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A Single Nucleotide Polymorphism in *Tyk2* Controls Susceptibility to Experimental Allergic Encephalomyelitis

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Abstract

Genes controlling immunopathologic diseases of differing etiopathology may also influence susceptibility to autoimmune disease. B10.D1-*H2^q/SgJ* mice with a 2538 G→A missense mutation in *tyrosine kinase-2 (Tyk2)* are susceptible to *Toxoplasma gondii*, yet resistant to autoimmune arthritis, unlike the wild-type B10.Q/Ai substrain. To understand if *Tyk2* is also important in a second autoimmune model, experimental allergic encephalomyelitis (EAE) was induced in B10.D1-*H2^q/SgJ (Tyk2^A)* and B10.Q/Ai (*Tyk2^G*) mice with myelin oligodendrocyte glycoprotein peptide_{79–96}. B10.D1-*H2^q/SgJ (Tyk2^A)* mice were resistant to EAE while B10.Q/Ai (*Tyk2^G*) mice were susceptible and a single copy of the *Tyk2^G* allele conferred EAE susceptibility in F₁ hybrids. Furthermore, EAE susceptibility in B10.D1-*H2^q/SgJ (Tyk2^A)* mice was complemented when pertussis toxin (PTX) was used to mimic the effects of environmental factors derived from infectious agents. Numerous cytokines and chemokines were increased when PTX was included in the immunization protocol. However, only RANTES, interleukin-6, and interferon- γ increased significantly with both genetic compensation and PTX complementation. These data indicate that *Tyk2* is a shared autoimmune disease susceptibility gene that can be complemented both genetically and environmentally. Single nucleotide polymorphisms like the one that distinguishes *Tyk2* alleles are of considerable significance given the potential role of gene-by-environment interactions in autoimmune disease susceptibility.

Keywords

EAE/MS; autoimmunity; neuroimmunology; protein kinases/phosphatases

INTRODUCTION

Autoimmune diseases have common features and understanding the commonalities underlying them may aid in the design of rational treatments. One approach to understanding these commonalities is to identify genes, termed shared autoimmune disease genes, whose alternately expressed alleles influence susceptibility to multiple autoimmune

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diseases. *Bphs/Hrh1*, which controls susceptibility to both experimental allergic encephalomyelitis (EAE) (1) and autoimmune orchitis (2) was the first non-antigen dependent shared autoimmune disease susceptibility gene to be identified and positionally cloned in the mouse (3). Another example of a potential shared autoimmune disease susceptibility gene is *Eae3/Idd3/Aod2* (4–6), which controls susceptibility to EAE, autoimmune insulin-dependent type I diabetes mellitus, and day 3 thymectomy induced autoimmune ovarian dysgenesis. In both mouse and humans, genetic clustering of autoimmune disease quantitative trait loci (QTL) supports the hypothesis that susceptibility to autoimmune disease may be controlled by shared genes (7). Moreover, relatives of multiple sclerosis (MS) and celiac disease patients are at increased risk of other autoimmune diseases suggesting a shared genetic susceptibility (8–11). Similarly, multiple autoimmune diseases are often observed within a single patient (12).

Tyrosine kinase 2 (*Tyk2*/*Tyk2*) participates in the signaling pathways of multiple cytokines in innate and acquired immunity (13,14). *Tyk2* is a member of the JAK/STAT signaling pathway (15) and contributes to the signaling of IFN- α/β (16), IL-6 (17), IL-10 (18), IL-12 (19), IL-13 (20) and IL-23 (21). Depending on the ligand, cytokine receptor aggregation activates *Tyk2* leading to phosphorylation of STAT 1, -3, -4, or -5 (15). The phospho-STAT dimerizes and translocates to the nucleus to promote gene transcription.

Although *Tyk2* activation has been implicated in the signaling of multiple cytokines (22), *Tyk2^{tm1Shmd}* (*Tyk2*^{-/-}) mice primarily exhibit defects in responses to IL-12 and type I IFN (14,23). B10.D1-*H2^q/SgJ* (B10.D1) mice are a substrain of B10.Q mice that have a naturally occurring mutation in *Tyk2*, designated *Tyk2^A* (24). The 2538 G→A base substitution is predicted to result in a non-conservative amino acid substitution (E775K) within a critical APE motif of the JH2 (pseudokinase) domain of *Tyk2*. The JH2 domain is required for *Tyk2* activation via ligand-activated cytokine receptors (16). Although *Tyk2^A*-specific transcripts are present at normal levels in B10.D1 mice, immunoreactive protein cannot be detected (24). B10.D1 splenocytes exhibit impaired STAT phosphorylation in response to IL-12, IL-23 and IFN α stimulation (24). In addition, neither T cells nor NK cells from B10.D1 mice produce IFN γ when stimulated with IL-12; however, this defect can be overcome by increasing the concentration of IL-12 and the incubation time or by stimulation through an IL-12-independent pathway (25,26).

Importantly, while B10.Q/Ai mice, which express a wild-type *Tyk2^G* allele, are susceptible to collagen-induced arthritis (CIA) and resistant to *Toxoplasma gondii* infections, the *Tyk2^A* mutation renders B10.D1 mice resistant to CIA and highly susceptible to *Toxoplasma gondii* (24–27), demonstrating that *Tyk2* is a shared immunopathology gene. Because autoimmune disease susceptibility genes can also be shared (7,28,29), we tested the hypothesis that *Tyk2* is a shared autoimmune disease gene by assessing susceptibility of B10.D1 and B10.Q/Ai mice to EAE, the principal animal model of MS. We found that *Tyk2* is a critical genetic regulator of EAE susceptibility and that the resistant *Tyk2^A* allele can be compensated by one copy of the wild-type *Tyk2^G* allele and by environmental factors such as pertussis toxin (PTX). These results are of particular significance given that *TYK2* polymorphisms are associated with increased risk of systemic lupus erythematosus (30,31) and that *TYK2* has recently been identified as a strong MS susceptibility gene in a genome-wide association study (32), and confirmed through independent replication (J. Oksenberg, personal communication).

