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**HISTAMINE RECEPTOR H₁ SIGNALING IN CENTRAL
NERVOUS SYSTEM AUTOIMMUNE DISEASE AND
IMMUNE DEVIATION**

A Dissertation Presented

by

Rajkumar Noubade

to

The Faculty of the Graduate College

of

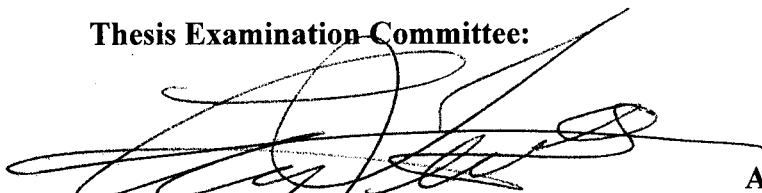
The University of Vermont

In Partial Fulfillment of the Requirements
for the Degree of Doctor of Philosophy
Specializing in Cell and Molecular Biology

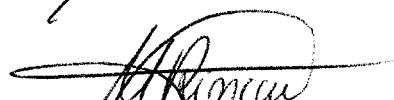
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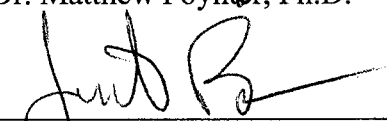
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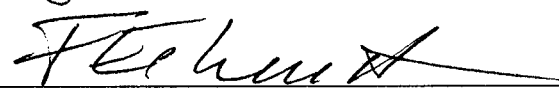
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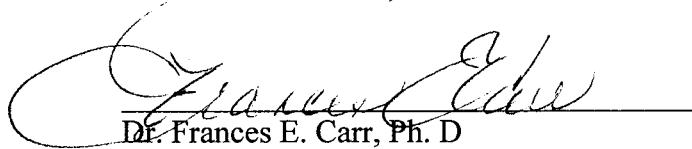
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ABSTRACT

Multiple Sclerosis (MS) is a demyelinating disorder of the central nervous system affecting 0.1% of the population in the Northern hemisphere. MS is a complex disease that depends on genetic and environmental factors and is controlled by multiple genes that exert a modest effect in the overall disease outcome. The complex nature of the disease complicates the study of individual genes and their contribution in the disease process.

To investigate mechanisms underlying the development of diseases like MS and how disease course can be manipulated, animal models have been extensively used, with Experimental Allergic Encephalomyelitis (EAE) being the principle autoimmune model for MS. Even though EAE, like MS, is a complex disease and polygenic in nature, it can be reduced to monogenic intermediate or subphenotypes, which allows for identification of the causative gene and its mechanism.

One such subphenotype of EAE in mice, *Bordetella pertussis* toxin-induced histamine sensitization (Bphs) is controlled by *Hrh1*, gene encoding mouse histamine receptor H₁ (H₁R), wherein sensitized animals of susceptible strains die upon histamine challenge and resistant strains do not. Moreover, mice deficient in H₁R (H1RKO) show delayed onset and reduced severity in the clinical course of EAE. However, the mechanism by which H₁R and its polymorphisms regulate EAE is unknown.

As a disease susceptibility gene, *Hrh1* could act in different cell types and at several checkpoints in the disease process. This includes endothelial cells that regulate blood-brain barrier, antigen presenting cells or T cells, which regulate the cytokine production. Using transgenic mice expressing H₁R exclusively in T cells, this study shows that H₁R expression in T cells is sufficient to restore the EAE severity and the disease associated cytokine production of H1RKO mice to wild type levels.

H₁R from susceptible and resistant strains of mice differ by three amino acids. The P-V-P haplotype (H₁R^S) is associated with disease susceptibility whereas the L-M-S (H₁R^R) haplotype is associated with less severe disease. In this study, using transgenic mice, we show that reexpression of H₁R^S fully complements the clinical EAE and the disease-associated cytokine production of H1RKO mice to wild type levels, however, reexpression of H₁R^R fails to do so. These data suggest that H₁R^R is not functional relative to H₁R^S. Mechanistically, using 293T cells, we show that the two H₁R alleles exhibit differential cell surface expression and altered intracellular trafficking, with the H₁R^R allele being retained within the endoplasmic reticulum (ER). Moreover, we show that all three residues (L-M-S) comprising the H₁R^R haplotype are required for altered expression. Thus, polymorphisms influencing cell surface expression of H₁R regulate immune functions and autoimmune disease susceptibility.

CITATIONS

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CHAPTER 1: COMPREHENSIVE LITERATURE REVIEW

Multiple Sclerosis

Multiple Sclerosis (MS), a prototypic demyelinating inflammatory disease of the central nervous system (CNS) (Hafler, 2004), has been the most common neurological disorder in young adults since it was first noted by Jean Martin Charcot in 1868 (Greenstein, 2007). More than 2.5 million people have been affected worldwide, with 350,000 individuals in the United States (US). The estimated prevalence rate in the year 2000, for the US Caucasian population was 1.91 per 1000 with an incidence rate of 7.3 per 100,000 (Berger et al., 2003). MS creates an economical burden to the individual, the health care system and the society. In 1994, the annual cost of MS in terms of direct care and loss of productivity in the US was estimated to be \$34,000/ patient with a mean life-time cost of \$2.2 million. This translates to a national cost of \$6.8 billion/year. MS is more common in females than in males (~ 2:1); however, affected men generally have a delayed onset with worse prognosis (Kantarci and Wingerchuk, 2006).

