

Genetic susceptibility to Grave's disease

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1. ABSTRACT

The variety of clinical presentations of eye changes in patients with Graves' disease (GD) suggests that complex interactions between genetic, environmental, endogenous and local factors influence the severity of Graves' ophthalmopathy (GO). It is thought that the development of GO might be influenced by genetic factors and environmental factors, such as cigarette smoking. At present, however, the role of genetic factors in the development of GO is not known. On the basis of studies with candidate genes and other genetic approaches, several susceptibility loci in GO have been proposed, including immunological genes, human leukocyte antigen (HLA), cytotoxic T-lymphocyte antigen-4 (CTLA-4), regulatory T-cell genes and thyroid-specific genes. This review gives a brief overview of the current range of major susceptibility genes found for GD.

2. INTRODUCTION

Graves' disease (GD) is a systemic autoimmune syndrome with manifestation in thyroid and orbital connective tissue. Graves' ophthalmopathy (GO) is clinically characterized by exophthalmos, periorbital edema, eyelid retraction, extraocular muscle dysfunction, pain and optic neuropathy (1,2). These symptoms are related to the pathologic processes within the orbit of the eye that increase the volume of retro-ocular tissue, in which the orbital fibroblasts are the principal target of autoimmune attack and are the key to the pathophysiology of GO (3–5).

Even weak to moderately severe ophthalmopathy impacts greatly on and reduces the quality of life in affected patients (6). The course of GD is unpredictable and a rapid worsening of GO can occur at any time (7,8). As the treatment of GO is often inadequate, there is a need to recognize

potential predisposing factors and to develop sensitive and specific diagnostic procedures with which to identify GD patients at high risk of developing ophthalmopathy (9,10).

The exact etiology of the immune response to the thyroid is not known but there is evidence for a strong genetic influence on the development of autoimmune thyroid diseases (AITDs), including GD. It is currently accepted that AITDs are complex diseases in which susceptibility genes, in combination with environmental triggers, initiate the autoimmune response to the thyroid (11).

Both endogenous (genetic factors, increasing age, male gender) and exogenous factors (cigarette smoking, thyroid dysfunction (hyperthyroidism and hypothyroidism) and treatment with radiolabeled iodine) could contribute to the development and/or severity of GO (12). On the basis of studies with candidate genes and other genetic approaches, several susceptibility loci in GO have been proposed; for example, immunological genes, human leukocyte antigen (HLA), cytotoxic T-lymphocyte antigen-4 (CTLA-4), regulatory T-cell genes and thyroid-specific genes (13). It is widely agreed that complex diseases are not controlled by an individual gene or DNA variation alone but by a combination of genes or DNA variations. We give a brief overview of the current range of the susceptibility genes found for Graves' disease.

3. IMMUNOLOGICAL GENES

The immunological synapse is the interface between antigen-presenting cells (APCs) and T-cells that is formed during T-cell activation. This immunological complex interface involves a peptide antigen bound to an HLA class II molecule and to the T-cell receptor, costimulatory molecules, receptors on the APC and T-cells, integrins and other molecules (14). Interestingly, several GD susceptibility genes participate in the immunological synapse, suggesting that abnormalities in antigen presentation are important mechanisms in the pathway leading to GD.

3.1. CD40/CD40L

CD40, which is expressed primarily on B-cells and other APCs (15), has a fundamental role in B-cell activation and antibody secretion (16,17). The whole-genome linkage study done by Tomer identified a locus on chromosome 20q that was linked with GD. Fine mapping identified the CD40 gene as the GD susceptibility gene at this locus, and further sequencing studies of the CD40 gene demonstrated that a C/T single nucleotide polymorphism (SNP) in the Kozak sequence of CD40 was the likely causative variant (18–23). The CC genotype of this SNP is associated with GD (20–23) but one study did not find this association, possibly because of ethnic differences among populations (24); however, a meta-analysis confirmed the association (22). Intriguingly, we showed recently that the association of the CC genotype was stronger in a subset of GD patients with persistently high levels of thyroid antibodies (25). Mechanistically, the CC genotype is located in the Kozak sequence of CD40 and can alter CD40 translation and expression.

Other studies have shown that the C-allele of the polymorphism increases the translation of CD40 mRNA transcripts by 20–30% compared to the T-allele. CD40 is expressed on B-cells (15) and on thyroid follicular cells (25,26), which are both involved in the development of GD, and it is possible that increased expression of CD40 on B-cells and/or thyrocytes driven by the C-allele predisposes to disease. Thus, increased expression of CD40 on B-cells can result in enhanced production of anti-TSHR-stimulating antibodies, whereas increased expression of CD40 on thyrocytes can trigger an autoimmune response to the thyroid by resident T-cells. These mechanisms are not mutually exclusive and could both be operative.

