

# PUBLISHED VERSION

Jwu Jin Khong, Kathryn P. Burdon, Yi Lu, Kate Laurie, Lefta Leonardos, Paul N. Baird, Srujana Sahebjada, John P. Walsh, Adam Gajdatsy, Peter R. Ebeling, Peter Shane Hamblin, Rosemary Wong, Simon P. Forehan, Spiros Furlanos, Anthony P. Roberts, Matthew Do  
**Pooled genome wide association detects association upstream of FCRL3 with Graves' disease**  
BMC Genomics, 2016; 17(1):939-1-939-10


© The Author(s). 2016 Open Access This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated.

Originally published at:

<http://doi.org/10.1186/s12864-016-3276-z>

## PERMISSIONS

<http://creativecommons.org/licenses/by/4.0/>




### Attribution 4.0 International (CC BY 4.0)

This is a human-readable summary of (and not a substitute for) the [license](#). [Disclaimer](#).

**You are free to:**


- Share** — copy and redistribute the material in any medium or format
- Adapt** — remix, transform, and build upon the material for any purpose, even commercially.

The licensor cannot revoke these freedoms as long as you follow the license terms.



---

**Under the following terms:**

-  **Attribution** — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.
- No additional restrictions** — You may not apply legal terms or [technological measures](#) that legally restrict others from doing anything the license permits.

27 June 2017


<http://hdl.handle.net/2440/105050>

METHODOLOGY ARTICLE

Open Access



# Pooled genome wide association detects association upstream of *FCRL3* with Graves' disease

Jwu Jin Khong<sup>1,2,3\*</sup> , Kathryn P. Burdon<sup>4</sup>, Yi Lu<sup>5</sup>, Kate Laurie<sup>6</sup>, Lefta Leonardos<sup>6</sup>, Paul N. Baird<sup>7</sup>, Srujana Sahebjada<sup>7</sup>, John P. Walsh<sup>8,9</sup>, Adam Gajdatsy<sup>10</sup>, Peter R. Ebeling<sup>11</sup>, Peter Shane Hamblin<sup>1,12</sup>, Rosemary Wong<sup>12</sup>, Simon P. Forehan<sup>13</sup>, Spiros Furlanos<sup>13</sup>, Anthony P. Roberts<sup>14</sup>, Matthew Doogue<sup>15</sup>, Dinesh Selva<sup>16</sup>, Grant W. Montgomery<sup>17</sup>, Stuart Macgregor<sup>5</sup> and Jamie E. Craig<sup>6</sup>

## Abstract

**Background:** Graves' disease is an autoimmune thyroid disease of complex inheritance. Multiple genetic susceptibility loci are thought to be involved in Graves' disease and it is therefore likely that these can be identified by genome wide association studies. This study aimed to determine if a genome wide association study, using a pooling methodology, could detect genomic loci associated with Graves' disease.

**Results:** Nineteen of the top ranking single nucleotide polymorphisms including HLA-DQA1 and C6orf10, were clustered within the Major Histo-compatibility Complex region on chromosome 6p21, with rs1613056 reaching genome wide significance ( $p = 5 \times 10^{-8}$ ). Technical validation of top ranking non-Major Histo-compatibility complex single nucleotide polymorphisms with individual genotyping in the discovery cohort revealed four single nucleotide polymorphisms with  $p \leq 10^{-4}$ . Rs17676303 on chromosome 1q23.1, located upstream of *FCRL3*, showed evidence of association with Graves' disease across the discovery, replication and combined cohorts. A second single nucleotide polymorphism rs9644119 downstream of *DPYSL2* showed some evidence of association supported by finding in the replication cohort that warrants further study.

**Conclusions:** Pooled genome wide association study identified a genetic variant upstream of *FCRL3* as a susceptibility locus for Graves' disease in addition to those identified in the Major Histo-compatibility Complex. A second locus downstream of *DPYSL2* is potentially a novel genetic variant in Graves' disease that requires further confirmation.

**Keywords:** Graves' disease, Genome-wide association study, Pooled blood

## Background

Graves' disease (GD) is an autoimmune thyroid disease which typically presents as thyrotoxicosis and goitre; other clinical findings include Graves' orbitopathy, dermopathy and acropachy. The incidence rate of GD is 15 per 100, 000 persons per year with an overall mean prevalence of 1152 per 100, 000 population in the

United States [1, 2]. Women are disproportionately more affected with the female to male ratio reported at 7.3:1 [1]. The disease also occurs in children at one tenth the prevalence rate of all ages [1].

GD is a complex disease with a strong familial predisposition; [3–7] the triggers are poorly understood but various environmental factors were linked to onset of GD such as stress, smoking and *Yersinia* infection in genetically susceptible individuals [8, 9]. GD shows a strong familial predisposition. The concordance rate for GD in monozygotic twins is significantly higher than dizygotic twins and model-fitting analysis predicted that genetic factors account for 79 % of disease heritability in

\* Correspondence: [jwujinkhong@gmail.com](mailto:jwujinkhong@gmail.com)

<sup>1</sup>Melbourne Medical School Western Campus, Department of Medicine, University of Melbourne, Sunshine Hospital, 176 Furlong Road, St Albans, VIC 3021, Australia

<sup>2</sup>Orbital, Plastics and Lacrimal Unit, The Royal Victorian Eye and Ear Hospital, Heidelberg, VIC, Australia

Full list of author information is available at the end of the article



twins [10]. With a concordance rate of 22–35 % for monozygotic twins, environmental and modifier factors are likely to play a key role [10, 11]. Clustering of GD with other autoimmune conditions including type I diabetes mellitus, myasthenia gravis, polymyositis, lupus erythematosus and Addison's disease suggest genes regulating the immune system shared by these diseases might also contribute towards the genetic susceptibility for GD [3].

The genetic susceptibility of GD can be broadly categorized into genes involved in immune regulation, and thyroid specific genes. Genes confirmed to be associated with GD include the following: multiple loci within the Human leukocyte antigen (HLA) I and II region, as well as non-HLA loci *CTLA4*, *PTPN22*, *CD40*, *IL2A*, *FCRL3* and *TSHR* [12–26]. The contributions from each of these genetic variants are modest. From candidate gene studies, HLA class II alleles *DRB1\*03(DR3)*, *DQA1\*0501*, *DQB1\*02* were significantly associated with GD with odd ratios of 2 to 3 for *DR3* [5, 15, 27, 28]. *CTLA4* A49G, and CT60 3'UTR polymorphisms were more frequent in GD with an odds ratio of 1.4 to 2, [12, 13, 29–31] and association with *PTPN22* polymorphism has an odds ratio of 1.5 to 1.9 [14, 16, 17].

Genome wide association studies (GWAS) have replicated earlier candidate gene study findings and identified additional new genetic loci. The earliest GWAS studies on autoimmune thyroid disease showed association of GD with multiple loci within the HLA class I and II regions, and also in *TSHR* and *FCRL3* [26, 32]. More recently two new risk loci for GD, the *RNASET2-FGFR1OP-CCR6* region at 6q27 and an intergenic region at 4p14 were reported, along with confirmation of positive association of GD with SNPs in HLA-*DPB1*, *TSHR*, *CLTA4* and *FCRL3* [33]. Using a custom array, association of SNPs near *PTPN22*, *CTLA4*, *TSHR*, *RNASET2-FGFR1OP-CCR6* loci with GD were replicated, and seven novel susceptibility loci, *MMEL1*, *LPP*, *BACH2*, *PRICKLE1*, *ITGAM*, rs1534422 at 2p25.1 and rs4409785 at 11q21 were identified but the results require confirmation in replication studies [24].