MATERIALS AND METHODS

Mice

B10.D1-*H2^q*/SgJ (B10.D1) (Strain #002024) mice bearing the *Tyk2^{rs2538-A}* (*Tyk^A*) allele were purchased from The Jackson Laboratory (Bar Harbor, ME) and B10.Q/Ai (Line #4059) mice with the *Tyk2^{rs2538-G}* (*Tyk^G*) allele were purchased from Taconic Farms (Tarrytown, NY) through the National Institute of Allergy and Infectious Diseases Animal Supply Contract. Reciprocal F₁ hybrid progeny were generated and bred at the University of Vermont. Mice were housed at 25°C with 12:12h light-dark cycles and 40–60% humidity. Naïve, age-matched male and female mice were used throughout. The experimental procedures performed in this study were approved by the Institutional Animal Care and Use Committee of the University of Vermont.

Induction and Evaluation of EAE

Mice were immunized for the induction of EAE using either the double injection or single injection protocols. For the double injection protocol mice were injected subcutaneously in the posterior right and left flank with a sonicated emulsion of 50 µg myelin oligodendrocyte glycoprotein peptide 79–96 [GKVALRIQNVRFSDEGGY] (MOG_{79–96}) (33) and 200 µg *Mycobacterium tuberculosis* H37Ra in CFA (Difco Laboratories, Detroit, MI) in 0.1 ml; one week later mice received the same injection on the right and left flank anterior of the original injection site (34). For the single injection protocol with PTX as an auxiliary adjuvant (MOG_{79–96}-CFA + PTX), mice were injected subcutaneously with 100 µg MOG_{79–96} and 200 µg *M. tuberculosis* H37Ra in CFA in 0.1 ml on the posterior right and left flank and the scruff of the neck. Immediately afterward, each mouse received 200 ng PTX (List Biological Laboratories, Campbell, CA) in 0.2 ml by intravenous injection (34). EAE was evaluated daily beginning at day 5 as follows: 0, no clinical expression of disease; 1, flaccid tail without hind limb weakness; 2, hind limb weakness; 3, complete hind limb paralysis and floppy tail; 4, hind leg paralysis accompanied by a floppy tail and urinary or fecal incontinence; 5, moribund. Clinical quantitative trait variables were generated as previously described (35). Mice were considered positive for incidence if they showed any clinical signs greater than or equal to one for two or more consecutive days. The severity index is the cumulative disease score per days affected. Histological assessment of EAE neuropathology was done as previously described (35–38). Briefly, brains and spinal cords were dissected from calvarias and vertebral columns, respectively, and fixed by immersion in phosphate buffered (pH 7.2) 10% formalin. Representative areas of the brain and SC, including brainstem, cerebrum, cerebellum, and the cervical, thoracic, and lumbar segments of the SC, were selected for histopathological evaluation. EAE pathology reflects the overall severity of the lesions observed, extent and degree of myelin loss and tissue injury (swollen axon sheathes, swollen axons, and reactive gliosis), severity of the acute inflammatory response (predominantly neutrophils), and the severity of the chronic inflammatory response (lymphocytes/macrophages).

Cell culture conditions and lymphokine assays

For *ex vivo* cytokine and chemokine analysis, spleens and draining lymph nodes were obtained from mice immunized by both methods 10 days earlier for EAE as described above. Single cell suspensions at 1×10^6 cells/ml in RPMI 1640 media (Cellgro Mediatech, Inc., Manassas, VA) plus 5% FBS (HyClone, Logan, UT) were stimulated with 50 µg MOG_{79–96}. Cell culture supernatants were recovered at 72 hours and 23 different cytokine and chemokine levels quantified in duplicate by Bioplex multiplex cytokine assay (Becton Dickinson Bioscience, San Jose, CA), including IL-1 α , IL-1 β , IL-2, IL-3, IL-4, IL-5, IL-6, IL-9, IL-10, IL-12 (p40), IL-12 (p70), IL-13, IL-17, Eotaxin, G-CSF, GM-CSF, IFN- γ , KC, MCP-1, MIP-1 α , MIP-1 β , RANTES, and TNF- α . To confirm the IL-17 and IFN- γ

results, ELISAs were performed as described (34), using primary anti-IL-17A and anti-IFN γ antibodies and their corresponding biotinylated secondary antibodies (BD Biosciences-Pharmingen, San Diego, CA). Other ELISA reagents included horseradish peroxidase-conjugated avidin D (Vector Laboratories, Burlingame, CA), TMB microwell peroxidase substrate and stop solution (Kirkegaard and Perry Laboratories, Gaithersburg, MD), and recombinant IFN- γ and IL-17 (R&D Systems, Inc., Minneapolis, MN) used as standards. IL-6 was confirmed using the mouse IL-6 DuoSet ELISA (R&D Systems, Inc., Minneapolis, MN).

Proliferation assays

Mice were immunized for EAE induction, and draining lymph nodes and spleens were harvested on day 10. Single cell suspensions were prepared, and 5×10^5 cells/well in RPMI 1640 media (5% FBS) were plated on standard 96-well U-bottom tissue culture plates and stimulated with 0, 2, 10 or 50 μ g MOG₇₉₋₉₆ for 72 h at 37°C. During the last 18 h of culture, 1 μ Ci of [³H]-thymidine (PerkinElmer, Stelton, CT) was added. Cells were harvested onto glass fiber filters and thymidine uptake was determined by liquid scintillation.

