Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease

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Australia, 42 Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Helsinki, Finland, 43 Institute of Human Genetics, Helmholtz Zentrum München, Munich, Germany, 44 Institute of Human Genetics, Technische Universität München, Munich, Germany, 45 Department of Cardiology and Internal Medicine, University Hospital Ghet and Faculty of Medicine, Ghent University, Ghent, Belgium, 46 Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge, United Kingdom, 47 Department of Medical Genetics, University of Helsinki and University Central Hospital, Helsinki, Finland, 48 Diagnostica Stago, Doncaster, Victoria, Australia, 49 Institute for Translational Genomics and Population Sciences, Los Angeles Biomedical Research Institute, Torrance, California, United States of America, 50 Department of Pediatrics, Harbor-UCLA Medical Center, Torrance, United States of America, 51 Institute for Community Medicine, University Medicine Greifswald, Greifswald, Germany, 52 Department of Twin Research and Genetic Epidemiology, King’s College London, London, United Kingdom, 53 School of Clinical and Experimental Medicine, College of Medical and Dental Sciences, University of Birmingham, Edgbaston, Birmingham, United Kingdom, 54 Diabetes, Endocrinology and Vascular Health Centre, Royal Devon and Exeter NHS Foundation Trust, Exeter, United Kingdom, 55 BIOIBIX Lab. for Bioinformatics and Computational Genomics, Dept. of Mathematical Modelling, Statistics and Bioinformatics. Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, 56 Faculty of Health Science, University of Copenhagen, Copenhagen, Denmark, 57 Department of General Practice and Primary Health Care, University of Helsinki, Helsinki, Finland, 58 Helsinki University Central Hospital, Unit of General Practice, Helsinki, Finland, 59 Folkhalsan Research Centre, Helsinki, Finland, 60 Vasa Central Hospital, Vasa, Finland, 61 Curtin Health Innovation Research Institute, Curtin University of Technology, Bentley, Western Australia, Australia, 62 Institute of Epidemiology I, Helmholtz Zentrum Munich, Munich, Germany, 63 Group Health Research Institute, Group Health Cooperative, Seattle, Washington, United States of America, 64 Department of Internal Medicine, Diabetes & Endocrinology Unit, San Raffaele Scientific Institute and Vita-Salute San Raffaele University, Milan, Italy, 65 Laboratory of Genetics, National Institute on Aging, Baltimore, Maryland, United States of America, 66 Institute for Maternal and Child Health - IRCCS “Burlo Garofolo”, Trieste, Italy, 67 University of Trieste, Trieste, Italy, 68 Biopharmacy, Department of Pharmaceutical Sciences, University Basel, Basel, Switzerland, 69 Netherlands Consortium for Healthy Aging, Netherlands Genomics Initiative, Leiden, The Netherlands, 70 Department of Internal Medicine, VU Medical Center, Amsterdam, The Netherlands, 71 Division of Endocrinology, Diabetes, and Metabolism, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, Pennsylvania, United States of America, 72 Institute of Molecular Genetics-CNR, Pavia, Italy

Abstract

Autoimmune thyroid diseases (AID) are common, affecting 2-5% of the general population. Individuals with positive thyroid peroxidase antibodies (TPOAbs) have an increased risk of autoimmune hypothyroidism (Hashimoto’s thyroiditis) as well as autoimmune hyperthyroidism (Graves’ disease). As the possible causative genes of TPOAbs and AID remain largely unknown, we performed GWAS meta-analyses in 18,297 individuals for TPOAb-positivity (1769 TPOAb-positives and 16,528 TPOAb-negatives) and in 12,353 individuals for TPOAb serum levels, with replication in 8,990 individuals. Significant associations (P<5x10^-8) were detected at TPO-rs11675434, ATXN2-rs653178, and BACH2-rs10944479 for TPOAb-positivity, and at TPO-rs11675434, MAGI3-rs1230666, and KALRN-rs210099 for TPOAb levels. Individual and combined effects (genetic risk scores) of these variants on (subclinical) hyper- and hypothyroidism, goiter and thyroid cancer were studied. Individuals with a high genetic risk score had, besides an increased risk of TPOAb-positivity (OR: 2.18, 95% CI 1.68–2.81, P = 8.1x10^-8), a higher risk of increased thyroid-stimulating hormone levels (OR: 1.51, 95% CI 1.26–1.82, P = 2.9x10^-8), as well as a decreased risk of goiter (OR: 0.77, 95% CI 0.66–0.89, P = 6.5x10^-8). The MAGI3 and BACH2 variants were associated with an increased risk of hypothyroidism, which was replicated in an independent cohort of patients with Graves’ disease (OR: 1.37, 95% CI 1.22–1.54, P = 1.2x10^-7) and OR: 1.25, 95% CI 1.12–1.39, P = 6.2x10^-5). The MAGI3 variant was also associated with an increased risk of hypothyroidism (OR: 1.57, 95% CI 1.18–2.10, P = 1.9x10^-3). This first GWAS meta-analysis for TPOAbs identified five newly associated loci, three of which were also associated with clinical thyroid disease. With these markers we identified a large subgroup in the general population with a substantially increased risk of TPOAbs. The results provide insight into why individuals with thyroid autoimmunity do or do not eventually develop thyroid disease, and these markers may therefore predict which TPOAb-positives are particularly at risk of developing clinical thyroid dysfunction.