A pooled GWAS strategy can effectively identify gene variants in multiple diseases. Using relatively small numbers of cases and controls, pooled GWAS has previously been used to identify the known susceptibility loci *CFH* and *ARMS2/HTRA1* in age related macular degeneration and *LOXL1* in pseudoexfoliation syndrome [34]. A pooled DNA study has also identified a new susceptibility locus, *HGF*, in keratoconus (a progressive corneal degeneration) and additional novel candidate genes related to platelet reactivity in diabetic patients [34–36]. The study design must be carefully considered to include multiple pools to minimise pooling errors and an appropriate array platform to extract maximal available information from the pooled DNA [37, 38].

The aim of this study was to determine if GWAS using DNA pooling methodology could replicate genomic loci associated with GD and discover new genetic loci.

## Methods

### Definition of Graves' disease

GD cases were participants with biochemically confirmed hyperthyroidism on thyroid function tests; and had either the presence of Graves' orbitopathy, or positive thyrotropin receptor (TSHR) antibodies or uniform increase in uptake on technetium-99 m pertechnetate thyroid scan.

### Discovery cohort

The Australian Thyroid-associated Orbitopathy Research (ATOR) discovery cohort consisting of 412 GD cases with and without Graves' orbitopathy of European descent was recruited from endocrinology and ophthalmology clinics in the hospitals and private practices from Victoria and South Australia.

A total of 498 controls were recruited from two Australian populations. These comprised 198 adult patients with keratoconus, a non-autoimmune eye disease unrelated to GD, who were recruited from eye clinics in Melbourne, and 300 healthy controls aged over 50 years recruited from retirement villages and the general community in South Australia. The control cohort was not actively screened for GD, but none of the controls reported having this condition.

### Replication cohort

An independent group of 539 GD cases and 1230 controls were recruited to form a replication cohort. The GD cases were new cases recruited into the ATOR cohort ( $n = 373$ ) from Melbourne, and endocrine and ophthalmology clinics from Western Australia ( $n = 166$ ). The controls were research participants of European descent with eye diseases without recognizable association with GD or other autoimmune diseases (angle closure glaucoma or suspect, pigment dispersion syndrome, steroid responsive ocular hypertension, myopia and keratoconus) recruited in a collaborative effort from South Australia and Victoria to study the genetics of these eye diseases (age ranging from 9 to 92 years).

### DNA pooling for GWAS study

Two methods of DNA pooling were used. For freshly collected samples, whole blood was pooled directly (pool 1) and for archived DNA samples, equimolar DNA pools were created (pools 2 and 3). Venous blood or DNA aliquots from all participants were thawed for 3 h before construction of 3 pool comparisons. Pool number 1 contained 154 GD cases and 198 controls, pool number 2 had 218 GD cases and 213 controls, and pool number 3 had 40 GD

cases and 87 controls, giving a total of 412 cases and 498 controls from the discovery cohort. For pool 1, 100  $\mu$ l of whole blood from each sample was mixed with protease and lysis buffer, vortexed and incubated, then samples were combined in one tube for whole blood pool construction, 1 tube each for cases and controls. DNA was extracted from the whole blood pool by using QIA-amp DNA blood maxi kit (Qiagen, Valencia, CA, USA) according to the manufacturer's protocol. For pool 2 and 3 samples, whole blood was lysed and DNA was extracted from each sample. Equimolar DNA pools were constructed in duplicate by step-wise dilutions of genomic DNA using QIA-amp DNA blood maxi kit (Qiagen, Valencia, CA, USA) to 75 ng/ $\mu$ l. We used Fluoroskan Ascent microplate fluorometer (ThermoFisher Scientific, Waltham, MA, USA) coupled with Picogreen reagents (Invitrogen, Carlsbad, CA) for DNA quantitation. Comparisons were made to a standard curve generated from serial dilutions of Lambda DNA (Invitrogen, Carlsbad, CA). A total of 451 ng of DNA from each sample was added to the equimolar DNA pool.

#### Pooling error

Previous studies showed that the majority of pooling errors arise from errors on the arrays rather than pool construction errors, [39] hence in this pooling design, multiple Illumina HumanOmni5-Quad arrays were used for each pool to reduce array errors. The pooling standard deviation is very small for the Illumina bead arrays, pooling standard deviation for HumanHap300 was estimated between 0.007 and 0.011, [38] and variance for the 1M array was  $6.8 \times 10^{-5}$  [34]. This encompasses both assays and pool construction errors. The Illumina HumanOmni5-Quad beadchip array supersedes its predecessor arrays; the HumanHap300 and 1M array, by virtue of its comprehensive coverage of the human genome but is similar in the way of the bead array design.

#### Pooled genotyping and analysis

Genome-wide genotyping was conducted at Queensland Institute of Medical Research (QIMR) Berghofer Medical Research Institute, using HumanOmni5-Quad beadchip microarray (Illumina, San Diego, CA, USA) which contained approximately 4.3 million markers. Three case and control pools, each replicated 2 to 4 times to minimise measurement error, were generated for comparisons.

The output of the raw beadscores from Illumina Beadstation were subjected to a series of data cleaning and quality control measures, as described previously for array-based DNA pooling studies [38, 40, 41]. SNPs with minor allele frequency (MAF) greater than 1 % from the reference panel of EUR samples in the 1000 Genomes Project were retained for subsequent analysis (i.e. 2.5 million SNPs). We excluded SNPs with more than 10 %

negative beadscores, and SNPs with the sum of mean red and green scores smaller than 1200 across each array. A correction factor (*corr*) was calculated to rescale the green beadscore to calibrate the mean value of the pooling allele frequency (PAF) at 0.5 over all SNPs on each strand of the array. The PAF was computed based on the raw red intensities and the corrected green intensities as  $PAF = red / (red + green / corr)$  [40]. We further filtered non-autosomal SNPs and any SNPs with a significant variance difference between cases and controls.

A final set of autosomal SNPs meeting the following criteria: (1) contain sufficient number of probes (i.e., over  $\frac{1}{2}$  of expected number of probes for SNPs with MAF 1–5 %, or over  $\frac{1}{3}$  of expected number of probes for SNPs with MAF >5 %; (2) display no larger than 0.3 differences between PAF and reference allele frequency from EUR samples in the 1000 Genomes Project were taken forward for association testing. After data cleaning and quality control, 2.2M SNPs were left for association testing. A linear model was used to test for allelic association in the three case-control pools from GD discovery cohort. The test statistic corrected for pooling error was used to rank SNPs; with *p* values derived from chi-squared distribution with 1 ° of freedom to assess the significance of allele frequency difference between cases and controls. We then conducted a meta-analysis weighted by inverse variance to combine the results of the three case-control pool comparisons. The top-ranking SNPs in the meta-analysis were counter checked for proxies (i.e., linkage disequilibrium  $r^2 > 0.5$  with the index SNPs in the EUR populations). If proxy SNPs were available, they should also show evidence of association to be considered valid. A genome-wide significance threshold was set at  $5 \times 10^{-8}$  to account for multiple testing but SNPs with  $p < 1 \times 10^{-6}$  were also included for further evaluation.

#### Individual genotyping and analysis

Top-ranked non-major histo-compatibility complex (MHC) SNPs with *p*-value  $\leq 1 \times 10^{-6}$  were selected for technical validation genotyping in individual DNA samples that made up the pool as well as for genotyping in the replication cohorts. The top ranking SNPs were individually genotyped in the discovery cohort in 412 GD cases and 480 normal controls. A subset of 18 controls had insufficient residual samples for individual genotyping, hence the discrepancy in the final pooling and validation sample sizes.