A remarkable heterogeneity is seen in clinical MS with multiple forms identified: (i) relapsing-remitting MS, observed in 85-90% of patients, with full or partial recovery between relapses, with most developing into (ii) secondary progressive MS with progressive clinical deterioration and, (iii) primary progressive MS with neurological dysfunction from the onset without any clinical relapses (Hafler, 2004; Holmoy and Vartdal, 2007). The symptoms vary depending on the component of the CNS involved, brain or spinal cord, and include motor, sensory, autonomic and cognitive disabilities. About 50% of MS patients become dependent on a walking

aid by year 15 of the disease (Kantarci and Wingerchuk, 2006; Weinshenker et al., 1989).

Etiology of MS

One hundred and fifty years after its discovery, the etiology of MS is still unknown; however, genetic (Mackay and Myriantopoulos, 1966; Sadovnick et al., 1988) as well as environmental factors (Dean et al., 1976; Kurtzke and Hyllested, 1987) have been implicated in its susceptibility. Considered to be a complex disease with multiple disease-susceptibility genes, MS lacks a clear pattern of inheritance. Hence it is believed that the disease is triggered by some kind of environmental factor in genetically susceptible individuals (Comabella and Martin, 2007; Hafler et al., 2005).

The support for the influence of genetic factors include: a 20-40 times greater risk in siblings and fraternal twins of patients, a 150-300 times greater risk in identical twins of patients and a lack of increased risk in adopted-relatives of patients (Allen et al., 1994; Ebers, 2005; Ebers et al., 1995; Hafler et al., 2005; Jersild et al., 1973; Kurtzke et al., 1982; Mackay and Myriantopoulos, 1966; Risch and Merikangas, 1996). Familial studies have suggested that even phenotypic heterogeneity of MS has a genetic basis with greater similarity of clinical course in patients who are relatives (Kantarci et al., 2002).

The support for the involvement of environmental factors in MS include: non-infectious factors such as geography and migration, with lower MS risk among individuals migrating from high-risk to low-risk areas (Alter et al., 1978; Alter et al., 1966; Dean, 1967; Hammond et al., 2000; Kurtzke et al., 1985; Kurtzke et al., 1970); latitude gradient, with 3% higher risk in individuals born in the north (42⁰ N and

above) than individuals born in the south latitude (37° N and below) (Hernan et al., 1999); exposure to sunlight; circulating levels of vitamin D, with low levels being associated to higher risk (Ascherio and Munger, 2007; Munger et al., 2004; Soilu-Hanninen et al., 2005; Soilu-Hanninen et al., 2007); and an incomplete concordance in monozygotic twins (Ebers, 2005; Weinshenker, 1996).

An infectious etiology with a variety of viral and bacterial agents associated with increased risk has been proposed, with Epstein-Barr virus (EBV) infection the most consistent and strongest risk factor (Ascherio and Munger, 2007; Coo and Aronson, 2004; Kurtzke, 1968, 1993; Marrie, 2004; Thacker et al., 2006). This multifactorial etiology triggers a disease in MS patients characterized, neuropathologically, by discrete lesions (or plaques) mostly in the white matter of the CNS tissue, causing inflammatory infiltrates, demyelination, astrocytic proliferation (astrogliosis) and axonal damage. It is widely believed that the inflammatory infiltrates are pathogenically the primary factors and that MS is an autoimmune disease with an immune attack against myelin proteins (McFarland and Martin, 2007).

Myelin structure and functions

The myelin sheath is a multilamellar membrane, uniquely found and essential to the functioning of the vertebrate nervous system (Tzakos et al., 2005). In the CNS, the myelin sheath is formed by the wrapping of plasma membrane extensions of oligodendrocytes, specialized glial cells, in highly regular concentric layers around the axons. These concentric layers are practically fused together with very little or no cytoplasm (Kursula, 2006). High-resolution electron microscopic studies of myelin sheath have demonstrated periodic electron-dense and -light layers. Dense

layers, spaced between 150-170 Å⁰ apart, are formed by the apposition of the cytoplasmic surfaces of the plasma membrane extensions of the oligodendrocytes. The light layers, also known as intraperiodic lines, are formed by the apposition of the extracellular surfaces of the plasma membrane (Baumann and Pham-Dinh, 2001). The thickness of the myelin sheath varies with the length of the axon, with longer axons having thicker myelin (Waxman and Sims, 1984). The longitudinal organization of the myelin sheath is also unique, with three distinct anatomical and functional domains (Porter and Tennekoon, 2000).