Statistical analysis

Statistical analyses (two way ANOVA, Kruskal-Wallis test followed by Dunn's post hoc multiple comparisons, nonlinear regression-based curve fitting (34), and Chi-square test) were performed using GraphPad Prism version 5 (GraphPad Software, San Diego, CA). A *p* value of < 0.05 was considered significant.

RESULTS

B10.D1 mice are resistant to myelin oligodendrocyte glycoprotein peptide₇₉₋₉₆ (MOG₇₉₋₉₆)-CFA induced EAE

To determine if *Tyk2* is a shared autoimmune disease gene, EAE susceptibility was assessed in B10.D1 and B10.Q/Ai mice using the MOG₇₉₋₉₆-CFA double-injection protocol. B10.D1 mice were resistant (0/46) to EAE whereas B10.Q/Ai mice were susceptible (31/36; *p*<0.001) (Fig. 1A and Table I). On day 30, EAE pathology in the brain and spinal cord was assessed using previously defined neuropathologic trait variables (35,37). The susceptible B10.Q/Ai mice had marked EAE pathology in the spinal cord while B10.D1 had no EAE pathology (Figure 2). Neither strain showed significant EAE pathology in the brain. (B10.D1 \times B10.Q/Ai) F₁ hybrids (16/18) and the reciprocal (B10.Q/Ai \times B10.D1) F₁ hybrids (26/31) were both susceptible to MOG₇₉₋₉₆-CFA induced EAE compared to B10.D1 mice (*p*<0.001). The F₁ hybrids had significantly greater disease severity for each clinical disease trait compared to B10.D1 (*p*<0.001), and did not differ significantly from B10.Q/Ai mice (Fig. 1B and Table I). Similarly, lesion severity, monocyte/lymphocyte infiltration, and total EAE pathology score was significantly greater in the reciprocal F₁ hybrids compared to B10.D1 mice but did not differ from B10.Q/Ai mice in the spinal cord, *p* < 0.05 (Figure 2). Again, very little EAE pathology was noted in the brains of reciprocal F₁ hybrids. These data indicate that *Tyk2* alleles determine EAE susceptibility and that the *Tyk2*^A allele is recessive. Therefore, EAE resistance in B10.D1 mice can be compensated genetically with a single copy of the wild-type *Tyk2*^G allele, and since *Tyk2* is also a susceptibility gene in CIA (25), it is by definition a shared autoimmune disease susceptibility gene.

Immune responses of *Tyk2*^A and *Tyk2*^G mice elicited by MOG₇₉₋₉₆-CFA immunization

To investigate the mechanism whereby *Tyk2* alleles control T cell effector responses, the MOG₇₉₋₉₆-specific immune responses of B10.D1, B10.Q/Ai, and F₁ hybrid mice were

compared ten days after MOG₇₉₋₉₆-CFA immunization. Although B10.D1 mice were resistant to MOG₇₉₋₉₆-CFA induced EAE, *ex vivo* proliferative responses did not differ between the strains (Fig. 3G). However, in *ex vivo* re-stimulation assays, B10.Q/Ai and F₁ mice produced significantly more IFN γ , IL-6, and RANTES compared to B10.D1 mice (Fig. 3). Surprisingly, IL-17 was not significantly higher in supernatants from B10.Q/Ai or F₁ cells, although a trend toward increased IL-17 production was noted when the results were grouped by strain (Fig. 3C). The three strains did not exhibit significant differences in any of the other cytokines and chemokines assayed (e.g., IL-4 and TNF α , Fig 3, and others not shown). Importantly, IL-12(p40) and IL-12(p70) were not different indicating IL-12 insufficiency is not responsible for EAE resistance in B10.D1 mice.

Tyk2^A-mediated resistance is abrogated by PTX

PTX is an example of an environmental factor derived from an infectious agent that influences susceptibility to EAE and is capable of overriding genetic checkpoints in this autoimmune disease (39). Therefore, we included PTX in the immunization protocol and tested the susceptibility of B10.D1 and B10.Q/Ai mice to EAE. In the MOG₇₉₋₉₆-CFA + PTX single injection protocol (34), mice receive the same total amount of MOG₇₉₋₉₆ in CFA as the double injection protocol but also receive an i.v. injection of PTX on day 0. In B10.Q/Ai mice injected with MOG₇₉₋₉₆-CFA + PTX (Fig. 4B), there was increased incidence and more severe disease compared to B10.Q/Ai mice injected with MOG₇₉₋₉₆-CFA alone (Table II). A more dramatic difference was seen in B10.D1 mice, which are much more susceptible (33/37) to EAE induced using PTX (Fig. 4A and Table II) than with MOG₇₉₋₉₆-CFA alone. Clearly, EAE susceptibility in B10.D1 (*Tyk2^A*) mice can be complemented by environmental factors derived from infectious agents such as PTX.

PTX complementation of EAE susceptibility correlates with increased cytokine production

The complementation of EAE susceptibility in B10.D1 (*Tyk2^A*) mice following immunization with PTX was not reflected in their antigen-specific *ex vivo* proliferative responses, which were not significantly different between immunization protocols (Fig. 5B). Inclusion of PTX in the immunization protocol, however, resulted in increased cytokine secretion by cultured cells from both strains, consistent with the increased severity of EAE induced by the PTX protocol. PTX is known to induce many cytokines that are proinflammatory and pathogenic in EAE, but PTX also induces T_H2 responses (40,41). The changes due to inclusion of PTX in the immunization of B10.D1 mice as assayed in cell culture supernatants were consistent with these published reports. For example, cytokines characteristic of T_H1 (IFN γ , IL-12, TNF α), T_H17 (IL-17, IL-6) and T_H2 (IL-4, IL-5, IL-9, and IL-13) responses were elevated compared to those elicited by immunization without PTX (Fig. 5A). In addition, members of the CC chemokine family, MIP-1 α and RANTES, were elevated more than fourfold compared to those induced by MOG₇₉₋₉₆-CFA alone, suggesting that there is likely to be a distinct mobilization of T_H1 cells in the PTX-exposed mice (42,43). Notably, among the changes in cytokine and chemokine production elicited in B10.D1 mice by the inclusion of PTX in the immunization protocol, IFN γ , IL-6, and RANTES were also significantly elevated by genetic compensation (Fig. 3).