Thirteen SNPs were genotyped on iPLEX Gold assay (Sequenom, San Diego, CA, USA) by using Sequenom MassARRAY® Analyzer in two batches. The ATOR discovery cohort and Western Australia replication cohort genotyping was performed at the Australian Genome Research Facility (Brisbane, Australia) and the ATOR

replication cohort at GeneWorks Pty Ltd (Adelaide, Australia). The allele association analysis was performed using chi-square test (--assoc) in PLINK, [42] independently for technical validation in the ATOR pooled discovery cohort, the replication cohorts and the overall in the discovery and replication cohorts. The odds ratio and 95 % confidence interval for allelic association was further adjusted for covariates age and sex using logistic regression analysis (--logistic --covar). SNPs with  $p \leq 1 \times 10^{-4}$  were considered validated in validation genotyping. For replication genotyping,  $p < 0.05$  was considered significant.

## Results

The GD cases were predominantly female and younger when compared with controls (Table 1), hence subsequent individual genotyping analysis was adjusted for age and sex.

In the discovery GWAS, 19 of the top 30 ranking SNPs clustered within the MHC region on chromosome 6p21 including rs9272937 in HLA-DQA1 ( $p 10^{-7}$ ), two SNPs within C6orf10 ( $p 10^{-7}$ ), and rs1613056 reaching genome wide significance ( $p = 5 \times 10^{-8}$ ) (Additional file 1: Table S1). One SNP, rs9676286 on chromosome 19, reached genome-wide significance in the pooled GWAS ( $p = 1.08 \times 10^{-8}$ ) for association with GD. However rs9676286 was not as strongly supported when we conducted technical validation genotyping of the individual DNA samples from the pools ( $p = 5.54 \times 10^{-3}$ ).

An additional 12 top ranked non-MHC SNPs suggestive of association ( $p \sim 10^{-6}$ ) were also selected for validation. Of these, four SNPs showed evidence of association with  $p < 1 \times 10^{-4}$  when we conducted technical validation genotyping in the individual DNA samples. They are rs1469893 on chr 15, rs17676303 on chr 1, rs78542322 on chr 6 and rs62469516 on chr 7 (Table 2). Amongst these four, rs1767303 was most strongly associated with GD with a  $P$  value at  $1.14 \times 10^{-8}$  (OR = 2.05, 95 % CI 1.57–2.67). When correlating odds ratio of effect allele frequencies in pooled GWAS with individual validation genotyping, the results showed strong correlation ( $r = 0.89$ ,  $p < 0.001$ ) (Additional file 2: Figure S1).

Genotyping in the replication cohort showed positive association of GD with rs17676303, located upstream of *FCRL3* on chromosome 1q23.1 (OR = 1.22, 95 % CI

1.01–1.46,  $p = 0.04$ ). The minor T allele was more frequent in GD cases than in normal controls (OR = 1.42, 95 % CI 1.22–1.64,  $p = 3.41 \times 10^{-6}$ ) in the combined discovery and replication cohorts, adjusted for sex and age. Rs62469516, rs1469893 and rs78542322 minor alleles were not associated with GD in the replication cohort, or the combined cohorts (Table 3).

We further examined the relationship between SNP rs17676303 and other annotated SNPs in *FCRL3* gene or its promoter region, namely rs7528684, rs3761969 and rs11264798, which have previously been identified as positively associated with GD, rheumatoid arthritis and systemic lupus erythematosus [25, 33, 43]. All three SNPs previously associated with GD showed high linkage disequilibrium with rs17676303 in the Caucasian HapMap population (Table 4). The result suggests that these SNPs reported with various auto-immune diseases may be tagging the same functional genetic variants around the *FCRL3* gene locus.

A second SNP, rs9644119, located downstream of *DPYSL2* on chromosome 8p21 is highly ranked for its association with GD in pooled GWAS with a  $P$  value approaching genome wide significance ( $p = 9.10 \times 10^{-8}$ ). The association was not validated in the discovery cohort and for the combined cohort the association with GD is less strong than the discovery pooled GWAS would suggest ( $p = 4.02 \times 10^{-3}$ ). In the replication cohort, the minor T allele conferred increased odds for GD compared to controls (OR = 1.33, 95 % CI 1.11–1.59,  $p = 1.95 \times 10^{-3}$ ); after adjusting for sex and age, the result remained significant. (OR = 1.28, 95 % CI 1.06–1.54,  $p = 9.34 \times 10^{-3}$ ). The results suggested this allele might be a genetic locus of interest for GD, but will need further confirmation in future studies.

## Discussion

This study investigated the genetic associations of GD using a pooled genome wide association study (GWAS) in 910 samples. Despite the relatively small number of samples for discovery GWAS, the pooled strategy in combination with increased sample size in a second stage of individual genotyping in both the validation and replication cohorts, readily detected evidence of association of a genetic locus upstream of *FCRL3* on chromosome 1q23. The association of *FCRL3* with GD has

**Table 1** Demographics of Graves' disease cases and controls in the discovery and replication cohorts

|                    | N    |         | Mean age (SD) |             | $p$ value | Sex                  |                      |           |
|--------------------|------|---------|---------------|-------------|-----------|----------------------|----------------------|-----------|
|                    | Case | Control | Case          | Control     |           | Graves' case         | Controls             | $p$ value |
| Discovery cohort   | 412  | 498     | 45.3 (14.5)   | 56.3 (24.4) | <0.001    | Male 71 (17.23 %)    | Male 192 (41.03 %)   | <0.001    |
|                    |      |         |               |             |           | Female 341 (82.77 %) | Female 276 (58.97 %) |           |
| Replication cohort | 539  | 1230    | 44.5 (14.8)   | 48.1 (17.4) | <0.001    | Male 109 (20.30 %)   | Male 596 (49.30 %)   | <0.001    |
|                    |      |         |               |             |           | Female 428 (79.70 %) | Female 613 (50.70 %) |           |

**Table 2** Top ranking SNPs identified from pooled genome wide association study and validation genotyping in the discovery cohort

