22.1) | 603 (20.7)   | 0.91 (0.82–1.02) | 0.15  | 1,346 (22.2) | 1,206 (20.7) | 1.00 (ref)  |
|           | AG          | 395 (13.7)       | 345 (12.2)   | 0.96 (0.86–1.07) | 0.64  | 395 (13.7) | 345 (12.2)   | 0.96 (0.86–1.07) | 0.64  | 780 (13.3) | 740 (13.3) | 1.00 (ref)  |

**PLOS ONE** | www.plosone.org 5 March 2013 | Volume 8 | Issue 3 | e57758
Ultimately, we also inspected a cell type–specific cis-eQTL database relevant to immunity and inflammation in purified B-cell and monocyte populations [27]. Of note, in the both-cis dataset, among a cluster of SNPs correlated with the expression of FCRL3, rs7528684 displayed higher correlation in the B cell.

| SNP       | Gene region | Chr. Position | Allele/ Cases Control | N (%) | OR (95% CI) | P     |
|-----------|-------------|---------------|-----------------------|-------|-------------|-------|
| rs7528684 | CD5L        | intron 1      | GG                    | 40 (2.8) | 1.62 (0.99–2.65) | 0.2494 |

SNP: single nucleotide polymorphism, N-number, OR- odds ratio for the minor allele, 95% CI- 95% confidence interval. We report a 1-df test P-value for allelic effects and a 2-df test P-value for genotype effects.

doi:10.1371/journal.pone.0057758.t001

Figure 2. Regional plots of association results and logistic regression analysis in the combined population at 1q21.1.
Panel A shows the linkage disequilibrium block analysis for the 12 SNPs with $P_{GWAS} < 0.0001$, which can be tagged by seven replicated SNPs in the combined population by using haploview software 4.2. Panel B shows the GD association of seven replicated SNPs in the combined population. The color of each genotyped SNP spot reflects its $r^2$ with the top SNP within each association locus shown as a large red diamond, and smaller values changing from red to white. Genetic recombination rates are shown in cyan. Genetic recombination rates, estimated using the 1000 Genomes pilot 1 CHB and JPT samples, are shown cyan. Physical positions are based on NCBI build 36. Panel C shows the two locus logistic regression results for seven SNPs at 1q21.1 in the combined population. The SNPs were improved by adding rs7528684 were shown in red points; whereas, the SNPs improved the model with rs7528684 were showed in blue triangles.

doi:10.1371/journal.pone.0057758.g002
**Table 2.** Frequencies of the haplotypes on 1q23.1 in the combined population.

| Haplotype | Control N(%) | Case N(%) | P     | OR (95% CI) |
|-----------|--------------|-----------|-------|-------------|
| T G A C G G | 1199 (12.4)  | 1476 (14.5) | 1.15 × 10⁻⁵ | 1.20 (1.11–1.30) |
| T G A C A G A | 1230 (12.7)  | 1405 (13.8) | 0.0214 | 1.10 (1.01–1.20) |
| T A A C A G A | 543 (5.6)    | 669 (6.6) | 0.0044 | 1.18 (1.05–1.33) |
| C A G T A G A | 562 (5.8)    | 633 (6.2) | 0.2154 | 1.08 (0.96–1.21) |
| T G G T A A A | 454 (4.7)    | 468 (4.6) | 0.7677 | 0.98 (0.86–1.12) |
| T A A C A G A | 534 (5.5)    | 490 (4.8) | 0.0262 | 0.87 (0.76–0.98) |
| C A G T A A A | 4668 (48.2)  | 4511 (44.3) | 4.73 × 10⁻⁸ | 0.86 (0.81–0.91) |

Bold letters indicate those haplotypes with significant differences between GD and normal subjects. All data shown here are haplotypes whose frequencies are more than 2%.

doi:10.1371/journal.pone.0057758.t002

(\(P = 7.43 \times 10^{-33}\) for nuID KV7kDSLO4uggquLXB4 and \(P = 5.93 \times 10^{-26}\) for nuID 67umrLpPjv_xuOezU; Figure 1E) than that in the mono-cell (\(P = 2.35 \times 10^{-26}\) for nuID KV7kDSLO4uggquLXB4 and \(P = 0.0001\) for nuID 67umrLpPjv_xuOezU; Figure 1E). In the B cell-cis dataset, rs7528684 also manifested the highest correlation with FCRL3 expression (\(P = 2.37 \times 10^{-30}\) for nuID ZUclXxUi6VEoBJeRT8; Figure 1F).