DISCUSSION

A naturally-occurring single nucleotide polymorphism (SNP) within the pseudokinase domain of *Tyk2* influences the immunopathologic outcomes of CIA (25) and *Toxoplasma gondii* infection in B10.Q/Ai and B10.D1 (26), making *Tyk2* a shared immunopathology gene. The data presented here showing that *Tyk2* alleles control EAE susceptibility demonstrate that *Tyk2* is also a shared autoimmune disease susceptibility gene. Specifically, B10.D1 mice which possess the *Tyk2^A* allele are completely resistant to MOG₇₉₋₉₆-CFA-

induced EAE while B10.Q/Ai substrain mice expressing the *Tyk2^G* allele are susceptible. Moreover, a single copy of the *Tyk2^G* allele fully confers EAE susceptibility in B10.D1 F₁ hybrids clearly establishing that *Tyk2* is important in controlling autoimmune disease susceptibility. When PTX was included in the immunization regime to mimic the effects of environmental agents derived from infectious agents, EAE susceptibility was also complemented thus emphasizing the contextual role that gene-by-environment interactions play in determining susceptibility to autoimmune diseases.

It is not surprising that *Tyk2* is a player in mouse autoimmunity and inflammation, due to its importance in supporting IL-12-induced IFN- γ responses (14,15,44), and its ability to down-regulate T_H2-mediated antibody production, especially IgE (45). There are differences between the requirements for *Tyk2* in mouse as compared to human immune responses. For example, human *TYK2*-deficient cell lines are completely unresponsive to type 1 IFN, and IL-6 and IL-10 signaling is severely impaired (13), whereas these phenotypes are leaky in *Tyk2^{-/-}* mice, and high concentrations of IFN α can overcome the mouse *Tyk2* deficiency MHC class I expression (23). However, evidence exists that *Tyk2* shares some functions between these two species. There is a report of one patient with a mutation in *TYK2*, who had a remarkably similar immune response to that seen in B10.D1 mice, with hyper-IgE syndrome, increased susceptibility to multiple microbial pathogens, an impaired STAT-4 phosphorylation pattern, and undetectable IFN γ production in response to IL-12 (13). This supports the hypothesis that human *TYK2* is also a shared immunopathology gene. Supporting the hypothesis that *TYK2* is a shared human autoimmune disease susceptibility gene, it has recently been identified as a strong MS susceptibility gene in a genome-wide association study (32), and confirmed through independent replication (J. Oksenberg, personal communication) and *TYK2* polymorphisms have also been associated with increased risk of systemic lupus erythematosus (30,31).

However, the manner by which *Tyk2* complements autoimmunity is not known. T cell proliferation induced by IL-12 is not *Tyk2* dependent (23) and likewise, no differences in antigen-specific proliferation were observed between B10.D1 and wild type B10.Q/Ai mice following immunization with MOG₇₉₋₉₆-CFA in this study. B10.D1 mice make IL-12 in normal abundance (26) and both IL-12 and TNF α levels were similar between B10.D1 and B10.Q/Ai and F₁ hybrid mice after induction of EAE without PTX. Therefore, differences in proliferation and/or levels of these cytokines are not likely an important mechanism by which B10.D1 mice are resistant to EAE. The *Tyk2^A* mutation impairs signaling through both IL-12R and IL-23R pathways (24). It is more likely therefore that their EAE resistance is due to this signaling defect, leading to an inability to up-regulate encephalitogenic levels of IFN γ (via IL-12R, reviewed in (44)) and IL-17 (via IL-23R, reviewed in (44)) or to activate T cells that make these cytokines. We observed differences between B10.D1 and B10.Q/Ai mice for both of these effector molecules, although the difference in IL-17 was only a trend. In addition, B10.D1 (*Tyk2^A*) mice had significantly impaired ability to produce pro-inflammatory molecules such as IL-6 and RANTES. IL-17 and IFN γ have well-documented roles in EAE (46–49), and the development of EAE is blocked by antibodies or antagonists of IL-6 and RANTES (50,51). It is important to note that the effects of the *Tyk2^A* allele may not be exclusively in T cells as *Tyk2* is also required in dendritic cells for IL-12, IL-23 and IFN γ production (52).

In the present study, PTX was included in the EAE induction protocol to reveal gene-by-environment interactions, and especially the effects of an environmental factor derived from an infectious agent. B10.D1 mice were susceptible to EAE only when it was induced with MOG₇₉₋₉₆-CFA + PTX, and they produced significantly higher levels of multiple T_H1-, T_H2-, and T_H17-type cytokines and chemokines compared to the MOG₇₉₋₉₆-CFA-inoculated mice (Fig. 5A). Of interest, both GM-CSF and IL-5 showed large increases with

PTX treatment. Multiple sclerosis patients in the active phase of disease have elevated levels of GM-CSF compared to patients in remission (53) and mice lacking GM-CSF are resistant to MOG₃₅₋₅₅-induced EAE (54). Taken together, these reports and the present study suggest that GM-CSF is critically important in EAE and MS pathogenesis. A small study of MS patients and controls found patients with highly proliferating MBP-specific T cells produced higher levels of IL-5 and IL-17 and this correlated with number of MRI-identified active plaques (55). However IL-5 has also been shown to increase in MS patients treated with IFN-beta (56) or glatiramer acetate (57).