| SNP name   | Location chr and bp       | Gene   | GWAS pooled genotyping<br>(Cases = 412, Controls = 498) |                       |       | Validation individual genotyping<br>(Cases = 412, Controls = 480) |       |                       |                     |
|------------|---------------------------|--|---|-----------------------|-------|---|-------|-----------------------|---------------------|
|            |                           |  | A1  | P value               | OR_A1 | F_A   | F_U   | P value*              | OR_A1*<br>(95 % CI) |
| Rs9676286  | Chr19q13.43<br>58126481   | ZNF134 intron                                      | A   | $1.08 \times 10^{-8}$ | 2.08  | 0.047   | 0.023 | $5.54 \times 10^{-3}$ | 2.28 (1.27, 4.09)   |
| rs9644119  | Chr8p21.2<br>26517817     | DPYSL2<br>2124 bp downstream                       | T   | $9.10 \times 10^{-8}$ | 1.78  | 0.177   | 0.128 | 0.033                 | 1.36 (1.03, 1.79)   |
| rs11722643 | Chr4p16.1<br>10127484     | Intergenic<br>WDR1 upstream, ZNF518B<br>downstream | T   | $1.03 \times 10^{-7}$ | 1.88  | 0.101   | 0.054 | $1.38 \times 10^{-3}$ | 1.91 (1.28, 2.83)   |
| Rs686806   | Chr 11q22.3<br>107228533  | CWF19L2 intron                                     | T   | $2.36 \times 10^{-7}$ | 1.70  | 0.242   | 0.168 | $9.6 \times 10^{-4}$  | 1.53 (1.19, 1.97)   |
| rs62469516 | Chr7q21.13<br>88958624    | ZNF804B intron                                     | A   | $2.68 \times 10^{-7}$ | 0.51  | 0.043   | 0.088 | $5.73 \times 10^{-5}$ | 0.41 (0.26, 0.63)   |
| rs73452600 | Chr 7q34<br>142828104     | PIP 1070 bp upstream                               | A   | $3.49 \times 10^{-7}$ | 1.90  | 0.099   | 0.061 | $3.37 \times 10^{-3}$ | 1.80 (1.22, 2.67)   |
| Rs1662312  | Chr 18p11.31<br>3220450   | MYOM1 upstream                                     | A   | $5.72 \times 10^{-7}$ | 0.51  | 0.040   | 0.080 | $5.33 \times 10^{-4}$ | 0.45 (0.29, 0.71)   |
| rs1469893  | Chr 15q14<br>34988664     | GJD2<br>56015 bp<br>Downstream                     | A   | $6.58 \times 10^{-7}$ | 0.58  | 0.05  | 0.104 | $6.86 \times 10^{-5}$ | 0.44 (0.29, 0.66)   |
| Rs17676303 | Chr 1q23.1<br>157679691   | FCRL3<br>9044 bp upstream                          | T   | $8.05 \times 10^{-7}$ | 1.68  | 0.254   | 0.150 | $1.14 \times 10^{-8}$ | 2.05 (1.57, 2.67)   |
| rs28578508 | Chr18q12.1<br>32316007    | DTNA intron  | A   | $8.16 \times 10^{-7}$ | 0.56  | 0.062   | 0.099 | $2.80 \times 10^{-3}$ | 0.56 (0.39, 0.82)   |
| rs78542322 | Chr 6q14.1<br>77291670    | Intergenic<br>IMPG1 upstream<br>HTR1B downstream   | T   | $9.82 \times 10^{-7}$ | 0.52  | 0.071   | 0.141 | $3.27 \times 10^{-5}$ | 0.47 (0.33, 0.67)   |
| Rs3818779  | Chr 10q26.11<br>121140671 | GRK5 intron  | A   | $1.51 \times 10^{-6}$ | 1.94  | 0.059   | 0.029 | $2.08 \times 10^{-3}$ | 2.30 (1.35, 3.9)    |
| rs2141440  | Chr 11q14.3<br>90898463   | Intergenic MIR4490 and FAT3                        | A   | $4.48 \times 10^{-6}$ | 0.58  | 0.078   | 0.097 | 0.34                  | 0.84 (0.59, 1.20)   |

F\_U is individual genotyping minor allele frequency A1 in normal control, F\_A is the allele frequency in Graves' disease

OR is odd ratio for having minor allele in Graves' cases compared to normal controls

\*P values and odds ratios in validation genotyping were adjusted for age and sex

previously been identified in large scale GWAS studies [25, 26, 33]. The pooled GWAS also detected association of GD with multiple SNPs within the MHC I and MHC II regions on chromosome 6p21. Susceptibility loci within both these regions which contain HLA genes involved in antigen presentation, are well established for GD by association studies, candidate gene analysis and GWAS [5, 25–27, 44]. Rs9272937 in the un-translated region of *HLA-DQA1* within the MHC class II region showed evidence of association with GD ( $p = 4.43 \times 10^{-7}$ ) in our study. The positive association of *HLA-DQA1* with GD has been replicated in multiple studies [15, 44, 45]. Two SNPs within the intron of the *C6orf10* gene suggesting association with GD ( $p 10^{-7}$ ), were also independently validated as a locus of susceptibility in GD in a previous GWAS study [26].

These replicative findings in GD prove the robustness of the two-stage study design for pooled GWAS. The pooled

GWAS study also found evidence of association for a gene locus marked by rs9644119, downstream of *DPYSL2* on chromosome 8, but the significance is less certain. The risk attributions from individual genetic variants for GD are known to be small with odds ratios  $<1.5$ , [23] therefore large sample sizes in the thousands will be needed to increase power for detecting significant association, and may in the future prove or disprove the significance for the rs9644119 locus.

For the two compelling signals we have detected in the vicinity of *FCRL3* and *DPYSL2*, genetic variants in *FCRL3* were associated with a modest increase in odds for GD at 1.2 to 1.35 [25, 33, 46]. Genetic variation in the promoter region of *FCRL3* i.e. *FCRL3* -169T>C allele is reportedly associated with other autoimmune diseases such as rheumatoid arthritis and systemic lupus erythematosus, [43, 47, 48] suggesting that the *FCRL3* locus may influence the susceptibility to multiple autoimmune

**Table 3** Genotyping results for top ranking single nucleotide polymorphisms in replication cohorts, and combined analysis of discovery and replication cohorts using individual genotyping

| SNP name   | Location chr and bp       | Gene   | Replication cohorts (Cases = 539, Controls = 1230) |       |       |                       |                   | Combined discovery and replication cohorts (Cases = 951, Controls = 1710) |       |                       |                    |  |
|------------|---------------------------|--|--|-------|-------|-----------------------|-------------------|---|-------|-----------------------|--------------------|--|
|            |                           |  | A1   | F_A   | F_U   | P value               | OR_A1 (95 % CI)   | F_A   | F_U   | P value*              | OR_A1*             |  |
| Rs9676286  | Chr19q13.43<br>58126481   | ZNF134 intron                                      | A  | 0.045 | 0.039 | 0.41                  | 1.17 (0.81–1.71)  | 0.046   | 0.034 | 0.04                  | 1.38 (1.02, 1.87)  |  |
| rs9644119  | Chr8p21.2<br>26517817     | DPYSL2<br>2124 bp downstream                       | T  | 0.219 | 0.174 | $9.34 \times 10^{-3}$ | 1.28 (1.06–1.54)  | 0.200   | 0.161 | $4.02 \times 10^{-3}$ | 1.25 (1.07, 1.45)  |  |
| rs11722643 | Chr4p16.1<br>10127484     | Intergenic<br>WDR1<br>upstream, ZNF518B downstream | T  | 0.096 | 0.095 | 0.94                  | 0.99 (0.76–1.29)  | 0.098   | 0.083 | 0.14                  | 1.17 (0.95, 1.44)  |  |
| Rs686806   | Chr 11q22.3<br>107228533  | CWF19L2 intron                                     | T  | 0.198 | 0.210 | 0.95                  | 0.99 (0.82, 1.20) | 0.217   | 0.197 | 0.04                  | 1.63 (1.004, 1.35) |  |
| rs62469516 | Chr7q21.13<br>88958624    | ZNF804B intron                                     | A  | 0.053 | 0.053 | 0.64                  | 1.09 (0.77–1.53)  | 0.048   | 0.063 | 0.06                  | 0.77 (0.59, 1.01)  |  |
| rs73452600 | Chr 7q34<br>142828104     | PIP 1070 bp upstream                               | A  | 0.090 | 0.084 | 0.71                  | 1.05 (0.81, 1.36) | 0.094   | 0.077 | 0.07                  | 1.22 (0.98–1.50)   |  |
| Rs1662312  | Chr 18p11.31<br>3220450   | MYOM1 upstream                                     | A  | 0.070 | 0.070 | 0.77                  | 0.93 (0.59, 1.50) | 0.049   | 0.073 | $1.72 \times 10^{-3}$ | 0.61 (0.44, 0.83)  |  |
| rs1469893  | Chr 15q14<br>34988664     | GJD2<br>56015 bp<br>Downstream                     | A  | 0.074 | 0.081 | 0.72                  | 0.95 (0.71, 1.27) | 0.064   | 0.088 | $7.29 \times 10^{-3}$ | 0.73 (0.57, 0.92)  |  |
| Rs17676303 | Chr 1q23.1<br>157679691   | FCRL3<br>9044 bp upstream                          | T  | 0.233 | 0.201 | 0.04                  | 1.22 (1.01–1.46)  | 0.242   | 0.186 | $3.41 \times 10^{-6}$ | 1.42 (1.22, 1.64)  |  |
| rs28578508 | Chr18q12.1<br>32316007    | DTNA intron  | A  | 0.069 | 0.083 | 0.13                  | 0.80 (0.60, 1.07) | 0.066   | 0.087 | $3.21 \times 10^{-3}$ | 0.71 (0.56, 0.89)  |  |
| rs78542322 | Chr 6q14.1<br>77291670    | Intergenic<br>IMPG1 upstream<br>HTR1B downstream   | T  | 0.094 | 0.096 | 0.89                  | 0.98 (0.76, 1.27) | 0.084   | 0.109 | $9.45 \times 10^{-3}$ | 0.76 (0.62, 0.93)  |  |
| Rs3818779  | Chr 10q26.11<br>121140671 | GRK5 intron  | A  | 0.055 | 0.049 | 0.58                  | 1.10 (0.78, 1.55) | 0.057   | 0.043 | 0.06                  | 1.31 (0.99, 1.72)  |  |
| rs2141440  | Chr 11q14.3<br>90898463   | Intergenic MIR4490 and FAT3                        | A  | 0.094 | 0.086 | 0.53                  | 1.09 (0.84, 1.41) | 0.087   | 0.089 | 0.88                  | 0.98 (0.80, 1.21)  |  |