Because CD40 is a major APC and B-cell costimulatory molecule, it is plausible that CD40 will have a role in the genetic susceptibility to other autoimmune diseases. Indeed, recent data show that CD40 is associated with and/or linked to high levels of IgE in asthma, rheumatoid arthritis, systemic lupus erythematosus and multiple sclerosis (27).

CD40L, which is expressed on activated T-cells, and its receptor CD40 have been shown to have a role in the onset and maintenance of autoimmune inflammation. Zhao *et al.* showed that CD40L can potentially induce ICAM-1 expression in orbital fibroblast cells through multiple signal pathways, such as the p38 MAPKs and NF- κ B pathways in orbital fibroblast cells.

3.2. The Fc receptor-like (FCRL) family

SNPs are the most common form of DNA variation and have great potential as a medical diagnostic tool. Wei *et al.* analyzed the association between combinations of SNPs and GD by investigating 108 SNPs in 384 cases and 652 controls. When this method was evaluated by differentiating between cases and controls in a five-fold cross-validation test, it achieved a prediction accuracy of 72.9% with a combination of 17 SNPs. The experimental results showed that SNPs, even those with a high *P*-value, have a greater effect on GD when acting in combination compared to their effect when acting individually (79).

The FCRL gene family, which encodes products that have a key role in controlling B-cell signaling (28,29) has been shown to be associated with several autoimmune diseases. A genome-wide screening of 15,000 non-synonymous SNPs in a UK Caucasian GD cohort confirmed the association of the previously detected GD susceptibility locus FCRL3 and detected the association of neighboring FCRL5 with GD (30). Simmonds *et al.* used tag SNP screening of FCRL5 in an enlarged data set and confirmed the association of this gene with GD. Although the association at FCRL5 was shown to be secondary to the association at FCRL3, it does not prove that FCRL3 contains the etiological variant represented by these associations. It is tempting to embark upon a functional analysis of rs11264798 (the most strongly associated FCRL3 tag SNP) but haplotype analysis suggests that this might not be the etiological variant, as the high-risk G allele is associated only when present with the rs10489678 C allele (not the rs10489678 T allele),

suggesting the etiological variant could be located elsewhere within this region (31).

3.3. Chromosome 5q31–q33

Chromosome 5q31–q33 encodes a large variety of cytokines, inflammatory mediators and other immune modulators [interleukin (IL)-3, -4, -5, -9 and -13] and represents a region of linkage that has generated much interest (32). There is strong evidence that the Chr.5q31–33 region is linked to autoimmune thyroid disorders in Chinese and Japanese populations. Linkage of microsatellite marker D5S436 located within chromosome 5q31–33 was first detected in a Japanese GD genome-wide screen (33) and replicated later in a Han Chinese GD dataset along with other more strongly associated microsatellite markers, including D5S2090 (34) and in a second Japanese GD cohort associated with an extended 5q12–q33 region (35). Although no Caucasian GD genome-wide microsatellite screen has reported linkage to 5q31–33 (36–39), some evidence for linkage to a separate region of chromosome 5, 5q11.2–5q14.3, has been reported (37). Several genes within 5q31–33 have been proposed to explain the association of this region with GD, including beta-2-adrenergic receptor (ADRB2) (40), IL-12b (41), interferon regulatory factor 1, IL-13 and IL-4, although replication of these loci has proved difficult. More recently, two independent studies designed to narrow down the association within this region have identified two distinct GD susceptibility loci approximately 15 Mb apart, which could potentially explain linkage to GD in this region (32).

3.4. The HLA gene

The major histocompatibility (MHC) complex region encoding the HLA glycoproteins is a highly polymorphic genetic region that includes many genes and is located on chromosome 6p21. It is subdivided into (1) the class I region, which encodes HLA antigens A, B and C, (2) the class II region, which encodes HLA antigens DR, DQ and DP, each with one or more α and β chains and (3) the class III region, which encodes several immune-regulatory molecules, including complement components, heat shock protein 70 (HSP70) and TNF (42). Initial studies analyzed the major HLA class II alleles in AITD (43).

Grumet *et al.* were the first to show the association between GD and the alleles of MHC class I, with a higher frequency of HLA-B8 in GD patients (47%) compared to the controls (21%). However, a stronger association of GD was found with the MHC class II allele HLA-DR3, which is in strong linkage disequilibrium with HLA-B8. In non-white populations, GD has been found to be associated with different HLA alleles; HLA B35, B46, A2 and DPB1*0501 in Japanese and B46, DR9, DRB1*303 and DQB1*0303 in Hong Kong Chinese (42).