Although it is not known how PTX restores EAE susceptibility in B10.D1 mice, several possibilities exist. PTX may act intrinsically in T cells because they express PTX-sensitive G_{i/o} proteins. Inhibitory G_{i/o} proteins are inactivated by PTX-mediated ADP-ribosylation (58). Following direct TCR stimulation, T cells from G_{αi2}^{-/-} mice produce more IL-2, IL-4 and IFN γ than wild type mice (59). Thus, the PTX-mediated abrogation of G_i coupled inhibitory signals in T cells would increase the magnitude of the cytokine responses. This may be one mechanism by which PTX complements EAE susceptibility in B10.D1 mice. Accordingly, PTX also increases the expression of the co-stimulatory molecule CD28 on T cells (41) which would therefore potentiate the immune response.

PTX could also increase T cell cytokine responses and complement EAE susceptibility through its effects on APCs. PTX increases secretion of proinflammatory cytokines such as IL-1 β (41), IL-6 (60), IL-12 (61) and TNF α (62). Increased IL-6 production by PTX-treated APCs promotes the generation of IL-17 producing T cells (60). Indeed, IL-6 and IL-17 were up-regulated by PTX in both B10.D1 (*Tyk2^A*) and B10.Q/Ai (*Tyk2^G*) mice. PTX also enhances the ability of the APC to activate T cells by inducing dendritic cell maturation (62) and up-regulating expression of the co-stimulatory molecules CD80 and CD86 in the spleen and spinal cord (40,41,63). PTX-induced cytokine production and T cell clonal expansion are thought to occur primarily through the CD28:CD80/86 costimulatory pathway (64). The PTX-induced changes in EAE susceptibility of B10.D1 mice cannot be attributed solely to effects on either T cells or APCs based on these experiments. Although it is tantalizing to speculate that PTX increases co-stimulatory molecules on APCs which then increases both APC maturation and T cell differentiation and clonal expansion as evidence suggests (40,63,65), leading to the cytokine differences we observed, careful bone marrow chimera experiments must be performed to conclude this. These experiments are underway to attempt to determine if the effect of PTX is directly on APC or T cells through APCs.

In B10.D1 (*Tyk2^A*) mice, IFN γ and IL-17 levels were both elevated, indicating that PTX must enhance their production via Tyk2-independent pathways, such as IL-18R-mediated IFN γ production (26). The *Tyk2*^{-/-} mouse has decreased expression of IL-18R (66), so if PTX modulated production of IFN- γ via IL-18, it would also have to up-regulate the IL-18R for this to occur. The role of IL-18 is paradoxical, despite its apparently excellent candidacy. IL-18R α -deficient mice are protected from EAE, in contrast to IL-18-deficient mice, which are susceptible (67). Further complicating matters, an alternative unidentified ligand for IL-18R on APCs responsible for Th17 pathogenicity has been postulated (68). Within the type I IFN pathway, alternate routes of STAT4 phosphorylation have also been noted (69). Additionally, PTX intoxication may produce sufficient IL-12 stimulation as to cause receptor aggregation leading to phosphorylation of Jak2 that can stand in for Tyk2. We observed high levels of active IL-12 after PTX inoculation (Fig. 5A), and it has been shown that greater exposure to IL-12 *in vitro* can overcome the effects of the *Tyk2^A* allele as measured by STAT4 phosphorylation (25). Thus, IL-12 alone could explain the results we have observed. Because the issue of direct and indirect effects on the pathogenic T cells is further complicated by the independent roles of IL-12, IL-18, and an unknown IL-18R-

ligand, it is unclear which pathway PTX uses to modulate IFN- γ and IL-17 in the B10.D1 mice.

The ability of environmental factors derived from infectious agents to alter autoimmune disease susceptibility controlled by a SNP highlights the contextual importance of gene-by-environment interactions in determining autoimmune disease susceptibility. There is increasing evidence that human autoimmune disease results from a complex interaction of environmental effects in genetically susceptible individuals. The 75% discordance rate for MS in monozygotic twins (70) suggests that environmental factors are important in MS. In particular, low ultraviolet light exposure (71–74) and the resulting low serum 25-(OH) $_2$ D $_3$ levels correlate with increased MS risk (75–78). It is therefore interesting in this regard, that *in vivo* treatment of mice with 1,25-dihydroxyvitamin D $_3$ ameliorates EAE (79), and treatment of activated T cells *in vitro* with 1,25-dihydroxyvitamin D $_3$ inhibits IL-12-induced tyrosine phosphorylation of Tyk2, thereby reducing T cell responses to antigen (80). Another important finding is that the sexual dimorphism observed in MS is increasing in the last 50 years suggesting that emergent factors such as environmental estrogens could selectively promote MS in women (81). The phytoestrogen quercetin, known to reduce signs of EAE in mice, is also capable of blocking IL-12 induced phosphorylation of Tyk2 (82). In preliminary work we note that EAE susceptibility in B10.D1 (*Tyk2^A*) and B10.Q/Ai (*Tyk2^G*) mice is in fact sexually dimorphic (Blankenhorn, Spach, and Teuscher, in preparation, 2009). In the context of the present report, therefore, the mutant *Tyk2^A* allele is a good candidate for an environmentally sensitive genetic modifier of demyelinating diseases, responding to a wide variety of environmental factors including 1,25-dihydroxyvitamin D $_3$, estrogenic compounds, and toxins produced by microorganisms, such as PTX.

In summary, we demonstrate that *Tyk2* is both a shared immunopathology gene and also a shared autoimmune disease susceptibility gene in mice. We further demonstrate that it can be complemented both genetically and environmentally. As such, this model provides a unique opportunity to identify additional environmental factors impacting a core genetic network underlying susceptibility to autoimmune disease.