The myelin sheath is segmented, forming internodes of about 150-200 µm length (Butt and Ransom, 1989). The internodes are separated by spaces where myelin is lacking and the axolemma is exposed to the extracellular milieu. These are called nodes of Ranvier and are enriched in voltage gated sodium channels (120,000/µm², the highest density in the nervous system) (Baumann and Pham-Dinh, 2001). Each successive myelin wrap, at its lateral margins, creates a loop containing some cytoplasm, called paranodal loops or paranodes (Porter and Tennekoon, 2000). The junction of paranodal loops with axons, known as juxtaparanodal region, is rich in potassium channels and thus segregates them from the voltage gated sodium channels in the nodes of Ranvier (Porter and Tennekoon, 2000; Rios et al., 2003). This organization is important for the normal conduction of electrical impulses along the axons (Kursula, 2006). Myelination alters the electrical properties of the axons because the myelin sheath has high resistance and low capacitance (Tolhurst and Lewis, 1992). Therefore, once an action potential is generated at one node of Ranvier, it flows down the axon quickly to the next node rather than leak back across the membrane. Thus, an

electrical impulse jumps from one node to the next node, a method of propagation known as saltatory conduction (Baumann and Pham-Dinh, 2001; Salzer, 2002). Myelin is very effective in increasing conduction velocity. An axon of about 1-5 μm in diameter can propagate an electrical impulse at about 20 meters per second if it is myelinated, while a non-myelinated axon needs to be 500-1000 μm thick in order to propagate an electrical impulse at the same rate (Hall, 1992).

Myelin constitutes about 40-50% of the CNS white matter on dry weight basis (Tzakos et al., 2005). It is a poorly hydrated structure containing about 40% water in contrast to the highly hydrated (80%) grey matter. Like all other cell membranes, it is composed of a lipid bilayer with intercalated proteins. However, in contrast to the other cell membranes, it is uniquely made of lipids (70% of the dry weight). The lipids are composed of cholesterol, phospholipids and glycolipids, with an enrichment of glycosphingolipids (Baumann and Pham-Dinh, 2001; Porter and Tennekoon, 2000). The low water content and lipid-rich composition of myelin contributes to its insulating properties and favor rapid nerve conduction velocity. When the myelin is damaged by diseases or when it is not formed due to genetic defects, it results in serious neurological conditions, including motor and sensory deficits (Porter and Tennekoon, 2000).

The myelin proteins, comprising the remainder 30% of the myelin dry weight, consist of a restricted set of proteins (Kursula, 2006). Most of these proteins are exclusively found in myelin and oligodendrocytes and are important in myelination and/or maintenance of myelin architecture (Tzakos et al., 2005). Myelin basic protein (MBP) is one of the most abundant proteins, constituting 30% of the total myelin

proteins, and is present at the cytoplasmic surfaces of the myelin membranes (Baumann and Pham-Dinh, 2001). MBP is essential for myelin compaction (Campagnoni and Macklin, 1988). Mutant mice, with a large deletion of the MBP gene (shiverer mice), lack the major dense line of myelin (Privat et al., 1979; Roach et al., 1985).

Proteolipid protein (PLP) and its splice variant, DM20, are the most abundant myelin proteins, constituting 50% of the total myelin proteins (Kursula, 2006). The absence of PLP/DM20 leads to a loosely wrapped myelin sheath and loss of intraperiodic lines, correlating with reduced physical stability (Boison et al., 1995). Therefore, PLP, along with MBP, is believed to cement the myelin sheath, like a zipper, by forming membrane junctions after myelin compaction (Boison et al., 1995; Klugmann et al., 1997) Further, the absence of PLP/DM20 leads to axonal damage and axonal degeneration, indicating that myelin plays a pivotal role in maintaining axonal integrity and function (Baumann and Pham-Dinh, 2001; Boison et al., 1995).

Myelin oligodendrocyte glycoprotein (MOG) is a minor myelin protein and is present on the outermost lamellae of the myelin sheath and is present in oligodendrocytes, particularly on the processes (Tzakos et al., 2005). MOG is a surface marker for oligodendrocyte maturation and its presence correlates with late stages of maturation (Baumann and Pham-Dinh, 2001; Solly et al., 1996). The amino acid sequence of MOG is highly conserved among animal species, suggesting an important biological function (Tzakos et al., 2005) in the completion, compaction and/or maintenance of myelin (Johns and Bernard, 1999).

Myelin associated glycoprotein (MAG) is another minor glycoprotein important in myelin compaction (Tzakos et al., 2005). Absence of MAG leads to increased

cytoplasm content between lamellae and lower number of myelin wraps (Li et al., 1994; Montag et al., 1994). Other myelin proteins include connexin32, a gap junction protein, and 2'3'-cyclic nucleotide-3'-phosphodiesterase (CNPase) found in the cytoplasm of paranodes (Tzakos et al., 2005).