Recent studies have shifted the focus from the association of the major HLA-DR allele groupings with AITD to the molecular structure of the peptide-binding pocket and its association with disease (44). This mechanistic-based approach has proved to be very fruitful. Because T-cells recognize and respond to peptide antigens when presented by APCs bound to HLA class II pockets, it was hypothesized that certain HLA-DR alleles permit autoantigenic peptides to fit into the peptide-

binding pocket and to be presented more efficiently to T-cells (45). We recently identified arginine at position 74 of the HLA-DRb1 chain (DRb-Arg74) as the crucial DR amino acid conferring susceptibility to GD. By contrast, the presence of glutamine at position 74 of the DRb1 chain is protective. These data were replicated in an independent dataset (46). Similarly, a pocket HLA-DR amino acid signature was identified that confers strong risk for Hashimoto's thyroiditis (HT) (44). As in GD, the key pocket amino acid was DRb-Arg74. Structural analysis demonstrated that this pocket amino acid signature has a unique pocket structure that is likely to influence pathogenic peptide binding and presentation to T-cells. Further studies identified the Tg peptides that could be presented by HLA-DR pockets containing arginine at position beta 74 (47). Thus, the peptide-binding pocket structure has a major role in the etiology of AITD (48).

3.5. CTLA-4

The CTLA-4 gene is an important negative regulator of T-cell activation (49). Because CTLA-4 controls normal T-cell responses by suppressing T-cell activation, it was postulated that CTLA-4 polymorphisms that reduce its expression and/or function might predispose to autoimmunity by creating over-reactive T-cells.

The first demonstration of an association between CTLA-4 and GD was reported by DeGroot *et al.* (50). They showed a significant association between a microsatellite in the 3'UTR of CTLA-4 and GD, which was the first report of an association between CTLA-4 and an autoimmune condition. CTLA-4 is now established as an autoimmunity gene linked to and/or associated with various autoimmune conditions, including both GD and HT (51–56), as well as the production of thyroid antibodies alone without clinical disease (57–59). The association has been shown to be consistent across ethnic and geographic groups (50,53,60–63).

Recent work by Vieland *et al.* showed that the involvement of CTLA-4 in the genetic susceptibility to AITD is more complex than originally thought. CTLA-4 alone predisposes to the development of thyroid antibodies, but it could have a role in the susceptibility to high levels of thyroid antibodies and clinical AITD when interacting with other loci (64). Moreover, both the G allele (reported to be associated with AITD) and the A allele (reported to be protective) of the A/G49 SNP of CTLA-4 might predispose to AITD when interacting with different loci (64).

It is not known which CTLA-4 variant is the causative variant or by what mechanism it confers susceptibility to autoimmunity. Three main CTLA-4 variants have been studied: an AT-repeat microsatellite at the 3'UTR of the CTLA-4 gene (50,53); an A/G SNP at position 49 in the signal peptide resulting in an alanine/threonine substitution (A/G49) (52,63); and an A/G SNP located downstream and outside of the 3'UTR of the CTLA-4 gene. Further studies are needed to determine which one is causative (65).

3.6. Regulatory T-cell genes

Regulatory T-cells (Tregs) are an important subset of T-cells that regulate T-cell activation (66) and Tregs are known to have an important role in immune

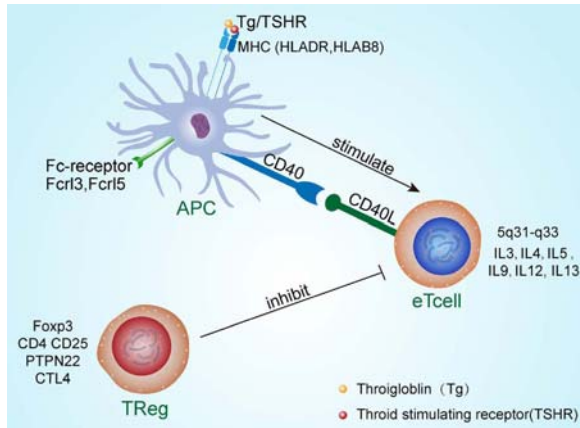


Figure 1. The susceptibility genes involved in Grave's disease: antigen presenting cells (APCs) capture the self-antigen thyroid globin and/or thyroid stimulating receptor and up-regulate CD40, the Fc-receptor and activating T-cells. The activated T-cells express cytokines IL-3, -4, -5, -9, -12 and -13. The Treg cell is a negative regulator of the immune response; it inhibits T-cell activation via up-regulation of Foxp3, CD25, PTPN22 and CTLA4.

regulation. In a murine model of GD, Tregs appear to be crucial in the pathogenesis of GD (31). Moreover, an apoptosis-induced decrease in the proportion of intrathyroidal Tregs in patients with AITD is reported (67).