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† These authors contributed equally to this work.

‡ SS, SN and RPP also contributed equally to this work.

Introduction

Autoimmune thyroid disease (AITD), including Hashimoto’s thyroiditis and Graves’ disease, is one of the most common autoimmune diseases, affecting 2–5% of the general population [1,2,3]. Thyroid dysfunction has been associated with osteoporosis, depression, atrial fibrillation, heart failure, metabolic syndrome, and mortality [4,5,6,7,8,9,10,11]. High serum antibodies against the enzyme thyroid peroxidase (TPO), which is located in the thyroid and plays a key role in thyroid hormone synthesis, are present in 90% of patients with Hashimoto’s thyroiditis [12,13], the most frequent cause of hypothyroidism and goiter. Although TPO antibodies (TPOAbs) are a useful clinical marker for the detection of early AITD, it remains controversial if these antibodies play a causative role in the pathogenesis of Hashimoto’s thyroiditis [14,15,16].

Interestingly, TPOAb-positive persons also have an increased risk of developing autoimmune hyperthyroidism (Graves’ disease) [17,18], which is caused by stimulating antibodies against the thyroid stimulating hormone (TSH) receptor [19]. Numerous studies have shown that Graves’ hyperthyroidism and Hashimoto’s thyroiditis show co-inheritance [17,20,21]. Finally, thyroid autoimmunity is the most common autoimmune disorder in women of childbearing age, and TPOAb-positive women have an increased risk of developing pregnancy complications such as miscarriage and pre-term delivery [17,18,22,23,24,25,26].

The prevalence of TPOAb-positivity in the general population ranges from 5–24%, but it is currently unknown why these people develop TPOAbs, nor is it known why not all individuals with thyroid autoimmunity develop clinical thyroid disease [27,28]. It is estimated that around 70% of the susceptibility to develop thyroid autoantibodies is due to genetic factors [29]. In this context it is remarkable to note that little is known about the genetic factors that determine TPOAb-positivity and the risk of AITD.

We therefore performed a genome wide association study (GWAS) meta-analysis for TPOAbs in the general population in 18,297 individuals from 11 populations. Newly identified genetic variants were studied in relation to subclinical and overt hypo- and hyperthyroidism, goiter, thyroid autoimmunity during pregnancy and thyroid cancer risk.

Results

Characteristics of the studied populations are shown in Table 1 and the Supplementary Material S1. Heritability estimates in the family-based cohorts SardiNIA, TwinsUK and Val Borbera were, respectively, 0.65, 0.66, and 0.54 for TPOAb-positivity, and 0.43, 0.66, and 0.30 for TPOAb levels.

Loci associated with TPOAb-positivity and TPOAb levels

See Table 1 and Supplementary Figure S1 for TPOAb measurements and Supplementary Table S1 for genotyping procedures. In most autoimmune diseases, both the presence and the level of autoantibodies are relevant for the disease onset [18,30,31]. Furthermore, different pathophysiological processes may be involved in the initiation and severity of the autoimmune response. We therefore performed a GWAS on TPOAb-positivity (including 1769 TPOAb-positives and 16,328 TPOAb-negatives), as well as a GWAS on continuous TPOAb levels (including 12,353 individuals) in stage 1. See Supplementary Figures S2 and S3 for QQ (quantile-quantile) and Manhattan plots.