To confirmed the cis-eQTL analysis, We then evaluated allele-specific effects for rs3761959 and rs7528684 on the mRNA expression of FCRL3 gene in PBMCs from 95 individuals and the result revealed both genotypes were correlated with the expression levels of FCRL3 (\(P = 0.0009\) for nuID 67umrLpPjv_xuOezU; Figure 1G). We then detected the expression of FCRL3 in distinct PBMC populations. Although FCRL3 was expressed in all subsets of PBMCs, there were higher expression levels of FCRL3 in CD19⁺ B cells and CD8⁺ T subsets than those in CD4⁺ T subsets and CD14⁺ monocytes (Figure 1H). More specifically, both risk alleles A of rs3761959 and C of rs7528684 can significantly up-regulate the mRNA level of FCRL3 in all subsets of PBMCs, especially in CD19⁺ B cells and CD8⁺ T subsets isolated from 95 healthy volunteers (\(P = 0.0001\) in CD4⁺ T subsets, \(1.72 \times 10^{-5}\) in CD8⁺ T subsets, 0.0122 in CD14⁺ monocytes, and 9.05 × 10⁻⁷ in CD19⁺ B cells; Table 1; Figure 1H).

**The Association Analysis in the Replication and Combined Cohort**

Among the 124 SNPs with \(P < 0.0001\) in FCRL3-CD5L gene region, 11 SNPs were genotyped and 113 SNPs were imputed in the initial scan (Figure 1A, Table S1, and Figure S1A). Next, six genotyped SNPs tagging 11 genotyped SNPs with \(P < 0.0001\) and one imputed SNP (rs7528684), which were all related to FCRL3 expression, were genotyped in the second cohort (Figure 2A). After quality control, the most significant association signal was observed at rs7528684 in 3,655 patients with GD and 3,385 controls (allele frequencies \(P_{\text{replication}} = 5.44 \times 10^{-7}, \text{OR} = 1.19, 95\% \text{CI} = 1.11–1.27; \) Table 1). Concordantly, among the seven SNPs genotyped for replication, rs7528684 displayed the highest significance in the combined datasets with 5,107 GD cases and 4,853 control individuals (allele frequencies \(P_{\text{combined}} = 7.11 \times 10^{-13}, \text{OR} = 1.23, 95\% \text{CI} = 1.16–1.30; \) and genotype distributions \(P_{\text{combined}} = 4.87 \times 10^{-12}, \text{TC: OR} = 1.20, 95\% \text{CI} = 1.19–1.21, \text{CC: OR} = 1.53, 95\% \text{CI} = 1.36–1.71; \) Table 1; Figure 2B). Meanwhile, rs3761959 also met the genome-wide association level in the combined cohort (allele frequencies \(P_{\text{combined}} = 2.27 \times 10^{-12}, \text{OR} = 1.22, 95\% \text{CI} = 1.16–1.30; \) and genotype distributions \(P_{\text{combined}} = 1.60 \times 10^{-12}, \text{GA: OR} = 1.19, 95\% \text{CI} = 1.09–1.30, \text{AA: OR} = 1.51, 95\% \text{CI} = 1.35–1.70; \) Table 1; Figure 2B). In addition, the forward and two-locus logistic regression analysis in the combined population demon-

**Figure 3.** The epigenetic analysis from the ENCODE database. The chromosome region containing rs7528684 displayed no DNaseI hypersensitivity and can bind the transcription factor. However, the region harboring rs3761959 shows no binding with the transcription factor.

doi:10.1371/journal.pone.0057758.g003
stratified that rs7528684 could not improve the model with rs3761959 and rs3761959 also could not improve the model with rs7528684 (Figure 2C).