Immunology of MS

MS is considered to be a coordinated immunological attack against myelin proteins in the CNS (Ferber et al., 1996). A large body of literature provides evidence that the immune system is involved in the disease process (McFarland and Martin, 2007). Even though specific self-antigen(s) has not been definitively demonstrated, it is generally accepted that CD4 T cells reactive to major constituents of the myelin sheath, MBP (Berger et al., 2003; Bielekova et al., 2000; Bielekova et al., 2004), PLP (Bielekova et al., 2004) and MOG (Genain et al., 1999; Olsson et al., 1992; Soderstrom et al., 1993) mediate the autoimmune pathology of the disease. Myelin-specific T cells are easily detected in normal individuals (Sospedra and Martin, 2005). The triggers that cause these cells to attack myelin are largely unknown.

A role of infectious agents has long been proposed to break the tolerance to myelin components in genetically susceptible individuals through molecular mimicry and bystander activation (Fujinami and Oldstone, 1985) (Lang et al., 2002; Tejada-Simon et al., 2003; Wucherpfennig and Strominger, 1995) (Anthony et al., 1997; Waldner et al., 2004). Environmental factors, described earlier, are also considered to trigger the activation of autoreactive CD4 T cells in genetically susceptible individuals. In this regard, histamine elicited by environmental factors or generated during an ongoing infection could act as a mediator of such a disease-inducing trigger. The myelin-

reactive CD4 T cells penetrate CNS through the blood-brain barrier (BBB), formed by specialized endothelial cells that are connected through tight junctions (Minagar and Alexander, 2003). These endothelial cells are typically ensheathed by basal lamina and astrocytic end-feet processes (Kim et al., 2006)

Astrocytes are the most abundant glial cells in CNS (Minagar et al., 2002). They are critical for the development, structural support and the maintenance of BBB. In co-culture systems, astrocytes upregulate the several proteins of tight junction structure that connects the endothelial cells (Dehouck et al., 1990; Rubin et al., 1991). The BBB endothelial cells exhibit an apical or luminal polarization of transporters like p-glycoprotein, glucose transporter 1 (GLUT1), thus forming a transport barrier (Abbott et al., 2006). Astrocytes up-regulate the expression and the polarized localization of these transporters (Kim et al., 2006). BBB also acts as a metabolic barrier and astrocytes upregulate several of the BBB-specific enzymes such as monoamine oxidase, superoxide dismutase, that support the protective and detoxifying roles of BBB (Haseloff et al., 2005). The perivascular end-feet of the astrocytes are highly specialized with high density of orthogonal array of particles containing the water channel aquaporin 4 and the potassium channel Kir4.1. The polarity of these proteins, which are anchored to the basal lamina through a proteoglycan protein called agrin, contributes to the integrity of BBB (Minagar et al., 2002). Moreover, astrocytes secrete several factors such as basic fibroblast growth factor, glial-derived neurotrophic factor, angiopoetin 1 and TGF β , that induce several aspects of BBB (Kim et al., 2006).

The entry of T cells into the CNS is a multistep process involving the induction of adhesion molecules such as vascular cell adhesion molecule (VCAM) on the

endothelial cells, mostly by cytokines including IFN- γ , TNF- α and IL-23 released during the inflammatory process. The interaction of these adhesion molecules with their binding partners, such as VLA-4, on the surface of activated CD4 T cells allows the CD4 T cells to adhere to the endothelial cells and diapedese into the CNS (Brocke et al., 1993; Butcher et al., 1999). Matrix metalloproteases (MMP), particularly MMP-2 and -9, surround the inflamed BBB endothelial cells and degrade the basal membrane as well as the extracellular matrix of parenchyma, thus enabling the T cells to spread in the CNS (Anthony et al., 1997; Clements et al., 1997; Lindberg et al., 2001; Pedotti et al., 2003).

After gaining access to the white matter, the CD4 T cells re-encounter the myelin antigens presented to them by the resident antigen presenting cells (APCs), particularly microglial cells (Minagar et al., 2002). Activated T cells produce several cytokines, which in turn activate more APCs and thus set up a pro-inflammatory loop that provides an infiltrate rich in activated T cells, macrophages and other cells of hematopoietic origin such as B cells and mast cells. The activated macrophages attack myelin and phagocytose large chunks of the myelin sheath (Ferber et al., 1996; Sospedra and Martin, 2005) and produce toxic materials such as nitric oxide (Brenner et al., 1997; Conlon et al., 1999). There is a myelin-directed cytotoxic T cell response, an auto-antibody response and an activation of the complement cascade (Compston et al., 1986; Keegan et al., 2005; Lalive et al., 2006; Laurell and Link, 1972; Lucchinetti et al., 1996; Morgan et al., 1984).

This concerted attack of T and B cells, complement cascade, inflammatory mediators including cytokines and nitric oxide on the myelin sheath results in areas

of severe demyelination. In addition, there is loss of myelin-producing oligodendroglial cells, an increase in the number of fibrous scar tissue-forming astrocytes, and permanent axonal damage (Conlon et al., 1999; Sospedra and Martin, 2005; Trapp et al., 1998), thus resulting in the pathophysiological defects observed in the affected individual.