In stage 2, we followed-up 20 stage 1 SNPs (P<5×10−6; 13 TPOAb-positivity and 10 TPOAb level SNPs, with 3 SNPs overlapping) in 5 populations, including up to 8,990 individuals for TPOAb-positivity (922 TPOAb-positives and 8068 TPOAb-negatives) and 8,159 individuals for TPOAb level analyses (see Supplementary Material S1). Results of the combined stage 1 and 2...
Individuals with thyroid peroxidase antibodies (TPOAbs) have an increased risk of autoimmune thyroid diseases (AITD), which are common in the general population and associated with increased cardiovascular, metabolic and psychiatric morbidity and mortality. As the causative genes of TPOAbs and AITD remain largely unknown, we performed a genome-wide scan for TPOAbs in 18,297 individuals, with replication in 8,990 individuals. Significant associations were detected with variants at TPO, ATXN2, BACH2, MAGI3, and KALRN. Individuals carrying multiple risk variants also had a higher risk of increased thyroid-stimulating hormone levels (including subclinical and overt hyperthyroidism), and a decreased risk of goiter. The MAGI3 and BACH2 variants were associated with an increased risk of hyperthyroidism, and the MAGI3 variant was also associated with an increased risk of hypothyroidism. This first genome-wide scan for TPOAbs identified five newly associated loci, three of which were also associated with clinical thyroid disease. With these markers we identified a large subgroup in the general population with a substantially increased risk of TPOAbs. These results provide insight into why individuals with thyroid autoimmunity do or do not eventually develop thyroid disease, and these markers may therefore predict which individuals are particularly at risk of developing clinical thyroid dysfunction.

Associations with thyroid disease in independent populations

a) Graves’ disease. As MAGI3 rs1230666 and BACH2 rs10944479 showed promising associations (i.e., P≤0.05) with hyperthyroidism in our meta-analyses, we tested these SNPs in an independent population of 2478 patients with Graves’ disease and 2682 controls (see Supplementary Material for further details). Both were associated with an increased risk of Graves’ disease (MAGI3 rs1230666: OR, 1.37 [95% CI, 1.22–1.54]; P = 1.2×10⁻⁷; BACH2 rs10944479: OR, 1.25 [1.12–1.39]; P = 6.2×10⁻⁷).

b) Thyroid cancer. Supplementary Table S6 shows the associations of the 5 GWAS significant SNPs with thyroid cancer. No statistically significant associations were detected, but a borderline significant signal with an increased risk of thyroid cancer was observed at ATXN2 rs653178 (OR, 1.32 [95% CI, 1.02–1.70]; P = 0.03).

Pathway analyses

Ingenuity Pathway Analyses (IPA; Ingenuity Systems, Ca, USA) and GRAIL analyses [32] were performed to identify potential pathways involved in AITD, the results of which are shown in Supplementary Tables S7 and S8, and Figure S6. The identified top pathways involved cell death, survival, movement, and OX40 signalling.

Discussion

This is the first GWAS meta-analysis investigating the genetics of TPOAbs in the normal population in up to 18,297 individuals from 11 populations with replication in up to 8,990 individuals from 5 populations. We identified 5 GWAS significant loci associated with TPOAb-positivity and/or levels.

The most significant hit for both TPOAb-positivity and TPOAb levels was located near the TPO gene itself. TPO is a membrane-bound protein located on the apical membranes of the thyroid follicular cell, catalyzing key reactions in thyroid hormone synthesis [33]. Mutations in TPO have been found in patients with congenital hypothyroidism [34,35]. Although TPOAbs are
<table>
<thead>
<tr>
<th>Study</th>
<th>Ethnic group (origin)</th>
<th>Sample characteristics</th>
<th>TPOAb specifications</th>
<th>TSH specifications</th>
<th>FT4 specifications</th>
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<td></td>
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<td>N with TPOAb and GWAS data</td>
<td>Age (yrs) Mean (SD)</td>
<td>TPOAb-positivity (%), TPOAb-positivity cut off</td>
<td>TSH Median (IQR), Assay (normal range)</td>
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<td></td>
<td>Men (%)</td>
<td>N continuous approach</td>
<td>Men (%)</td>
<td>Continuous approach</td>
<td>N case-control approach (cases/controls)</td>
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<td>BHS</td>
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<td>1363 47</td>
<td>1316 (197/1119)</td>
<td>1316 43%</td>
<td>15.0% 35</td>
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<td>CHS</td>
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<td>2024 0</td>
<td>2024 (281/1743)</td>
<td>1817 41%</td>
<td>13.9% 34</td>
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<td>HBCS</td>
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<td>15.1% 12</td>
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<td>KORA</td>
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<td>1475 (74/1401)</td>
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<tr>
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<td>1829 (287/1542)</td>
<td>1829 50%</td>
<td>15.7% 12</td>
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<tr>
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<td>1577 (137/1440)</td>
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<td>972 (108/864)</td>
<td>1257 49%</td>
<td>11.1% 35</td>
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<tr>
<td>SHIP</td>
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<td>3803 (265/3538)</td>
<td>1818 52%</td>
<td>7.0% 60</td>
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<td>2369 (461/1893)</td>
<td>774 0%</td>
<td>19.5% 6</td>
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<tr>
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<td>1571 (161/1410)</td>
<td>1571 46%</td>
<td>10.2% 60 and 50</td>
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### Table 1. Cont.