Because multiple SNPs may act in combination to increase the risk of disease, haplotypes of the SNPs in the combined population were investigated and their frequencies in the GD and control groups were compared. The results displayed that seven haplotypes with a frequency of more than 4% were formed from seven SNPs and accounted for about 95% of all haplotypes (Table 2). Four of seven haplotypes exhibited significantly higher frequencies among individuals with GD than the control group. As shown in Table 2, the haplotype TGGACGG was the highest statistical difference \( (P=1.15 \times 10^{-8}, OR=1.20, 95\% CI=1.11-1.30) \); Table 2), followed by haplotypes TGGACAGA and TGGACAAA \( (P=0.0214, OR=1.10, 95\% CI=1.01-1.20); \) and \( P=0.0044, OR=1.18, 95\% CI=1.05-1.33, \) respectively; Table 2). In contrast, haplotypes CAGTAAA and TGTTAAA were more frequently observed in controls than in patients with GD \( (P=4.73 \times 10^{-9}, OR=0.86, 95\% CI=0.81-0.91); \) and \( P=0.0262, OR=0.87, 95\% CI=0.76-0.98, \) respectively; Table 2). Notably, all the risk haplotypes of GD contained the risk allele A of rs3761959 and risk allele C of rs7528684 and all the protected haplotypes of GD contained the protected allele G of rs3761959 and protected allele T of rs7528684 (Table 2).

Ultimately, we used the ENCODE databases of epigenetic study to narrow down the candidate regulatory regions and polymorphisms (http://genome.ucsc.edu/ENCODE/) [29]. The data from ENCODE manifested the chromosome region containing rs7528684 was without a DnaseI hypersensitivity, however, can bind the transcription factor (Figure 3). Also, we found the risk allele C of rs7528684 can bind the transcription factor NF-KB utilizing the Searching Transcription Factor Binding Sites (TFSEARCH, ver 1.3) (score: 96.9) [30]. The previous study also found rs7528684 could affect the FCRL3 expression in the luciferase assay [16]. Whereas, the chromosome region containing rs3761959 could not bind the transcription factors (Figure 3), suggesting the association between rs3761959 and GD because of its high LD with rs7528684.

The false positive report probability (FPRP) of the SNPs with significant association to GD in the combined Chinese Han cohort was also analyzed. In the present study, the FPRP value was calculated for each genetic variant using the assigned prior probability range, the statistical power to detect an odds ratio of 1.5, and detected odds ratios and \( P \) values. As shown in Table 3, among the seven genetic variants, the FPRP values of five SNPs were below 0.2 for the prior probability from 0.25 to 0.00001, which was a relatively high prior probability range. In addition, the FPRP values for rs7528684 were still the lowest even for a prior probability of 0.00001 (Table 3). Interestingly, the case-control association study for these seven SNPs with significant differences in allele frequencies between the 5,107 patients with GD and 4,853 control individuals has 100% statistical power to detect a SNP with a \( z \) level equal to their reported \( P \) value, corresponding to relative risks of 1.5 for GD (Table 3).

### Discussion

Our refined association study of the SNPs on 1q21.1 region verified that FCRL3 was the susceptibility gene for GD in the Chinese Han population. Moreover, the logistic regression analysis revealed that 8 SNPs including rs3761959 may be the most likely susceptibility variant. Cis-eQTL analysis from three databases indicated that the most significant signals correlated to the expression of FCRL3 were located at a cluster of SNPs including rs3761959 and rs7528684. In the combined population analysis, the risk haplotypes containing the risk allele A of rs3761959 and risk allele C of rs7528684 were associated with the predisposition of GD. Furthermore, the risk allele A of rs3761959 and risk allele C of rs7528684 increased FCRL3 expression whether in PBMCs or in its subsets, especially in CD19+ B cells and CD8+ T subsets. However, only rs7528684 can bind the NF-KB transcription factor to affect the FCRL3 expression. Intriguingly, the FPRP value for SNP rs7528684 was very low for the prior probability range and was quite robust even for low prior probabilities. These results suggested that rs7528684 in the promoter of FCRL3 was associated with GD etiology in the combined Chinese Han population.