Tregs have a major role in the peripheral tolerance to self-antigens. Indeed, up-regulation of Tregs suppressed experimental autoimmune thyroiditis in mice (68) and depletion of Tregs in mice increased their susceptibility to experimental GD (69). Several subtypes of Tregs have been identified. One subtype, the natural Tregs, are characterized by constitutive expression of CD25, CTLA-4 and glucocorticoid-induced tumor necrosis factor receptor. In addition, their development is regulated by the FOXP3 gene. And, interestingly, both FOXP3 and CD25 have been found to be associated with GD.

The FOXP3 gene, which is the key to the differentiation of T-cells into natural Tregs, has been examined in a U.S. Caucasian and a Japanese cohort of AITD patients. The results demonstrated an association of a microsatellite inside the FOXP3 gene with AITD in the Caucasian but not the Japanese patients, demonstrating ethnic differences in disease susceptibility (70). Further analysis found the association of FOXP3 with AITD was mostly in patients with juvenile GD (71).

3.7. The protein tyrosine phosphatase-22 gene

Lymphoid tyrosine phosphatase, encoded by the protein tyrosine phosphatase-22 (PTPN22) gene, is a negative regulator of T-cell activation. The PTPN22 gene is associated with GD and the causative SNP is a tryptophan/arginine variant at position 620. The disease-associated variant is a gain-of-function variant and, therefore, the mechanism by which it predisposes to autoimmunity is not trivial because it would be expected to

suppress T-cell activation. It is possible that the decreased activation of T-cells enables self-reactive T-cells to escape the thymic central tolerance mechanisms, but this possibility awaits experimental confirmation (65).

3.8. Thyroid-specific genes

3.8.1. Thyroglobulin (Tg)

Tg is one of the main targets of the immune response in GD (72) and, therefore, an obvious candidate gene for GD. Indeed, a whole-genome linkage study done by Tome *et al.* identified the Tg gene as an important GD susceptibility gene. These findings were replicated by several other studies of several ethnic groups (73,74). Sequencing the Tg gene identified A734S, V1027M and W1999R as amino acid variants associated with GD. Mechanistically, it is possible that the Tg variants predispose to disease by altering Tg degradation in endosomes, resulting in a pathogenic Tg peptide repertoire.

3.8.2. TSHR

GD is defined by the presence of stimulating TSHR antibodies. Not surprisingly, TSHR was the first gene (after HLA) to be tested for association with GD. Earlier studies that tested three non-synonymous SNPs in the TSHR gene for association with GD, D36H, P52T and D727E gave mixed results (75). However, studies from Japan consistently reported association of TSHR with GD in Japanese (61). Finally, it was found more recently that non-coding intronic SNPs in TSHR are associated with GD (76). The most consistent association in Caucasians is with an intron 1 SNP (77). Mechanistically, intron 1 SNPs in TSHR can alter its splicing; Indeed, several splice variants of TSHR are known. The major splice variant of TSHR identified by us in 1992 is a 1.3 kb variant that includes most of the extracellular domain of TSHR. Other minor splice variants have been reported (78).

4. CONCLUSION

It is widely agreed that complex diseases are not controlled by an individual gene or DNA variation but by a combination of genes or DNA variations; however, knowledge of individual susceptibility genes in GD might lead the way to fully understanding the mechanism underlying GD. As we showed earlier, the self-antigens are captured by the APC cells and this activates the effector T-cells and releases a number of cytokines and chemokines. As a negative regulator, the Treg cell might suppress this response by inhibiting the effector T-cells. There are quite a number of genes known to be involved (Figure 1) but the details of this complex process remain to be elucidated. A better understanding of the susceptible genes and their interactions might provide a novel therapeutic tool in the near future.

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Abbreviations: GD: Graves' disease, GO: Graves' ophthalmopathy, HLA: human leukocyte antigen, CTLA-4: cytotoxic T-lymphocyte antigen-4, APCs: antigen-presenting cells, SNP: single nucleotide polymorphism, FCRL: Fc receptor-like, MHC: major histocompatibility complex, HSP70: heat shock protein 70, HT: Hashimoto's thyroiditis, Tregs: regulatory T-cells, PTPN22: protein tyrosine phosphatase-22

Key Words: Graves' disease, Graves' ophthalmopathy, CTLA-4, APCs, HSP70, Review

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