<table>
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<tr>
<th>Study</th>
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<td>N using thyroid medication</td>
<td>N continuous approach (cases/controls)</td>
<td>Age (yrs) Mean (SD)</td>
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<td></td>
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<td>270</td>
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<td>EFSTOH</td>
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<td>-</td>
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<td>Health2006 Study</td>
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<td>-</td>
<td>3287 (204/3083)</td>
<td>64%</td>
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<tr>
<td>SardiNIA2</td>
<td>Caucasian (Italy)</td>
<td>1387</td>
<td>30</td>
<td>765 (104/661)</td>
<td>41%</td>
</tr>
</tbody>
</table>

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valid clinical biomarkers ofAITD, they are generally considered to be secondary to the thyroid damage inflicted by T-cells.

The FOXE1 gene has been previously associated with hypothyroidism [36,37] and is known to regulate transcription of TPO [38]. In this context it is interesting to note that we did not find any associations of the variant near TPO with hypothyroidism. Most genes that have been associated with AITD (predominantly Graves’ disease) by candidate gene and GWAS studies so far are located in the HLA class I and II regions, or in genes involved in T-cell (i.e., CTLA-4, PTPN22) or other autoimmune responses [28,39]. Until now, the TPO gene itself had not been associated with AITD, except in one recent candidate gene analysis in a small cohort (n = 188) without replication [40]. A variant near TPO (rs11675434), which is in LD with rs11675434 (r2 = 0.97 in HapMap2), has previously been associated with TSH levels by Gudmundsson et al [41]. However, various other GWAS on serum TSH and FT4 levels have not found any significant associations in or near this locus, including a recent similar sized GWAS by Porcu et al [42].

Three of the four loci identified here are located in or are in linkage disequilibrium (LD) with genes previously associated with other autoimmune diseases. Rs1230666 is located in intron 9 of MAGE3, encoding a protein that modulates activity of AKT/PKB. AKT/PKB is expressed in the thyroid and regulates apoptosis [43], which seems to play an important role in the development of AITD [44,45]. In addition, rs1230666 is in LD with rs2476601 (r2 = 0.70 in HapMap2), a variant causing a R620W substitution in PTPN22. PTPN22 is a lymphoid-specific intracellular phosphatase involved in the T-cell receptor signaling pathway. Variations in PTPN22, and specifically R620W, are associated with various autoimmune disorders including type 1 diabetes, rheumatoid arthritis, systemic lupus erythematosus, and Graves’ disease [46,47,48,49]. The associations of the MAGE3 locus with TPOAb-positivity and Graves’ disease may therefore also be explained by linkage with disease-associated variants in PTPN22 [50]. Of note, the association signal at rs2476601 is one order weaker than that of the top variant rs1230666.

The BACH2 locus has been implicated in the susceptibility to several autoimmune diseases, including celiac disease, type 1 diabetes, vitiligo, Crohn’s disease, and multiple sclerosis [46,51,52,53,54]. A recent candidate gene analysis associated the BACH2 locus with an increased risk ofAITD, including Hashimoto’s thyroiditis and Graves’ disease [55]. However, the associations were not significant when Hashimoto’s thyroiditis and Graves’ disease were studied separately. BACH2 is specifically expressed in early stages of B-cell differentiation and represses different immunoglobulin genes [56]. Interestingly, BACH2 can bind to the co-repressor SMRT (silencing mediator of retinoid and thyroid receptor), which may suggest a more direct effect on thyroid hormone secretion and action as well.

Polymorphisms in ATXN2 have been associated with multiple neurodegenerative diseases, including spinocerebellar ataxia and Parkinson’s disease [57,58,59]. Different epidemiological studies have associated thyroid dysfunction with cerebellar ataxia [60,61]. Furthermore, the identified SNP in ATXN2 has been previously associated with renal function, serum urate levels and blood pressure [62,63,64]. However, this SNP is in high LD with rs3184504 (r2 = 0.873), a variant causing a Trp262Arg substitution in SH2B3 (SH2B3). SH2B3 encodes the adaptor protein LNK, a key negative regulator of cytokine signaling playing a critical role in hematopoiesis. This variant is associated with susceptibility to several autoimmune diseases, including celiac disease, type 1 diabetes, vitiligo, and rheumatoid arthritis [46,51,53,65], suggesting more relevance for TPOAb levels than ATXN2. This is supported by a recent study which showed that variants in LD with SH2B3, BACH2, and PTPN22 are associated with TPOAb levels in patients with type 1 diabetes [66].