\*P values and odds ratios are adjusted for age and sex

**Table 4** Haploview linkage disequilibrium between known susceptibility loci in Graves' disease and rs17676303 identified in pooled GWAS for Graves' disease in Hapmap CEU population data

| Locus 1    | Locus 2    | D'  | Log of the Odds (LOD) | R <sup>2</sup> | CI low | CI High |
|------------|------------|-----|-----------------------|----------------|--------|---------|
| rs11264798 | rs17676303 | 1.0 | 4.44                  | 0.142          | 0.64   | 1.0     |
| rs3761959  | rs17676303 | 1.0 | 5.83                  | 0.221          | 0.71   | 1.0     |
| rs7528684  | rs17676303 | 1.0 | 5.73                  | 0.224          | 0.7    | 1.0     |

diseases in a similar manner to the immune regulating *CTLA4*, *PTPN22* and MHC genes [24, 25, 32]. To pinpoint the exact locus associated with *FCRL3*, the entire *FCRL* region on chromosome 1q21 was previously investigated using imputation, and the strongest signals associated with GD were located in a cluster of SNPs including rs7528684 and rs3761959 [49]. SNP rs7528684 in the promoter region of *FCRL3* was also previously reported as positively associated with rheumatoid arthritis, systemic lupus erythematosus and GD [43]. Rs3761959 tagging rs7522061 and rs7528684 in the *FCRL3* gene showed association with GD in the Wellcome Trust Case Control Consortium GWAS study ( $p = 9.4 \times 10^{-3}$ ), and the association was further confirmed by The China Consortium for the Genetics of Autoimmune Thyroid disease, reaching genome wide significance ( $p = 2.22 \times 10^{-8}$ ) [25, 33]. In addition, rs11264798 in *FCRL3* was also associated with GD ( $p = 1.6 \times 10^{-5}$ ) [25]. We found high linkage disequilibrium of rs17676303, the SNP associated with GD in our study, with rs7528684, rs3761959 and rs11264798, that strongly suggest these SNPs were tagging the same functional variants in the vicinity of the *FCRL3* gene.

Functional analysis suggests *FCRL3* has immune regulating roles. *FCRL3* is an Fc receptor like molecule that shares a genomic location (chr 1q21-23) and gene structure as a receptor for the Fc portion of immunoglobulin with other members of the immunoglobulin superfamily [50]. Unlike the Fc receptor, the *FCRL* molecule has not been shown biochemically to bind immunoglobulin [50]. *FCRL3* molecules are preferentially expressed by B cells [51, 52]. *FCRL3* possesses both tyrosine based activating and inhibitory motifs in its cytoplasmic tail, indicating these may be used to transmit immune-modulatory signals via tyrosine phosphorylation in regulating B cell differentiation and response [50]. The strongest evidence linking *FCRL3* polymorphisms with autoimmunity is derived from linkage disequilibrium mapping of the chr1q21-23 region in rheumatoid arthritis, which identified 4 SNPs (rs7528684, rs11264799, rs945635 and rs3761959) in a Japanese population [43]. Of the 4 SNPs positively associated with rheumatoid arthritis, *FCRL3* -169T>C (marked by rs7528684 in the promoter region of *FCRL3*) substitution substantially increased promoter activity in *FCRL3* and enhanced binding affinity to the consensus NF- $\kappa$ B binding motif, where NF- $\kappa$ B widely

regulates genes involved in immune response [43]. In addition, *FCRL3* transcripts in peripheral B cells and genomic DNA are higher in heterozygous individuals with genotype -169C/T +358C/G, and increased *FCRL3* expression in synovial tissue and peripheral CD19+ B cell population suggest that higher expression of *FCRL3* is potentially pathogenic [43]. Further correlation of B cell abnormalities with *FCRL3* expression is afforded by significant positive correlation of rheumatoid factor autoantibody titre in individuals with rheumatoid arthritis with the number of susceptible -169 C alleles [43]. However not all studies showed consistent association with polymorphisms in *FCRL3*, specifically no discernible association with *FCRL3* were noted in some other rheumatoid arthritis populations including Caucasians in North American and European countries [53–55]. When the susceptibility effect of *FCRL3* was stratified by NF- $\kappa$ B1 genotypes, association of *FCRL3* polymorphisms with rheumatoid arthritis was observed in patients heterozygous for the NF- $\kappa$ B1 promoter in a Spanish population [54].

The second gene of interest, *DPYSL2*, produces collapse response mediator protein 2 (CRMP2). It was first described in the central nervous system as an effector cytosolic protein for semaphorin mediated axonal growth cones navigation during neural development and plasticity [56]. Dysregulation of CRMP2 phosphorylation and expression, have been associated with neuropsychiatric diseases including Alzheimer's disease and schizophrenia [56]. CRMP2 is also highly expressed in activated T lymphocytes from peripheral blood bearing CD69 and HLA-DR markers. CRMP2 is distributed in the trailing uropod in polarized T cells binding to cytoskeletal structures particularly to vimentin [57]. The observations of enhanced spontaneous and chemokine-directed T cell transmigration by induced expression of CRMP2 in Jurkat T cells, and high expression of CRMP2 in migrating T cells suggest CRMP2 may regulate T cell motility and migration [57]. The mechanism underlying CRMP2 induced T cell migration seems to involve phosphorylation of CRMP2 Tyr-479 residue, acting as transducer for chemokine stromal cell-derived factor-1 $\alpha$  (CXCL12) signaling [58]. The discovery of CRMP2 cellular function in T cells defines its potential role in the pathogenesis of immune mediated inflammation, specifically neuroinflammation [59].