The cytokine-producing phenotype of myelin-specific T cells determines the ability of these cells to cause inflammation in the CNS. Organ-specific autoimmune diseases such as MS are thought to be primarily mediated by Th1 type of CD4 T cells. These cells are differentiated in the presence of interleukin (IL)-12 and are characterized by the production of large amounts of IFN- γ , TNF- α and IL-2 (Ferber et al., 1996; McFarland and Martin, 2007; Sospedra and Martin, 2005). Increased levels of IFN- γ , TNF- α in the serum (Hohnoki et al., 1998) and of IL-12 in cerebrospinal fluid (CSF) (Dormond et al., 2002) of MS patients have been observed. However, these cytokines worsened the disease upon systemic administration (Panitch et al., 1987; Sharief and Hentges, 1991). The disease-enhancing effect of these cytokines has been associated with their ability to enhance the expression of adhesion molecules on the vascular endothelium (Ferber et al., 1996). Recently, IL-17 and IL-23 are being considered to be the important proinflammatory cytokines in autoimmune diseases (McFarland and Martin, 2007). Accordingly, an augmentation of *IL-17* mRNA in mononuclear cells of CSF and in brain tissues of MS patients is observed (Dormond et al., 2002; Matusевичius et al., 1999). IL-23 is present in both active and chronic lesions (Lundmark et al., 2007). Myeloid dendritic cells from MS patients express higher IL-23 than those from normal individuals (Vaknin-Dembinsky et al., 2006). All

these proinflammatory cytokines, in addition to orchestrating the inflammation, play an important role in the demyelination process by activating phagocytic cells and by inducing apoptosis of myelin producing cells, which lead to impaired saltatory conduction along the axon and pathological effects (Pouly et al., 2000; Selmaj et al., 1991).

Genetics of MS

The evidence for genetic factors in MS susceptibility is compelling. Several approaches including genetic linkage, candidate gene association and gene expression studies have been used (Becanovic et al., 2004; Fernald et al., 2005). However, all have failed to demonstrate a clear mode of inheritance in the disease. Consequently, it has been concluded that MS is polygenic and affected by multiple genes, each exerting a modest effect in the overall disease outcome (Sawcer, 2006). The most consistent association has been with the major histocompatibility complex (MHC) class II or human leukocyte antigen (HLA), specifically HLA-DRB1*1501-DQB1*0602 haplotypes located on chromosome 6 (Hafler et al., 2007; Haines et al., 1996; Haines et al., 1998). In spite of its strong linkage, HLA association explains only about 50% of the genetic etiology of MS (Ebers and Sadovnick, 1994). Evidence for additional linkages to several chromosomes outside HLA has been observed, supporting the complexity. Candidate gene studies have suggested more than 100 such non-MHC genes, a conservative estimate suggesting about 30 genes, but no consensus has been accepted (Becanovic et al., 2006; GAMES, 2001, 2003).

Recently, using a large-scale genomewide association scan, The International Multiple Sclerosis Genetic Consortium has identified IL-2 receptor alpha (IL-2RA)

and IL-7 receptor alpha (IL-7RA) alleles, along with those in the HLA locus, as risk factors for MS (Hafler et al., 2007). The risk conferred by polymorphisms in IL-7RA is confirmed by two additional, independent studies (Gregory et al., 2007; Lundmark et al., 2007). However, risk contributed by IL-2RA and IL-7RA is minimal and explains only 0.2% of the variance (Peltonen, 2007). Moreover, the approaches used in these studies have little statistical power to detect rare variants that could confer a relatively large genetic risk (Hafler et al., 2007; Sawcer, 2006). Overall, it has been difficult to identify genes associated with MS because of the genetic complexity of the disease, the genetic diversity of the human population, the relatively small sample sizes, and the environmental influence and possible variations in the disease diagnosis (Andersson and Karlsson, 2004).

Animal models of MS

Due to the complex genetic architecture of MS, to investigate mechanisms of disease development and disease manipulation, animal models have been extensively used. The most important advantage of animal models, compared to humans, is the better control of genetic background and environment. In addition, large numbers of animals can be studied. The disease can be deliberately induced and animals can be genetically manipulated. Animal models have the potential to significantly reduce the genetic complexity inherent in autoimmune diseases into intermediate or subphenotypes, such as histamine sensitivity. In addition, animal models permit the refinement of candidate regions to an interval small enough to allow identification of the causative gene using classical positional cloning and candidate gene screening. Thus, even though animal models do not completely display all the disease parameters found in the human

disease they model, specific traits of animal models reflect a particular pathway and give better mechanistic understanding of a particular stage of the human disease (Andersson and Karlsson, 2004).

There are two major strategies of discovering genetic contribution to the development of disease using animal models. The first one, “gene-to-disease” pursues a hypothesis-based role of a particular gene in the disease development and is performed using gene-knock out and transgenic mice. The other, “disease-to-gene” strategy, is an unbiased, hypothesis-free approach aimed at identifying the disease-relevant part of the genome. This strategy involves the use of hybrids of one susceptible strain of mice crossed with a resistant strain. Development of the disease is studied in these mice followed by a marker assisted genome screen. Statistical linkage analysis is used to relate disease development to a genetic variant at a defined genetic location. Subsequent refinement will yield identification of the candidate gene, which can further be investigated for genetic polymorphisms between the parental strains and the influence of these polymorphisms on the disease development process. Both the strategies of genetic analysis of susceptibility genes have their advantages and are complementary to each other (Andersson and Karlsson, 2004).