Whereas the above four loci are located in genes involved in the immune response or the autoantigen, the KALRN (Kalrin) gene encodes a multi-domain guanine nucleotide exchange factor for GTP-binding proteins of the Rho family. The relation of KALRN with levels of TPOAbs is unclear. This gene has recently been found to be associated with megakaryopoiesis and platelet formation [67], which may suggest a function in the immune system [68]. We furthermore performed pathway analyses on the stage 1 TPOAb-positivity and TPOAb level lead SNPs, and identified the cell death, survival and movement pathway as an important pathway for TPOAbs. This finding is supported by previous studies, which show an important role for apoptosis in the

**Table 2.** Newly identified loci associated with TPOAb-positivity and/or serum TPOAb levels reaching genome wide significance.

<table>
<thead>
<tr>
<th>Alleles</th>
<th>Stage 1 + 2 meta-analysis: up to 2691 cases and 24,596 controls</th>
</tr>
</thead>
<tbody>
<tr>
<td>TPOAb-positivity SNP</td>
<td>Chr.</td>
</tr>
<tr>
<td>rs11675434</td>
<td>2</td>
</tr>
<tr>
<td>rs6533178</td>
<td>12</td>
</tr>
<tr>
<td>rs10944479</td>
<td>6</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Alleles</th>
<th>Stage 1 + 2 meta-analysis: up to 20,512 subjects</th>
</tr>
</thead>
<tbody>
<tr>
<td>TPOAb levels SNP</td>
<td>Chr.</td>
</tr>
<tr>
<td>rs11675434</td>
<td>2</td>
</tr>
<tr>
<td>rs1230666</td>
<td>1</td>
</tr>
<tr>
<td>rs2010099</td>
<td>3</td>
</tr>
</tbody>
</table>

Chr., chromosome

aRisk allele frequency: Weighted mean frequency of the risk allele across all included cohorts.

bAdjusted for age and gender

cExpressed in sd of natural logarithm transformed serum TPOAb level, adjusted for age and gender

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**Table 2.** Newly identified loci associated with TPOAb-positivity and/or serum TPOAb levels reaching genome wide significance.
development of AITD [44,45]. Another top pathway involved was the OX40 signalling pathway, and it is of interest to note that OX40 is a T-cell activator promoting the survival of CD4+ T-cells at sites of inflammation [69].

Our results have potential clinical relevance for several reasons. Genetic risk scores based on these novel common (risk allele frequencies: 9–40%) TPOAb-associated SNPs enabled us to identify a large subgroup in the general population with a two-fold
increased risk of TPOAb-positivity (10.4% vs 5.4%). These individuals also have a higher risk of increased TSH levels and a lower risk of goiter, suggesting an advanced stage of destruction of the thyroid due to autoimmune processes. Furthermore, pregnant women with high genetic risk scores had a 2.4 times increased risk of TPOAb-positivity during pregnancy. In this context it is interesting to note that TPOAb-positive pregnant women have an increased risk of miscarriages and preterm births independent of thyroid function [70].

Associations with thyroid disease were also found on an individual SNP level. The MAGI3 SNP was associated with a substantially increased risk of hypothyroidism, and the BACH2 SNP showed a borderline significant association ($P = 0.011$) with a higher risk of increased TSH levels, which includes subjects with subclinical and overt hypothyroidism. Furthermore, both loci were significantly associated with an increased risk of Graves' hyperthyroidism in an independent population. To predict which patients with first or second degree relatives with documented Hashimoto’s or Graves’ disease will develop clinical thyroid disease, a clinical algorithm has been developed (i.e., the THEA score) [18]. Future studies should analyze if these genetic markers increase the sensitivity of the THEA score.

The prevalence of TPOAb-positivity in the general population is high (5–24%), but it is currently unknown why part of the individuals with thyroid autoimmunity develop clinical thyroid disease whereas others do not [27,28]. In this context it is interesting to note that the TPOAb-associated SNPs located in TPO and ATXN2 were not associated with clinical thyroid disease. This suggests that the TPOAbs in these individuals may be of less clinical relevance, providing insight into why TPOAb-positive individuals do or do not eventually develop clinical thyroid disease.