## Conclusions

In conclusion, the pooled GWAS is an effective methodology for detecting common genetic variants in GD. The study confirmed *FCRL3* region as a susceptibility locus for GD in addition to MHC. A second locus downstream of *DPYSL2* is potentially a novel genetic variant in GD that requires further confirmation.

## Additional files

**Additional file 1: Table S1.** Top 30 single nucleotide polymorphism associated with Graves' disease compared with controls in genome wide association study. This table denoted the top ranking SNPs and highlighted SNPs in major histocompatibility complex region and non-HLA SNPs that were chosen for subsequent validation. (DOCX 141 kb)

**Additional file 2: Figure S1.** Scatterplot for odds ratio of 13 effect allele frequencies comparing pooled GWAS Graves' disease with individual genotyping in the discovery cohort. This figure showed the correlation between odds ratio derived from pooled GWAS genotyping and individual genotyping in the ATOR discovery cohort; the correlation is high  $r = 0.89$ . (TIF 9765 kb)

## Abbreviations

ATOR: Australian thyroid-associated orbitopathy research; GD: Graves' disease; GWAS: Genome wide association study; HLA: Human leukocyte antigen; MAF: Minor allele frequency; MHC: Major histo-compatibility complex; PAF: Pooling allele frequency; SNP: Single nucleotide polymorphism; TSHR: Thyrotropin receptor

## Acknowledgements

Drs Peter Colman, Duncan Topliss, Mark Stein, Cherie Chiang, Jennifer Conn, Alan McNab, Thomas Hardy, Richard Stawell, Garry Davis for referring patients to the study. Prof Duncan Topliss for assisting with ethics application at Alfred Health. Ms Stacey Rylander and Mr Chamika De Silva for patients recruitment.

## Funding

Ophthalmic Research Institute of Australia (JJK), National Health and Medical Research Council of Australia (JC), Australian Research Council Fellowship (SM), National Health and Medical Research Council of Australia Fellowship (GM and 1028444 to PNB), Early Career Fellowship (YL), University of Melbourne Early Career Researcher (SS) and Australian Postgraduate Award (JJK). Centre of Eye Research Australia receives operational infrastructure support from the Victorian Government.

## Availability of data and material

The dataset supporting the conclusions of this article were included within the article and the supplementary material.

## Authors' contributions

JJK, contributed to conception and design, acquisition, analysis and interpretation of data and manuscript draft preparation. KPB, YL, GWM, SM, JEC contributed to conception and design of the study, analysis and interpretation of data and draft revision. KL, LL contributed to acquisition and processing of data. PNB, SS, JW, AG contributed to acquisition of additional data, and critical revision of manuscript. PRE, PSH, RW, SF, SF, AR, MD, DS contributed to data acquisition and critical manuscript revision. All authors read and approved the final manuscript.

## Competing interests

The authors declare that they have no competing interests.

## Consent for publication

No identifiable individual data were contained in this publication.

## Ethics approval and consent to participate

The study was approved at multiple recruitment sites by the Royal Victorian Eye and Ear Hospital Human Research Ethics Committee, Melbourne Health Human Research Ethics Committee and the Alfred Health Human Research Ethics Committee in Melbourne, Victoria, Australia; Southern Adelaide Clinical Human Research Ethics Committee and the Royal Adelaide Hospital Human Research Ethics Committee in Adelaide, South Australia. The genetic research was conducted in accordance with the Declaration of Helsinki. Written consents to participate were obtained from all patients.

## Author details

<sup>1</sup>Melbourne Medical School Western Campus, Department of Medicine, University of Melbourne, Sunshine Hospital, 176 Furlong Road, St Albans, VIC 3021, Australia. <sup>2</sup>Orbital, Plastics and Lacrimal Unit, The Royal Victorian Eye and Ear Hospital, Heidelberg, VIC, Australia. <sup>3</sup>Department of Ophthalmology and Department of Surgery, University of Melbourne, Austin Health, Heidelberg, VIC, Australia. <sup>4</sup>Menzies Institute for Medical Research, University of Tasmania, Hobart, TAS, Australia. <sup>5</sup>Statistical Genetics, Queensland Institute of Medical Research (QIMR) Berghofer Medical Research Institute, Herston, QLD, Australia. <sup>6</sup>Department of Ophthalmology, Flinders University of South Australia, Bedford Park, South Australia, Australia. <sup>7</sup>Department of Surgery, Centre for Eye Research Australia and Ophthalmology, University of Melbourne, East Melbourne, VIC, Australia. <sup>8</sup>Department of Endocrinology and Diabetes, Sir Charles Gairdner Hospital, Nedlands, WA, Australia. <sup>9</sup>School of Medicine and Pharmacology, The University of Western Australia, Crawley, WA, Australia. <sup>10</sup>Centre for Ophthalmology and Visual Sciences, University of Western Australia, Western Australia, Australia. <sup>11</sup>Department of Medicine, School of Clinical Sciences, Monash University, Clayton, VIC, Australia. <sup>12</sup>Department of Endocrinology and Diabetes, Western Health, St Albans, VIC, Australia. <sup>13</sup>Department of Diabetes and Endocrinology, Royal Melbourne Hospital, Parkville, VIC, Australia. <sup>14</sup>Department of Endocrinology, The Royal Adelaide Hospital, Adelaide, South Australia, Australia. <sup>15</sup>Department of Medicine, University of Otago, Christchurch, New Zealand. <sup>16</sup>South Australian Institute of Ophthalmology, University of Adelaide, South Australia, Australia. <sup>17</sup>Molecular Epidemiology, Queensland Institute of Medical Research (QIMR) Berghofer Medical Research Institute, Herston, QLD, Australia.

Received: 26 May 2016 Accepted: 9 November 2016

Published online: 18 November 2016

## References

- Jacobson DL, Gange SJ, Rose NR, Graham NM. Epidemiology and estimated population burden of selected autoimmune diseases in the United States. *Clin Immunol Immunopathol.* 1997;84(3):223–43.
- Cooper GS, Stroehla BC. The epidemiology of autoimmune diseases. *Autoimmun Rev.* 2003;2(3):119–25.
- Hemminki K, Li X, Sundquist J, Sundquist K. The epidemiology of Graves' disease: evidence of a genetic and an environmental contribution. *J Autoimmun.* 2010;34(3):J307–13.
- Manji N, Carr-Smith JD, Boelaert K, Allahabadi A, Armitage M, Chatterjee VK, Lazarus JH, Pearce SH, Vaidya B, Gough SC, et al. Influences of age, gender, smoking, and family history on autoimmune thyroid disease phenotype. *J Clin Endocrinol Metab.* 2006;91(12):4873–80.
- Tomer Y, Davies TF. Searching for the autoimmune thyroid disease susceptibility genes: from gene mapping to gene function. *Endocr Rev.* 2003;24(5):694–717.
- Villanueva R, Greenberg DA, Davies TF, Tomer Y. Sibling recurrence risk in autoimmune thyroid disease. *Thyroid.* 2003;13(8):761–4.
- Strieder TG, Prummel MF, Tijssen JG, Ender E, Wiersinga WM. Risk factors for and prevalence of thyroid disorders in a cross-sectional study among healthy female relatives of patients with autoimmune thyroid disease. *Clin Endocrinol (Oxf).* 2003;59(3):396–401.
- Prummel MF, Strieder T, Wiersinga WM. The environment and autoimmune thyroid diseases. *Eur J Endocrinol.* 2004;150(5):605–18.
- Prummel MF, Wiersinga WM. Smoking and risk of Graves' disease. *JAMA.* 1993;269(4):479–82.
- Brix TH, Kyvik KO, Christensen K, Hegedus L. Evidence for a major role of heredity in Graves' disease: a population-based study of two Danish twin cohorts. *J Clin Endocrinol Metab.* 2001;86(2):930–4.