Animal models of MS-experimental allergic encephalomyelitis (EAE)

Animal models that simulate features of MS provide a powerful tool for investigating the pathogenesis of the disease. Several mouse models, virus-induced and/or autoimmune, have been developed that reflect clinical and pathological attributes. The viral models for MS include the Theiler’s murine encephalomyelitis virus (TMEV) (Lipton and Dal Canto, 1976), recombinant- TMEV (Olson et al., 2001), murine

hepatitis virus (MHV) (Matthews et al., 2002), Semliki forest virus (Mokhtarian and Swoveland, 1987) and Sindbis virus (Mokhtarian et al., 1989). All these neurotropic viruses induce demyelination either by directly infecting the neurons or by activating autoreactive T cells through molecular mimicry (Ercolini and Miller, 2006; Grigoriadis and Hadjigeorgiou, 2006).

EAE is the principle autoimmune animal model for MS. With 70 years of history, it is one of the most endured animal models of a human disease (Pedotti et al., 2003). EAE was originally developed by Rivers and colleagues as a model for neuroparalytic accidents in patients who received anti-rabies vaccine, by inducing disseminated encephalomyelitis in monkeys by repeated injections of rabbit brain extracts (Rivers et al., 1933). The introduction of adjuvants, such as Freund's complete adjuvant (CFA), greatly facilitated the induction of the disease with a single or fewer injections of antigen (Freund et al., 1947). Subsequently, the disease has been induced in several animals including non-human primates (Genain et al., 1995), guinea pigs (Freund et al., 1947), rats (Lipton and Freund, 1952), rabbits (Morrison, 1947), hamsters (Tal et al., 1958), goats (Lumsden, 1949), sheep (Innes, 1951), dogs (Thomas et al., 1950), and mice (Olitsky et al., 1950). It is now well established that the experimental disease is mediated by T cells reactive to components of the myelin sheath. This prototypical model for cell-mediated autoimmune disease in general is the best available animal model for human CNS inflammatory demyelinating disease. EAE simulates several features of MS including its pathology, histopathology and pathogenesis making it a powerful tool in the investigation of the pathophysiology (Baxter, 2007; Blankenhorn et al., 2000; Gold et al., 2006; Martin and McFarland, 1995; Palakal et al., 2007).

EAE can be induced in genetically susceptible animals by inoculation with either crude CNS tissue-homogenate or their components, such as PLP, MBP, MOG, MAG, myelin oligodendrocyte basic protein, or the encephalitogenic peptides in an appropriate adjuvant (Encinas et al., 1996; Kuchroo et al., 2002; Trotter et al., 1987; Zamvil et al., 1985). CFA containing *Mycobacterium tuberculosis* H37RA, and *Bordetella pertussis* toxin (PTX) are the most commonly used adjuvants in disease induction. EAE can also be induced by adoptive transfer of CD4 T cells from immunized animals into naïve mice, which underscores the importance of these cells in the immunopathology of the disease (Baron et al., 1993; Bernard et al., 1976; Bernard and Mackay, 1983; Krueger et al., 2005; Langrish et al., 2005).

The development of EAE in the immunized mice occurs in two distinct stages, the induction phase and the effector phase. During the induction or the initial priming phase, up to day 10 post immunization, APCs present the immunized-component of the myelin sheath to CD4 T cells as “foreign” antigen in lymph node and/or spleen and activate them (Powell et al., 1990; Sayed and Brown, 2007).

Optimal activation of T cells requires two signals (Bretscher, 1999). The first signal is delivered by the interaction of T cell receptor (TCR) with antigen presented by MHC molecule on the surface of APCs. The second signal consists of engagement of costimulatory molecules such as CD28, inducible costimulatory molecule (ICOS), programmed death pathway 1 (PD-1), and CD154 expressed on T cells with CD80/CD86, ICOS ligand, PD-1 ligand 1 (PD1-L1)/PD-1 ligand 2 (PD-L2) and CD40 respectively, expressed on APCs (Agata et al., 1996; Hutloff et al., 1999; McAdam et al., 1998; Sharpe and Freeman, 2002). The critical regulatory role in EAE of ICOS and optimal T cell

activation is supported by complete absence of EAE in CD28-deficient mice (Chitnis et al., 2001; Oliveira-dos-Santos et al., 1999), blockade of disease by administration of anti-CD28 antibodies (Perrin et al., 1999), resistance of CD80/CD86-deficient mice to the induction of EAE (Chang et al., 1999; Girvin et al., 2000), exacerbation of disease in ICOS-deficient (Chitnis et al., 2001) and anti-PD1 antibody treated mice (Salama et al., 2003). Another costimulatory molecule, CTLA-4, is expressed on activated CD4 T cells and its interaction with CD80/CD86 is a negative regulator of T cell activation (Karandikar et al., 1996). Administration of anti-CTLA4 blocking antibody during the priming phase of EAE exacerbates the disease (Karandikar et al., 1996). In addition, factors such as histamine play a critical role during priming of autoreactive T cells (Chapter 2). In the presence of proper secondary signals, autoreactive CD4 T cells get activated and differentiated into distinct lineages such as Th1 or Th17 cells, defined by the unique set of cytokines they produce upon re-activation (Furuzawa-Carballeda et al., 2007).