Our study has some limitations. The validity of the results is restricted to individuals from populations of European ancestry. Future GWASs in populations from non-European descent will be required to determine to which extent our results can be generalized to other ethnic groups. Secondly, we did not perform conditional analyses to further identify secondary association signals within the identified loci, nor did we perform functional studies for the identified variants. Further research is therefore needed to unravel the exact biological mechanism behind the observed associations. The fact that various TPOAbs assays were used across the participating cohorts could lead to bias. We
Therefore used TPOAb-positivity cut-off values as provided by the respective assay manufacturer, instead of using one fixed cut-off value. This is also of clinical importance as in clinical practice most institutions rely on the TPOAb-positivity cut-off as provided by the assay manufacturer. Furthermore, we did not detect heterogeneity in our results, supporting the fact that results obtained with different assays can be combined across cohorts using the z-score based meta-analysis. Finally, as AITD coincides with other autoimmune diseases, our results could be driven by indirect associations with other autoimmune diseases. However, AITD is the most common autoimmune disease in the general population. We furthermore show that carriage of multiple risk alleles is associated with an increased risk of thyroid dysfunction, which underlines the clinical importance of our findings.

In conclusion, this first GWAS for TPOAbs identified five newly associated loci, three of which were also associated with clinical thyroid disease. Furthermore, we show that carriage of multiple risk variants is not only associated with a substantial increased risk of TPOAb-positivity, but also with a higher risk of increased TSH levels (including subclinical and overt hypothyroidism) and a lower risk of goiter. These genetic markers not only help to identify large groups in the general population with an increased risk of TPOAb-positivity, but may also predict which TPOAb-positive persons are particularly at risk of developing clinical thyroid disease.

Materials and Methods

Study cohorts

For the TPOAb GWAS stage 1 and 2 analyses, and the hypothyroidism, hyperthyroidism and goiter analyses, individuals were recruited from 16 independent community-based and family studies. For the Graves’ disease analyses, cases were recruited from the United Kingdom Graves’ disease cohort and controls from the British 1958 Birth Cohort. Thyroid cancer cases and controls were recruited from the Nijmegen and Ohio thyroid cancer cohorts. A detailed description of the original cohorts contributing samples is provided in Table 1 and in the Supplementary Material. All participants provided written informed consent and protocols were approved by the institutional review boards or research ethics committees at the respective institutions, and conducted according to the Declaration of Helsinki.

Phenotype definitions

Serum TPOAb levels were determined with a range of assays. TPOAb-positives were defined as subjects with TPOAb levels above the assay-specific TPOAb-positivity cut-off, as defined by the manufacturer (Table 1). Serum TSH and free thyroxine (FT4) levels were determined using a range of assays (Table 1). Assay-specific TSH and FT4 reference ranges were used, as provided by the manufacturer (Table 1). Overt hypothyroidism was defined as a high TSH (i.e., a TSH level above the TSH reference range) and a low FT4. Increased TSH was defined as a high TSH, including persons with overt hypothyroidism or subclinical hypothyroidism (i.e., high TSH with a normal FT4). Overt hyperthyroidism was defined as a low TSH and a high FT4. Decreased TSH was defined as a low TSH, including persons with subclinical or overt hyperthyroidism.

The diagnosis of goiter is described in the Supplementary Material, and the diagnosis of Graves’ disease and thyroid cancer in the respective cohorts have been described previously [41].

Genotyping

Samples were genotyped with a range of GWAS genotyping arrays (Supplementary Table S1). Sample and SNP quality control procedures were undertaken within each study. For each GWAS, over 2.5 million SNPs were imputed using CEU samples from Phase 2 of the International HapMap project (www.hapmap.org). Genotyping procedures in the stage 2, Graves’ disease and thyroid cancer populations are described in the Supplementary Material.

Association analyses

The heritabilities of TPOAb-positivity and serum TPOAb levels were estimated, as described in the Supplementary Material. In stage 1, we performed a GWAS on TPOAb-positivity as well as a GWAS on continuous TPOAb levels. Persons taking thyroid medication were excluded. Each SNP was tested for association with TPOAb-positivity using logistic regression analyses, adjusting for age and sex. For cohorts with family structure, we approximated the probability of being affected with a linear mixed model adjusting for age and sex. The produced model was used to predict the expected proportion of “risk” (effective) alleles in cases and controls, hence giving the means to estimate odds ratios. Only unrelated individuals were considered for the SardiNIA cohort.