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Abbreviations used in this paper

| | |
|----------------------------|--|
| CIA | collagen-induced arthritis |
| MOG_{79–96} | myelin oligodendrocyte glycoprotein peptide _{79–96} |
| PTX | pertussis toxin |
| Tyk2 | tyrosine kinase 2 |

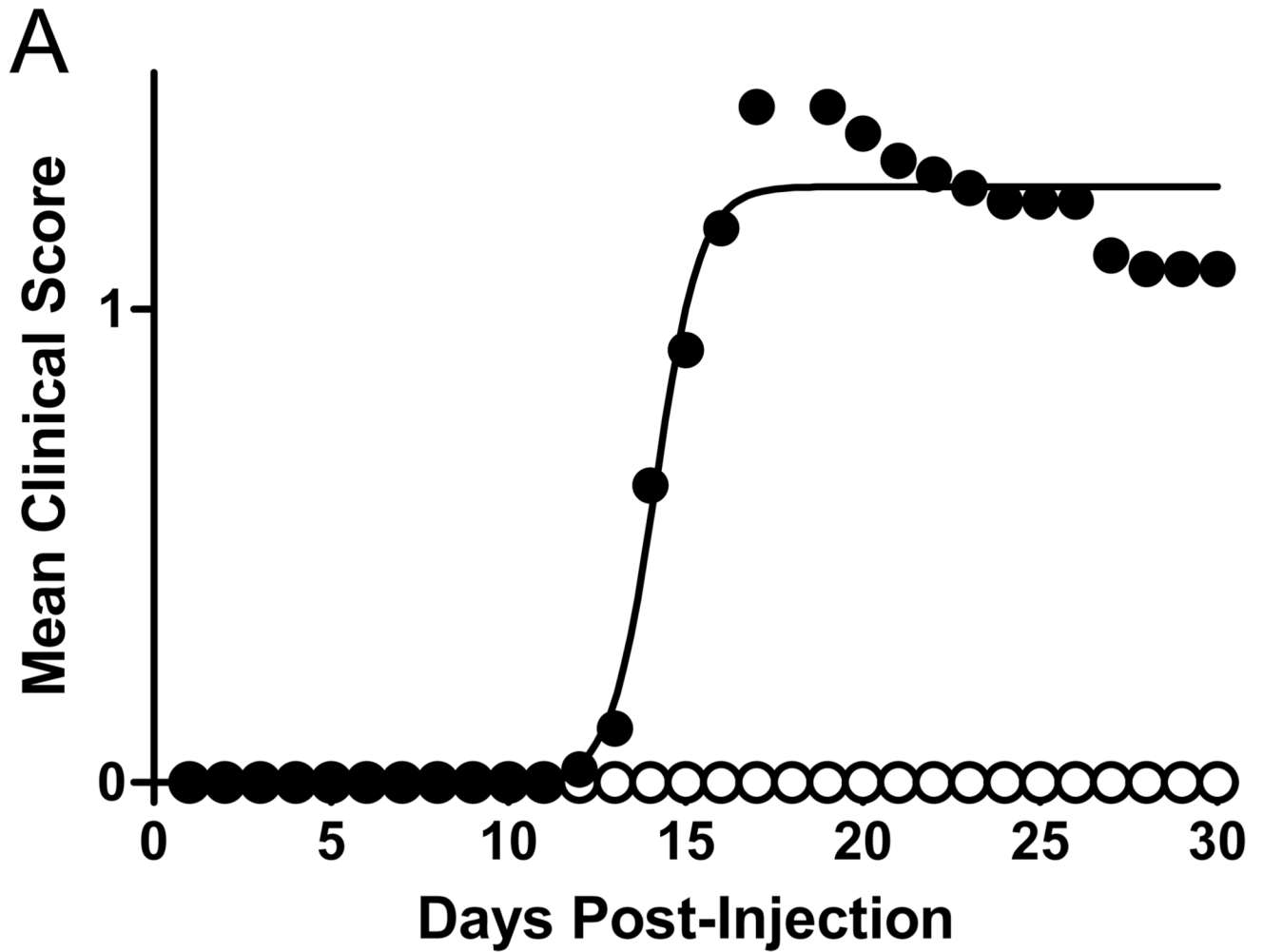


Figure 1. *Tyk2* alleles determine EAE susceptibility

(**A**) EAE was elicited by immunization with MOG₇₉₋₉₆-CFA on days 0 and 7. B10.Q/Ai mice (●, n = 36) were susceptible to EAE whereas B10.D1 mice bearing the *Tyk2*^A allele (○, n = 46) were resistant to EAE. (**B**) (B10.Q/Ai × B10.D1) (Δ, n = 31) and (B10.D1 × B10.Q/Ai) F₁ hybrids (◇, n = 18) were also fully susceptible to EAE, indicating that *Tyk2*^A is recessive. Regression lines and mean clinical scores are shown.

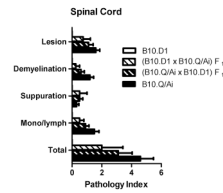


Figure 2. Quantification of EAE pathology in B10.Q/Ai, B10.D1 and reciprocal F₁ hybrid mice
 EAE was elicited by immunization with MOG_{79–96}-CFA on days 0 and 7. EAE pathology in the spinal cords of B10.Q/Ai mice was more severe on day 30 compared with B10.D1 mice for lesion severity, monocyte/lymphocyte infiltration and total EAE pathology ($p < 0.001$) with B10.D1 $<$ (B10.D1 \times B10.Q/Ai) F₁ = (B10.Q/Ai \times B10.D1) F₁ = B10.Q/Ai ($n = 4–11$ /group). Significance of differences was assessed using the Kruskal-Wallis test followed by Dunn's multiple comparisons.