The first reported variant about the association of FCRL3 with GD was rs7528684 located at position –169 in promoter of FCRL3 with GD in a Japanese population \( (P=7.4 \times 10^{-10}) \) [16], which was confirmed by the later study in 1,056 UK patients with GD and 864 controls \( (P=0.024) \) [31]. Our two-stage GWAS analysis also confirmed rs7528684 was associated with GD in Chinese Han population. Although there were two negative conclusions regarding association of rs7528684 in FCRL3 with GD in two small samples studies: one was in a Chinese population with 436 cases and 316 controls [32], and the other was in a UK population.

### Table 3. False positive report probability (FPRP) values for seven SNPs with significant difference between 5,300 patients with GD and 4,916 health individuals.

| SNP    | Odds ratio [95% CI] | Reported p-Value | Statistical power under recessive model* | Prior probability |
|--------|------------------|-----------------|----------------------------------------|-----------------|
| rs10098583 | 1.16 (1.10-1.23) | 8.55 \times 10^{-8} | 1.0000 | 0.25 |
| rs2210911  | 1.16 (1.09-1.23) | 4.98 \times 10^{-7} | 1.0000 | 0.1 |
| rs3761959  | 1.22 (1.16-1.30) | 2.27 \times 10^{-12} | 1.0000 | 0.01 |
| rs7528684  | 1.23 (1.16-1.30) | 7.11 \times 10^{-13} | 1.0000 | 0.001 |
| rs7517644  | 1.19 (1.10-1.28) | 1.70 \times 10^{-5} | 1.0000 | 0.001 |
| rs2765493  | 1.16 (1.10-1.23) | 2.16 \times 10^{-7} | 1.0000 | 0.001 |
| rs2260040  | 1.15 (1.07-1.24) | 0.0003 | 1.0000 | 0.001 |

*Statistical power is the power to detect an odds ratio of 1.5 for the homozygotes with the rare genetic variant, with an \( z \) level equal to the reported \( p \)-Value. FPRP values below 0.2 are in bold face.

doi:10.1371/journal.pone.0057758.t003
based on 625 cases and 490 controls (Table S2) [33], we still regarded SNP rs7528684 as a susceptibility GD locus in FCR3 region in the Chinese Han population. Meanwhile, all of the risk haplotypes of GD contained the risk allele C of rs7528684, which can increase FCR3 expression both from cis-eQTL analysis and from the real-time PCR results. Later, WTCCC in an analysis including 2,500 UK GD cases and 2,500 controls found an association at rs3761959 (a perfect proxy of rs7528684, $r^2=1$ in our data; Figure 2A) with GD ($P=0.0094$; Table S2) [19]. Also, rs3761959 showed the significant association with GD in our two-stage GWAS analysis and could affect the expression of FCR3 from our cis-eQTL analysis and real-time PCR. Noteworthy, in the WTCCC study, a stronger association was found with rs11264798 (in high LD with rs7528684 in our data, $r^2=0.99, P=1.6\times10^{-5}$; Table S2), located in the intron 8 of FCR3 [19]. More recently, the WTCCC genotyped 743 SNPs across FCR3 in 7,894 control samples and about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 1,600 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34]. Unfortunately, the fine mapping data about 2,000 GD subjects to define the causal GD-associated SNPs using Bayes theorem [34].

In summary, our study provided the unequivocal evidence that FCR3 was the susceptibility gene of GD and its proxy SNP rs7528684 may be the etiology variant to predispose to GD in Chinese Han population.