For the GWAS of continuous TPOAb levels, samples with a TPOAb level lower than the minimum TPOAb assay detection limit (Table 1) were excluded. TPOAb levels were natural log-transformed, and sex-specific, age adjusted standardized residuals were calculated. Each SNP was tested for association with these TPOAb level residuals using linear regression analyses (additive model),

### Table 5. Newly identified TPOAb associated loci, genetic risk scores and the risk of goiter.

<table>
<thead>
<tr>
<th>Nearby gene</th>
<th>SNP</th>
<th>Risk allele</th>
<th>Other allele</th>
<th>OR (95% CI)*</th>
<th>P value</th>
<th>GRS Quartile</th>
<th>% Goiter (N cases/total)</th>
<th>OR (95% CI)*</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>TPO</td>
<td>rs11675434</td>
<td>T</td>
<td>C</td>
<td>0.95 (0.88–1.02)</td>
<td>0.17</td>
<td>1 (reference)</td>
<td>35.2% (588/1669)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>ATXN2</td>
<td>rs653178</td>
<td>A</td>
<td>G</td>
<td>0.94 (0.85–1.05)</td>
<td>0.28</td>
<td>3</td>
<td>33.7% (570/1691)</td>
<td>0.92 (0.79–1.06)</td>
<td>0.21</td>
</tr>
<tr>
<td>BACH2</td>
<td>rs10944479</td>
<td>A</td>
<td>G</td>
<td>0.90 (0.81–1.00)</td>
<td>0.05</td>
<td>4</td>
<td>30.4% (517/1702)</td>
<td>0.77 (0.66–0.89)</td>
<td>6.5×10^-4</td>
</tr>
<tr>
<td>MAGI3</td>
<td>rs1230666</td>
<td>A</td>
<td>G</td>
<td>0.93 (0.81–1.05)</td>
<td>0.23</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

GRS, genetic risk score (based on rs11675434, rs653178, rs10944479, rs1230666, rs2010099).

*Adjusted for age, gender, and body surface area.

ATXN2/rs653178 is in high LD with SN283-rs3184504.

MAGI3/rs1230666 is in high LD with PTPN22-rs24756601.

doi:10.1371/journal.pgen.1004123.t005
correcting for relatedness in studies with family structure. See Supplementary Table S1 for the software used for these analyses.

Before meta-analysis, SNPs with a minor allele frequency (MAF) <1% or a low imputation quality were excluded (Supplementary Material). After the results for each GWAS were combined in a population size weighted z-score based meta-analysis using METAL [71]. Genomic control was applied to individual studies if λ>1.0.

In stage 2, we followed-up stage 1 GWAS significant SNPs, as well as promising SNPs not reaching GWAS significance, in an attempt to reach GWAS significant associations by increasing sample size (Supplementary Material). Results from stage 1 and 2 were combined in a population size weighted z-score based meta-analysis using METAL [71]. A z-score based meta-analysis was used to reduce bias that might be induced by different assays. As this method does not provide betas, and we wanted to provide a rough estimate of the actual effect sizes for convenience, we calculated betas using the fixed effects (inverse variance based) meta-analysis method. Heterogeneity was tested, applying Bonferroni based P-value thresholds of \(P=0.004\) for the TPOAb-positivity analyses and \(P=0.005\) for the TPOAb level analyses.

All studies assessed and, if present, corrected for population stratification using principal-component analysis (PCA) and/or multidimensional-scaling (MDS), with the exception of SardiNIA and ValBorbera where the high isolation substantiates a lack of stratification (Table S1) [72,73]. Lambda values were all \(\sim1\), indicating that population stratification was overall properly accounted for (Table S1). To fully remove residual effects, we applied genomic correction to studies were lambda was \(>1\). The final meta-analyses reported a lambda of 1.01 for both the TPOAb-positivity and the TPOAb level GWAS, thus no genomic correction was applied.

The variances explained by the GWAS significant SNPs were calculated. We subsequently studied the individual as well as the combined effects of the GWAS significant SNPs on the risk of clinical thyroid disease, as specified in the Supplementary Material. In short, to study combined effects, a genetic risk score was calculated for every person as the weighted sum of TPOAb risk alleles. The associations between the individual SNPs, genetic risk scores and the risk of abnormal thyroid function tests were studied using logistic regression analyses. Logistic regression analyses were used to study the associations with goiter, Graves’ disease and thyroid cancer (Supplementary Material). The results of each study were combined in a population size weighted z-score based meta-analysis using METAL [71].

Various bioinformatic tools were searched for evidence for functional relevance of the GWAS significant SNPs and pathway analyses were performed on the Stage 1 lead SNPs (see Supplementary Material).