11. Brix TH, Christensen K, Holm NV, Harvald B, Hegedus L. A population-based study of Graves' disease in Danish twins. *Clin Endocrinol (Oxf)*. 1998;48(4):397–400.
12. Kavvoura FK, Akamizu T, Awata T, Ban Y, Chistiakov DA, Frydecka I, Ghaderi A, Gough SC, Hiromatsu Y, Ploski R, et al. Cytotoxic T-lymphocyte associated antigen 4 gene polymorphisms and autoimmune thyroid disease: a meta-analysis. *J Clin Endocrinol Metab*. 2007;92(8):3162–70.
13. Furugaki K, Shirasawa S, Ishikawa N, Ito K, Kubota S, Kuma K, Tamai H, Akamizu T, Hiratani H, Tanaka M, et al. Association of the T-cell regulatory gene CTLA4 with Graves' disease and autoimmune thyroid disease in the Japanese. *J Hum Genet*. 2004;49(3):166–8.
14. Velaga MR, Wilson V, Jennings CE, Owen CJ, Herington S, Donaldson PT, Ball SG, James RA, Quinton R, Perros P, et al. The codon 620 tryptophan allele of the lymphoid tyrosine phosphatase (LYP) gene is a major determinant of Graves' disease. *J Clin Endocrinol Metab*. 2004;89(11):5862–5.
15. Allahabadi A, Heward JM, Nithiyananthan R, Gibson SM, Reuser TT, Dodson PM, Franklyn JA, Gough SC. MHC class II region, CTLA4 gene, and ophthalmopathy in patients with Graves' disease. *Lancet*. 2001;358(9286):984–5.
16. Skorka A, Bednarczuk T, Bar-Andziak E, Nauman J, Ploski R. Lymphoid tyrosine phosphatase (PTPN22/LYP) variant and Graves' disease in a Polish population: association and gene dose-dependent correlation with age of onset. *Clin Endocrinol (Oxf)*. 2005;62(6):679–82.
17. Ichimura M, Kaku H, Fukutani T, Koga H, Mukai T, Miyake I, Yamada K, Koda Y, Hiromatsu Y. Associations of protein tyrosine phosphatase nonreceptor 22 (PTPN22) gene polymorphisms with susceptibility to Graves' disease in a Japanese population. *Thyroid*. 2008;18(6):625–30.
18. Kurylowicz A, Kula D, Ploski R, Skorka A, Jurecka-Lubieniecka B, Zebracka J, Steinhof-Radwanska K, Hasse-Lazar K, Hiromatsu Y, Jarzab B, et al. Association of CD40 gene polymorphism (C-1 T) with susceptibility and phenotype of Graves' disease. *Thyroid*. 2005;15(10):1119–24.
19. Tomer Y, Concepcion E, Greenberg DA. A C/T single-nucleotide polymorphism in the region of the CD40 gene is associated with Graves' disease. *Thyroid*. 2002;12(12):1129–35.
20. Tomer Y, Huber A. The etiology of autoimmune thyroid disease: a story of genes and environment. *J Autoimmun*. 2009;32(3–4):231–9.
21. Brand OJ, Lowe CE, Heward JM, Franklyn JA, Cooper JD, Todd JA, Gough SC. Association of the interleukin-2 receptor alpha (IL-2Ralpha)/CD25 gene region with Graves' disease using a multilocus test and tag SNPs. *Clin Endocrinol (Oxf)*. 2007;66(4):508–12.
22. Brand OJ, Barrett JC, Simmonds MJ, Newby PR, McCabe CJ, Bruce CK, Kysela B, Carr-Smith JD, Brix T, Hunt PJ, et al. Association of the thyroid stimulating hormone receptor gene (TSHR) with Graves' disease. *Hum Mol Genet*. 2009;18(9):1704–13.
23. Simmonds MJ. GWAS in autoimmune thyroid disease: redefining our understanding of pathogenesis. *Nat Rev Endocrinol*. 2013;9(5):277–87.
24. Cooper JD, Simmonds MJ, Walker NM, Burren O, Brand OJ, Guo H, Wallace C, Stevens H, Coleman G, Franklyn JA, et al. Seven newly identified loci for autoimmune thyroid disease. *Hum Mol Genet*. 2012;21(23):5202–8.
25. Burton PR, Clayton DG, Cardon LR, Craddock N, Deloukas P, Duncanson A, Kwiatkowski DP, McCarthy MI, Ouwehand WH, Samani NJ, et al. Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nat Genet*. 2007;39(11):1329–37.
26. Nakabayashi K, Tajima A, Yamamoto K, Takahashi A, Hata K, Takashima Y, Koyanagi M, Nakaoka H, Akamizu T, Ishikawa N, et al. Identification of independent risk loci for Graves' disease within the MHC in the Japanese population. *J Hum Genet*. 2011;56:772–8.
27. Yarman S, Oguz F, Carin M. HLA-DRB1\*03 is a susceptibility gene in patients with Graves' disease with and without ophthalmopathy. *Int J Immunogenet*. 2007;34(1):23–5.
28. Bednarczuk T, Gopinath B, Ploski R, Wall JR. Susceptibility genes in Graves' ophthalmopathy: searching for a needle in a haystack? *Clin Endocrinol (Oxf)*. 2007;67(1):3–19.
29. Esteghamati A, Khalilzadeh O, Mobarra Z, Anvari M, Tahvildari M, Amir HM, Rashidi A, Solgi G, Parivar K, Nikbin B, et al. Association of CTLA-4 gene polymorphism with Graves' disease and ophthalmopathy in Iranian patients. *Eur J Intern Med*. 2009;20(4):424–8.
30. Buzzetti R, Nistico L, Signore A, Cascino I. CTLA-4 and HLA gene susceptibility to thyroid-associated orbitopathy. *Lancet*. 1999;354(9192):1824.
31. Bednarczuk T, Hiromatsu Y, Fukutani T, Jazdzewski K, Miskiewicz P, Osikowska M, Nauman J. Association of cytotoxic T-lymphocyte-associated antigen-4 (CTLA-4) gene polymorphism and non-genetic factors with Graves' ophthalmopathy in European and Japanese populations. *Eur J Endocrinol*. 2003;148(1):13–8.
32. Wellcome Trust Case Control Consortium. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature*. 2007;447(7145):661–78.
33. Chu X, Pan CM, Zhao SX, Liang J, Gao GQ, Zhang XM, Yuan GY, Li CG, Xue LQ, Shen M, et al. A genome-wide association study identifies two new risk loci for Graves' disease. *Nat Genet*. 2011;43(9):897–901.
34. Craig JE, Hewitt AW, McMellon AE, Henders AK, Ma L, Wallace L, Sharma S, Burdon KP, Visscher PM, Montgomery GW, et al. Rapid inexpensive genome-wide association using pooled whole blood. *Genome Res*. 2009;19(11):2075–80.
35. Burdon KP, Macgregor S, Bykhovskaya Y, Javadiyan S, Li X, Laurie KJ, Muszynska D, Lindsay R, Lechner J, Haritunians T, et al. Association of polymorphisms in the hepatocyte growth factor gene promoter with keratoconus. *Invest Ophthalmol Vis Sci*. 2011;52(11):8514–9.
36. Postula M, Janicki PK, Rosiak M, Kaplon-Cieslicka A, Trzepla E, Filipiak KJ, Kosior DA, Czlonkowski A, Opolski G. New single nucleotide polymorphisms associated with differences in platelets reactivity in patients with type 2 diabetes treated with acetylsalicylic acid: genome-wide association approach and pooled DNA strategy. *J Thromb Thrombolysis*. 2013;36(1):65–73.
37. Teumer A, Ernst FD, Wiechert A, Uhr K, Nauck M, Petersmann A, Volzke H, Volker U, Homuth G. Comparison of genotyping using pooled DNA samples (allelotyping) and individual genotyping using the affymetrix genome-wide human SNP array 6.0. *BMC Genomics*. 2013;14:506.
38. Macgregor S, Zhao ZZ, Henders A, Nicholas MG, Montgomery GW, Visscher PM. Highly cost-efficient genome-wide association studies using DNA pools and dense SNP arrays. *Nucleic Acids Res*. 2008;36(6):e35.
39. Macgregor S. Most pooling variation in array-based DNA pooling is attributable to array error rather than pool construction error. *Eur J Hum Genet*. 2007;15(4):501–4.
40. Lu Y, Dimasi DP, Hysi PG, Hewitt AW, Burdon KP, Toh T, Ruddle JB, Li YJ, Mitchell P, Healey PR, et al. Common genetic variants near the Brittle Cornea Syndrome locus ZNF469 influence the blinding disease risk factor central corneal thickness. *PLoS Genet*. 2010;6(5):e1000947.
41. Brown KM, Macgregor S, Montgomery GW, Craig DW, Zhao ZZ, Iyadurai K, Henders AK, Homer N, Campbell MJ, Stark M, et al. Common sequence variants on 20q11.22 confer melanoma susceptibility. *Nat Genet*. 2008;40(7):838–40.
42. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet*. 2007;81(3):559–75.
43. Kochi Y, Yamada R, Suzuki A, Harley JB, Shirasawa S, Sawada T, Bae SC, Tokuhira S, Chang X, Sekine A, et al. A functional variant in FCRL3, encoding Fc receptor-like 3, is associated with rheumatoid arthritis and several autoimmunities. *Nat Genet*. 2005;37(5):478–85.
44. Maciel LM, Rodrigues SS, Dibbern RS, Navarro PA, Donadi EA. Association of the HLA-DRB1\*0301 and HLA-DQA1\*0501 alleles with Graves' disease in a population representing the gene contribution from several ethnic backgrounds. *Thyroid*. 2001;11(1):31–5.
45. Barlow AB, Wheatcroft N, Watson P, Weetman AP. Association of HLA-DQA1\*0501 with Graves' disease in English Caucasian men and women. *Clin Endocrinol (Oxf)*. 1996;44(1):73–7.
46. Simmonds MJ, Heward JM, Carr-Smith J, Foxall H, Franklyn JA, Gough SC. Contribution of single nucleotide polymorphisms within FCRL3 and MAP3K7IP2 to the pathogenesis of Graves' disease. *J Clin Endocrinol Metab*. 2006;91(3):1056–61.
47. Newman WG, Zhang Q, Liu X, Walker E, Ternan H, Owen J, Johnson B, Greer W, Mosher DP, Maksymowych WP, et al. Rheumatoid arthritis association with the FCRL3 -169C polymorphism is restricted to PTPN22 1858 T-homozygous individuals in a Canadian population. *Arthritis Rheum*. 2006;54(12):3820–7.
48. Eike MC, Nordang GB, Karlsen TH, Boberg KM, Vatn MH, Dahl-Jorgensen K, Ronningen KS, Joner G, Flato B, Bergquist A, et al. The FCRL3 -169 T > C polymorphism is associated with rheumatoid arthritis and shows suggestive evidence of involvement with juvenile idiopathic arthritis in a Scandinavian panel of autoimmune diseases. *Ann Rheum Dis*. 2008;67(9):1287–91.
49. Zhao SX, Liu W, Zhan M, Song ZY, Yang SY, Xue LQ, Pan CM, Gu ZH, Liu BL, Wang HN, et al. A refined study of FCRL genes from a genome-wide association study for Graves' disease. *PLoS One*. 2013;8(3):e7758.