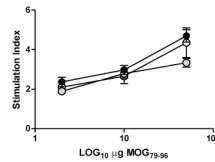


Figure 3. *Ex vivo* MOG₇₉₋₉₆-specific cytokine profiles and proliferation of MOG₇₉₋₉₆-CFA immunized B10.D1, B10.Q/Ai and F₁ hybrid mice

Cytokine production was assessed by stimulating splenocytes and lymphocytes from draining lymph nodes on day 10 post MOG₇₉₋₉₆-CFA immunization with 50 μg MOG₇₉₋₉₆ for 72 hr and measuring levels in supernatants by Bioplex assay (n = 8–10/group). The significance of differences was determined using the Kruskal-Wallis test followed by Dunn's post hoc multiple comparisons, * p<0.05, **p<0.01, ***p<0.001. IL-4 (A), TNFα (B) and IL-17 (C) did not differ significantly with EAE susceptibility whereas IFNγ (D) (F=4.1; p<0.05), RANTES (E) (F=9.9, p<0.01) and IL-6 (F) (F=7.3; p<0.01) increased significantly with increasing EAE susceptibility. Data for B10.D1 (open bars), B10.Q/Ai (blank bars) and F₁ hybrid (gray bars) from one representative experiment of two is shown. (G) Proliferation was assessed by stimulating splenocytes and lymphocytes from draining lymph nodes on day 10 post MOG₇₉₋₉₆-CFA immunization with and without MOG₇₉₋₉₆ for 72 hrs total and [³H]-thymidine incorporation measured in the final 18 h. Stimulation indices were calculated as average counts / background counts. B10.D1 (○), B10.Q/Ai (●) and reciprocal F₁ hybrid (●) samples (n = 8–10/group) were analyzed by two-way ANOVA (comparison: concentration of MOG₇₉₋₉₆, p<0.0001; strain differences, p=0.11; interaction, p=0.49). Data from one representative experiment of two is shown.

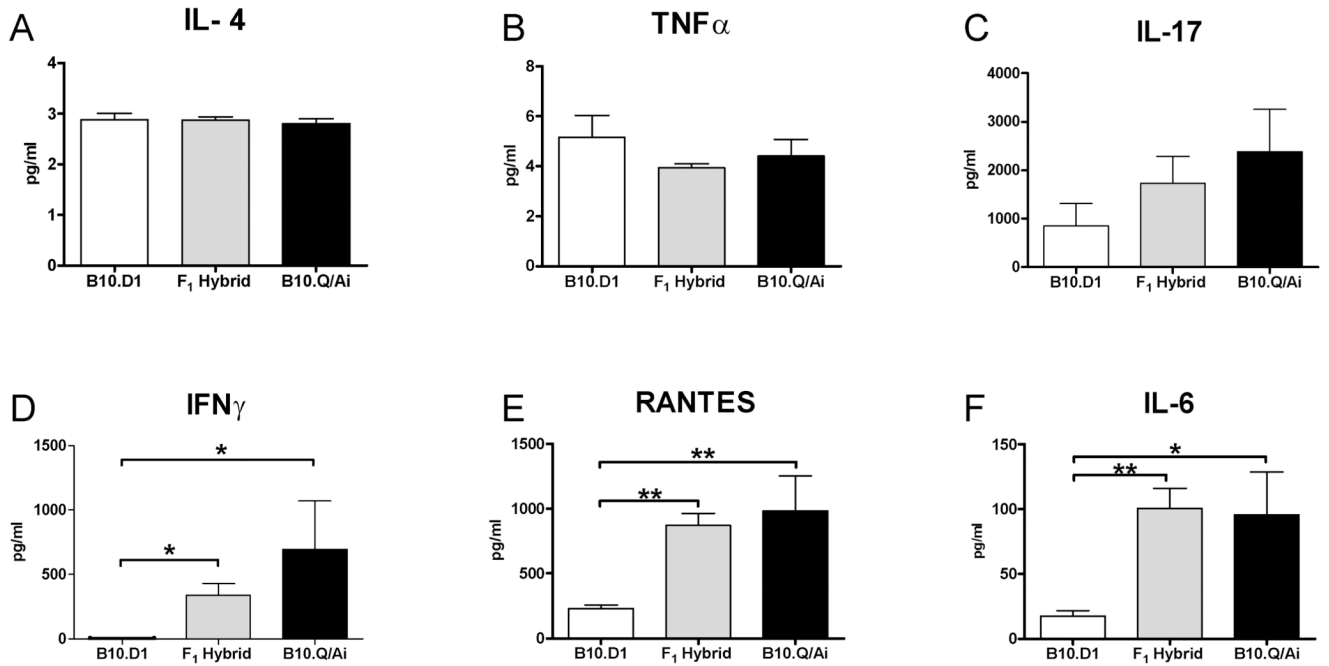


Figure 4. PTX complements EAE susceptibility of B10.D1 mice

EAE was induced by immunization with MOG₇₉₋₉₆-CFA + PTX on day 0. (A) B10.D1 (○, n = 37) were susceptible to EAE induced by MOG₇₉₋₉₆-CFA + PTX, in contrast to their resistance when immunized with MOG₇₉₋₉₆-CFA alone (●, n = 46) (also shown in Fig. 1A). (B) Both B10.Q/Ai (●, n = 44) and B10.D1 (○, n = 37) mice were susceptible to MOG₇₉₋₉₆-CFA + PTX induced EAE. The significance of differences in the course of clinical disease was assessed by regression analysis. Regression lines and daily mean clinical scores are shown.