Supporting Information

Figure S1 Regional plots of association results and linkage disequilibrium structure of 58 SNPs. Panel A shows the linkage disequilibrium (LD) structure for the 8 SNPs with high LD with rs3761959 in the first LD block and 50 SNPs that could not be improved in the model with rs3761959 in the second LD block in the GWAS samples. Panel B shows the GD association of 58 SNPs with $P<2.30\times10^{-6}$ the linkage disequilibrium (LD) structure for the 51 SNPs in the GWAS samples. The color of each genotyped SNP spot reflects its $r^2$ with the top SNP within each association locus shown as a large red diamond, and smaller values changing from red to white. Genetic recombination rates are shown in cyan. Genetic recombination rates, estimated using the 1000 Genomes pilot 1 CHB and JPT samples, are shown cyan. Physical positions are based on NCBI build 36. (TIF)

Figure S2 The linkage disequilibrium structure of 210 SNPs including rs6679793 in the GWAS scan cohort. The 210 SNPs contains 209 SNPs correlated to the FCR3 expression and rs6679793 is the top SNP correlated to the FCR5 expression. (TIF)

Figure S3 The linkage disequilibrium structure for the region 155,744-156,152 Kb at 1q21.1 in the CEU (A) and CHB and JPT (B) population from the HapMap phase II 24 release. Coloring in the figure is according to $r^2$. (TIF)

Table S1 Association results of the imputed and typed SNPs in 1q21.1 region with GD in initial genome-wide scan. (XLS)

Table S2 The comparison among the results from three studies on FCR3 genes in 1q21.1. (XLS)

Acknowledgments

Membership of The China Consortium for the Genetics of Autoimmune Thyroid Disease:
Huai-Dong Song: State Key Laboratory of Medical Genomics, Molecular Medicine Center, Ruijin Hospital Affiliated to Shanghai Jiaotong University (SJTU) School of Medicine, Shanghai, China; Shanghai Institute of Endocrinology and Metabolism, Department of Endocrinology, Ruijin Hospital Affiliated to SJTU School of Medicine, Shanghai, China.
Shuang-Xia Zhao: State Key Laboratory of Medical Genomics, Molecular Medicine Center, Ruijin Hospital Affiliated to Shanghai Jiaotong University (SJTU) School of Medicine, Shanghai, China; Shanghai Institute of Endocrinology and Metabolism, Department of Endocrinology, Ruijin Hospital Affiliated to SJTU School of Medicine, Shanghai, China.

Chun-Ming Pan: State Key Laboratory of Medical Genomics, Molecular Medicine Center, Ruijin Hospital Affiliated to Shanghai Jiaotong University (SJTU) School of Medicine, Shanghai, China.

Jun Liang: Department of Endocrinology, The Central Hospital of Xuzhou Affiliated to Xuzhou Medical College, Xuzhou, Jiangsu Province, China.

Xiao-Mei Zhang: Department of Endocrinology, The First Hospital Affiliated to Bengbu Medical College, Bengbu, Anhui Province, China.

Guo-Yue Yuan: Department of Endocrinology, The Hospital Affiliated to Zhejiang University, Zhenjiang, Jiangsu Province, China.

Chang-Gui Li: Department of Endocrinology and Geriat Laboratory, Medical School Hospital of Qingdao University, Qingdao, Shandong Province, China.

Jia-Jun Zhao: Department of Endocrinology, Shandong Province Hospital, Shandong University, Jinan, China.

We thank all patients and normal individuals for participating in this study.

Author Contributions
Conceived and designed the experiments: HDS. Performed the experiments: SXZ WL MZ YSY QLY QCM JLC HDS. Analyzed the data: SXZ ZHG LL HNW. Contributed reagents/materials/analysis tools: SXZ WL MZ YSY QLY QCM BLY JLC GGQ XGY CGL. Wrote the paper: SXZ GGQ MDC JLC HD8.

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