50. Davis RS. Fc receptor-like molecules. *Annu Rev Immunol.* 2007;25:525–60.
51. Miller I, Hatzivassiliou G, Cattoretti G, Mendelsohn C, Dalla-Favera R. IRTAs: a new family of immunoglobulinlike receptors differentially expressed in B cells. *Blood.* 2002;99(8):2662–9.
52. Davis RS, Wang YH, Kubagawa H, Cooper MD. Identification of a family of Fc receptor homologs with preferential B cell expression. *Proc Natl Acad Sci U S A.* 2001;98(17):9772–7.
53. Choi CB, Kang CP, Seong SS, Bae SC, Kang C. The -169C/T polymorphism in FCRL3 is not associated with susceptibility to rheumatoid arthritis or systemic lupus erythematosus in a case–control study of Koreans. *Arthritis Rheum.* 2006;54(12):3838–41.
54. Martinez A, Sanchez E, Valdivia A, Orozco G, Lopez-Nevot MA, Pascual-Salcedo D, Balsa A, Fernandez-Gutierrez B, de la Concha EG, Garcia-Sanchez A, et al. Epistatic interaction between FCRL3 and NFkappaB1 genes in Spanish patients with rheumatoid arthritis. *Ann Rheum Dis.* 2006;65(9):1188–91.
55. Hu X, Chang M, Saiki RK, Cargill MA, Begovich AB, Ardlie KG, Criswell LA, Seldin MF, Amos CI, Gregersen PK, et al. The functional -169 T->C single-nucleotide polymorphism in FCRL3 is not associated with rheumatoid arthritis in white North Americans. *Arthritis Rheum.* 2006; 54(3):1022–5.
56. Hensley K, Venkova K, Christov A, Gunning W, Park J. Collapsin response mediator protein-2: an emerging pathologic feature and therapeutic target for neurodegeneration. *Mol Neurobiol.* 2011;43(3):180–91.
57. Vincent P, Collette Y, Marignier R, Vuaillet C, Rogemond V, Davoust N, Malcus C, Cavagna S, Gessain A, Machuca-Gayet I, et al. A role for the neuronal protein collapsin response mediator protein 2 in T lymphocyte polarization and migration. *J Immunol.* 2005;175(11):7650–60.
58. Varrin-Doyer M, Vincent P, Cavagna S, Auvergnon N, Noraz N, Rogemond V, Honnorat J, Moradi-Ameli M, Giraudon P. Phosphorylation of collapsin response mediator protein 2 on Tyr-479 regulates CXCL12-induced T lymphocyte migration. *J Biol Chem.* 2009;284(19):13265–76.
59. Varrin-Doyer M, Nicolle A, Marignier R, Cavagna S, Benetollo C, Wattel E, Giraudon P. Human T lymphotropic virus type 1 increases T lymphocyte migration by recruiting the cytoskeleton organizer CRMP2. *J Immunol.* 2012; 188(3):1222–33.

Submit your next manuscript to BioMed Central and we will help you at every step:

- We accept pre-submission inquiries
- Our selector tool helps you to find the most relevant journal
- We provide round the clock customer support
- Convenient online submission
- Thorough peer review
- Inclusion in PubMed and all major indexing services
- Maximum visibility for your research

Submit your manuscript at  
[www.biomedcentral.com/submit](http://www.biomedcentral.com/submit)