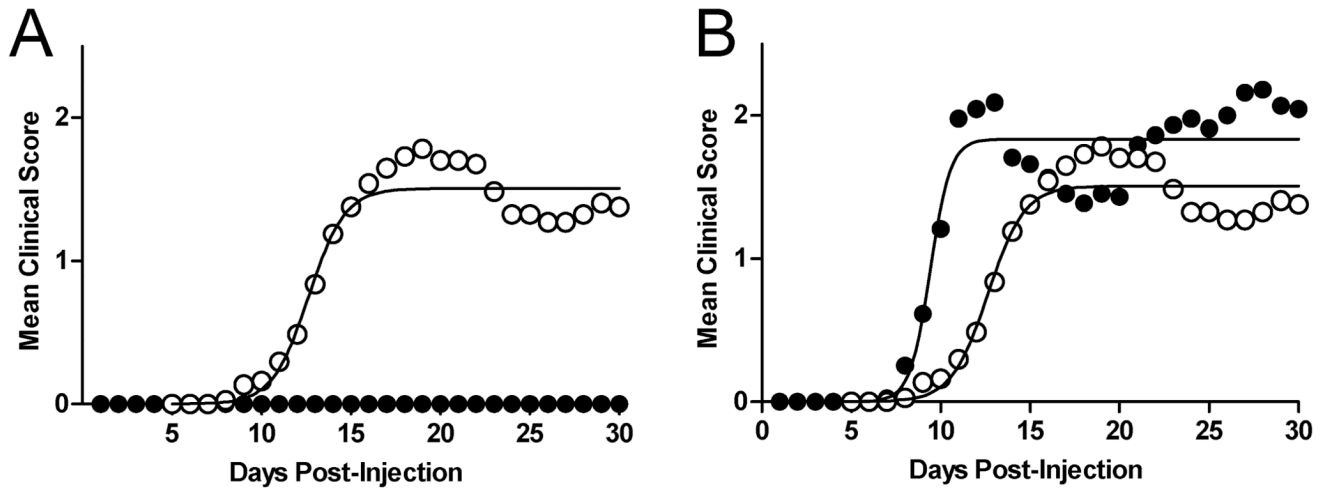


Figure 5. MOG₇₉₋₉₆-CFA + PTX immunization increased *ex vivo* MOG₇₉₋₉₆-specific cytokine and chemokine production compared to MOG₇₉₋₉₆-CFA in B10.D1 mice but proliferative responses did not differ between strains

Cytokine production and proliferation were assessed by stimulating splenocytes and lymphocytes from draining lymph nodes on day 10 after immunization with MOG₇₉₋₉₆-CFA or MOG₇₉₋₉₆-CFA + PTX. (A) Single cell suspensions were stimulated with 50 μ g MOG₇₉₋₉₆ for 72 hr and measuring levels in supernatants by cytometric bead assay. Samples (n=10/group) were analyzed by one way ANOVA. Cytokines that changed significantly have their average fold change represented in graph A above, p<0.05. (B) Proliferation was assessed by stimulating splenocytes and lymphocytes with and without MOG₇₉₋₉₆ for 72 hrs total and [³H]-thymidine incorporation measured in the final 18 h. Stimulation indices were calculated as average counts / background counts. Samples (n = 10/group) from B10.D1 mice immunized with MOG₇₉₋₉₆-CFA with PTX (\circ) or without PTX (\bullet) were analyzed by two -way ANOVA (comparison: concentration of MOG₇₉₋₉₆, p=0.002; strain, p=0.3; interaction, p=0.44). Data from one representative experiment of two is shown.

Table 1

Summary of clinical disease traits in B10.D1, B10.Q/Ai and reciprocal F₁ hybrids following MOG₇₉₋₉₆-CFA immunization^A.

| Strain | Overall Incidence ^B | Day of Onset | Cumulative disease score | Peak Severity | Severity Index ^C | Days Affected |
|-----------|--------------------------------|--------------|--------------------------|---------------|-----------------------------|---------------|
| B10.D1 | 0/46 | N/A | 0.0 | 0.0 | 0.0 | 0.0 |
| B10.Q/Ai | 31/36 | 14.8 | 20.5 | 1.7 | 1.3 | 13.0 |
| (Ai × D1) | 26/31 | 14.9 | 21.5 | 1.5 | 1.5 | 13.5 |
| (D1 × Ai) | 16/18 | 15.4 | 18.7 | 1.3 | 1.3 | 13.7 |
| | χ^2 89* | F 415.3* | 32.0* | 43.5* | 74.2* | 67.6* |

^A Trait values among B10.Q/Ai and the reciprocal F₁ hybrids were not significantly different whereas all were significantly different from B10.D1 mice, $p < 0.001$. Means are shown. The significance of differences for the trait values among the strains was assessed by Chi-square or Kruskal-Wallis followed by Dunn's post hoc multiple comparisons.

* $p < 0.0001$.

^B Animals were considered affected that showed clinical signs of ≥ 1 for two or more consecutive days.

^C The severity index is the cumulative disease score/days affected.

Table II

Summary of EAE clinical traits in B10.D1 and B10.Q/Ai mice with and without PTX included in the immunization protocol^A.

| Strain | Immunization protocol | Overall Incidence | Day of Onset | CDS ^B | Peak Severity | Severity Index | Days Affected |
|----------|-------------------------------|-------------------|--------------|------------------|---------------|----------------|---------------|
| B10.D1 | MOG ₇₉₋₉₆ -CFA | 0/46 | N/A | 0.0 | 0.0 | 0.0 | 0.0 |
| B10.D1 | MOG ₇₉₋₉₆ -CFA+PTX | 33/37* | 13.8* | 27.1* | 2.3* | 1.9* | 12.9* |
| B10.Q/Ai | MOG ₇₉₋₉₆ -CFA | 31/36 | 14.8 | 20.5 | 1.7 | 1.3 | 13.0 |
| B10.Q/Ai | MOG ₇₉₋₉₆ -CFA+PTX | 44/44* | 10.1* | 38.8* | 3.1* | 2.0* | 19.3* |

^A Clinical traits were calculated as detailed in Table I legend. Within each strain, trait values for both B10.D1 and B10.Q/Ai were significantly different between MOG₇₉₋₉₆-CFA + PTX and MOG₇₉₋₉₆-CFA protocols as assessed by Chi-square or Student's *t* test.

* $p < 0.001$. Means are shown.

^B CDS, cumulative disease score.