During the effector phase of the disease, the activated autoreactive T cells leave the secondary lymphoid organs, traffic to the CNS and persist there to orchestrate the inflammatory events. In healthy individuals, the traffic of lymphocytes into the CNS is very low and tightly regulated by a highly specialized structure called the blood-brain-barrier (BBB) formed by endothelial cells connected through tight junctions (Engelhardt, 2006). Therefore, loss of BBB integrity is a critical checkpoint in the pathogenesis of CNS inflammatory diseases (Noubade et al., 2007)(Appendix A of this thesis). Only activated T cells, not naïve T cells, can penetrate the BBB, a process mediated by adhesion molecules, chemokines and their respective chemokine receptors (Engelhardt

and Ransohoff, 2005; Hickey et al., 1991; Matejuk et al., 2002; Wekerle et al., 1987). Activated T cells express adhesion molecules such as lymphocyte function associated antigen 1 (LFA-1) and very late antigen 4 (VLA-4). Endothelial cells are induced to express adhesion molecules such as intracellular adhesion molecule 1 (ICAM-1), vascular cell adhesion molecule 1 (VCAM-1), platelet/endothelial cell adhesion molecule 1 (PECAM-1) on their surface, mostly by cytokines such as IFN- γ and TNF- α (Baron et al., 1993; Butter et al., 1991; Graesser et al., 2002; Wilcox et al., 1990). ICAM-1 and VCAM-1 are ligands for LFA-1 and VLA-4, respectively. Interaction of the adhesion molecules on T cells with their binding partners on endothelial cells (Baron et al., 1993; Yednock et al., 1992) and the degradation of the type IV collagen of the basement membrane underlying the endothelial cells by MMPs, results in extravasation of T cells through BBB endothelial cells into the CNS tissue. Type IV collagen is present only in the endothelial cell basement membrane and has distinct binding sites important for T cell binding to the basement lamina of endothelial cells (Sacca et al., 2003).

MMPs are a family of proteolytic enzymes present at low levels in a normal CNS but most of them, particularly MMP-2 and -9, are elevated during EAE. MMPs also assist T cells to spread in the white matter by degrading the brain parenchyma (Agrawal et al., 2006; Anthony et al., 1998; Clements et al., 1997; Dwyer et al., 1998; Harrington et al., 2005; Kieseier et al., 1998; Pagenstecher et al., 1998; Toft-Hansen et al., 2004). Once within the CNS, the T cells are re-activated when the normally-expressed myelin antigens are presented by the resident microglial cells and/or astrocytes (Matsumoto et al., 1992; Constantinescu et al., 2005; Stuve et al., 2002). The re-activation of CD4 T cells is necessary for them to be retained within the CNS and exert their effector functions.

Otherwise, the T cells exit rapidly or undergo apoptosis (Hickey, 2001).

The re-activation of CD4 T cells results in the increase of a number of pro-inflammatory molecules including MMPs, adhesion molecules, chemokines such as RANTES, MCP1, MIP1 α , MIP1 β , osteopontin (Butterfield et al., 1999; Chabas et al., 2001; Dogan and Karpus, 2004; Glabinski et al., 1995; Godiska et al., 1995), and cytokines such as IFN- γ , TNF- α , IL-1, IL-6, IL-12, IL-17, IL-22 and IL-23. These cytokines, particularly IFN- γ and IL-23, activate macrophages and microglial cells, which in turn upregulate their MHC class II molecules, re-present myelin antigen to CD4 T cells, and thus set up an inflammatory loop (Becher et al., 2003; Constantinescu et al., 2005; Ferber et al., 1996; Gutcher and Becher, 2007; Kuchroo et al., 1993). Consequently, there is a sustained breach of BBB integrity and rapid, massive infiltration of cells including CD4 T cells, CD8 T cells, macrophages, B cells, monocytes, mast cells and neutrophils, into the CNS white matter.