**Supporting Information**

**Figure S1** TPOAb level distributions in persons with detectable TPOAb levels in stage 1 and 2 populations. (PPTX)

**Figure S2** Quantile-quantile (QQ) plots for the TPOAb-positivity and TPOAb level stage 1 meta-analyses. (PPTX)

**Figure S3** Manhattan plots for stage 1 meta-analyses for TPOAb-positivity (a) and TPOAb levels (b). SNPs are plotted on the x-axis according to their chromosomal position against TPOAb-positivity (a) or TPOAb levels (b) (shown as \(-\log_{10}(P)\) value) on the y-axis. The horizontal grey line indicates the threshold for genome-wide statistical significance (\(P<5 \times 10^{-8}\)). Genome-wide significant associations were observed near TPO (Chr 2p25; \(P=1.5 \times 10^{-13}\), at ATXN2 (Chr 12q24.1; \(P=1.6 \times 10^{-38}\)) and near HCPS (Chr 6p21.3; \(P=4.1 \times 10^{-5}\)) for TPOAb-positivity, and near TPO (Chr 2p25; \(P=5.4 \times 10^{-13}\)) and at ATXN2 (Chr 12q24.1; \(P=1.1 \times 10^{-38}\)) for TPOAb levels. (PPTX)

**Figure S4** Regional association plots of stage 1 lead loci for TPOAb-positivity (panels a-m). The y-axis on the left indicates the \(-\log_{10}(P)\) value for the association with TPOAb –positivity. SNPs are plotted on the x-axis according to their chromosomal position. The most significant stage 1 SNP is indicated in purple. The combined stage 1 and 2 result of this SNP is indicated in yellow. The SNPs surrounding the most significant SNP are color-coded to reflect their LD with this SNP. Symbols reflect functional genomic annotation, as indicated in the legend. The blue y-axes on the right of each plot indicate the estimated recombination rates (based on HapMap Phase II); the bottom of each panel shows the respective annotated genes at the locus and their transcriptional direction. Mb, megabases. (PPTX)

**Figure S5** Regional association plots of stage 1 lead loci for TPOAb levels (panels a-j). The y-axis on the left indicates the \(-\log_{10}(P)\) value for the association with TPOAb levels. SNPs are plotted on the x-axis according to their chromosomal position. The most significant stage 1 SNP is indicated in purple. The combined stage 1 and 2 result of this SNP is indicated in yellow. The SNPs surrounding the most significant SNP are color-coded to reflect their LD with this SNP. Symbols reflect functional genomic annotation, as indicated in the legend. The blue y-axes on the right of each plot indicate the estimated recombination rates (based on HapMap Phase II); the bottom of each panel shows the respective annotated genes at the locus and their transcriptional direction. Mb, megabases. (PPTX)

**Figure S6** GRAIL results for the stage 1 TPOAb-positivity and TPOAb level lead SNPs. GRAIL circle plot of locus connectivity where each locus is plotted in a circle, where significant connections (\(P<0.05\)) based on PubMed abstracts are drawn spanning the circle. Analyses were based on the 20 stage 1 TPOAb-positivity and TPOAb level lead SNPs. (PPTX)

**Table S1** Study sample genotyping, quality control and association analyses for stage 1 populations. (DOCX)

**Table S2** Associations of stage 1 lead SNPs with TPOAb-positivity in stage 1 and 2. (DOCX)

**Table S3** Associations of stage 1 lead SNPs with serum TPOAb levels in stage 1 and 2. (DOCX)

**Table S4** Stage 1 TPOAb-positivity and TPOAb level meta-analyses results for GWAS significant SNPs reported in previous GWAS on thyroid related phenotypes. (XLSX)

**Table S5** Genetic risk score and the risk of increased TSH levels. (DOCX)

**Table S6** Newly identified TPOAb associated loci and the risk of thyroid cancer. (DOCX)
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Author Contributions

Conceived and designed the experiments: MM SJR RAJ RR AA HJG ER JIR HH LC DT Ti BV TdM TJ JGE BMP AHo DS HW Ahid TMF AL LR KAK AGU JPW KS EWA CMe MDh TJV TDS SGW HV AC DTo SS SN RPP. Performed the experiments: MM EP GP AT LC SJR RAJ RR GLR TSP SHV JL MJ SS LLN RMF BMS CG YSA AL TJV SS SN RPP. Analyzed the data: MM EP GP AT SJR RAJ RR GLR TSP SHV JL MJ SS LLN RMF Sg BS LM CB CG EC TK ET YET AA MeVd CMA TcG MT NP YSA Ahid RN TtNM SGLG JMk AL JWAS FR MhS SS RPP. Contributed reagents/materials/analysis tools: MM RR GLR TSP JL MJ SS LLN BN MG SN Csa UV JBR JAF BV TdM TJ JGE BMP Ti Ahod HW Ahid RN TtNM SGLG HM AS TMF AL FR AGU JPW CMe TJV TDS SGW HV AC DTo SS RPP. Wrote the paper: MM AT LC SJV SGW AC SS SN RPP.