The activated macrophages phagocytose myelin and myelin-producing cells leading severe demyelination (Ferber et al., 1996; Pender, 1987). Myelin-reactive CD8 T cells (Chabas et al., 2001; Huseby et al., 2001), B cells, myelin-specific antibodies (Iglesias et al., 2001; Lebar et al., 1986; Svensson et al., 2002), complement proteins that form membrane attack complexes at the surface of oligodendrocytes (Jegou et al., 2007; Piddlesden et al., 1993), opsonization of myelin by autoantibodies and complement proteins (Jegou et al., 2007), all contribute to the demyelination. Proteolytic enzymes (Guyton et al., 2005) and toxic products, such as reactive oxygen and nitrogen intermediates (MacMicking et al., 1992), are released by infiltrated cells. Increasing evidence suggests that inflammatory mediators released from the

infiltrated cells cause a considerable axonal loss (Park et al., 2005). All these events result in an ascending paralytic disease, that begins with weakness and loss of tone in the tail and progresses to complete paralysis of forelimbs, hind limbs, fecal and urinary incontinence, moribund state in some animals, and occasional mortality.

CD4 T cell subsets and their cytokines in EAE

Historically, CD4 T cells of Th1 type, characterized by their ability to secrete IFN- γ , are believed to be sufficient to orchestrate the inflammatory events and initiate myelin destruction in CNS. IL-12 drives the differentiation of CD4 T cells into Th1 type cells (Harrington et al., 2006). Mice deficient in IL-12p40 are resistant MBP-induced EAE (Segal et al., 1998). CD4 T cells differentiated *in vitro* in the presence of IL-12 induce disease in naïve recipients upon adoptive transfer (Baron et al., 1993; Bernard et al., 1976; Bernard and Mackay, 1983). Administration of anti-IL-12p40 antibodies suppresses EAE in adoptive transfer recipients (Leonard et al., 1995). IL-18 also promotes Th1 differentiation (Okamura et al., 1995). Mice deficient in IL-18 are resistant to EAE (Shi et al., 2000) and anti-IL-18 antibodies significantly reduce the IFN γ production and disease development during MBP-induced EAE in rats (Wildbaum et al., 1998). The number of Th1 CD4 T cells in inflammatory lesions correlate with disease severity (Merrill et al., 1992). Encephalitogenic MBP- and PLP-specific CD4 T cells clones are Th1 type (Ando et al., 1989; Baron et al., 1993; Kuchroo et al., 1993). Mice deficient in T-bet, the key transcription factor for the development of Th1 CD4 T cells (Szabo et al., 2000) do not develop EAE (Bettelli et al., 2004). Silencing T-bet by RNA interference ameliorated EAE (Gocke et al., 2007). TNF- α is upregulated in CNS during EAE (Juedes et al., 2000). The

encephalitogenicity of MBP-specific T cell clones is strongly correlated with the TNF- α production (Powell et al., 1990). However mice deficient in TNF- α , IFN- γ or IFN- γ R are susceptible to EAE (Ferber et al., 1996; Frei et al., 1997; Willenborg et al., 1996). Similar observations were made in mice deficient in IL-12, particularly IL-12p35 (Becher et al., 2002; Ghosh et al., 2002).

In contrast, mice deficient in IL-23, a member of IL-12 family, were completely resistant to EAE (Cua et al., 2003; Langrish et al., 2005). Further, these EAE-induced IL-23-deficient mice completely lacked IL-17- positive cells in the CNS while IFN- γ -positive cells were present. These discrepancies led to the identification of a distinct subset of CD4 T cells called IL-17 producing-Th17 cells (Harrington et al., 2005; Krueger et al., 2005). IL-17-deficient mice are resistant to EAE (Komiyama et al., 2006). Subsequently, in addition to IL-17, the Th17 CD4 T cells have been shown to produce IL-1 β , IL-6, TNF- α , IL-22, GM-CSF (Furuzawa-Carballeda et al., 2007). The presence of IL-6, TGF- β and IL-1 β is essential for the generation of these cells and mice deficient in IL-6 as well as IL-1R are resistant to EAE (Okuda et al., 1998; Schiffenbauer et al., 2000). Additionally, IL-23-derived Th17 CD4 T cells induced EAE in naïve recipients upon adoptive transfer (Krueger et al., 2005; Langrish et al., 2005). However, adding complexity to the Th17 pathway is the observation that mice deficient in IL-17E, also known as IL-25, have increased IL-23 expression and are hypersusceptible to EAE (Kleinschek et al., 2007). Thus the relative contribution of Th1 versus Th17 CD4 T cells to the development of EAE remains to be elucidated.

CD8 T cells in EAE

Initial studies suggested that CD8 T cells may play a protective role in EAE when a significant reduction in disease relapses was observed in CD8 knock-out or CD8 T cell-depleted mice (Jiang et al., 1992; Koh et al., 1992). However, several lines of evidence such as predominance of CD8 over CD4 T cells in the brain of MS patients and the close association of CD8 T cells with MS lesions (Booss et al., 1983; Cabarrocas et al., 2003; Hauser et al., 1986; Neumann et al., 2002; Skulina et al., 2004) led to a more careful analysis of these cells in EAE pathogenesis. One criticism for CD4 T cell predominance in EAE has been that when EAE is induced by immunizing the mice with myelin antigens in appropriate adjuvant, the antigens are presented by MHC class II molecules and thus activate CD4 T cells rather than by MHC class I molecules (Ji and Goverman, 2007). Therefore, when MHC class I restricted MBP-specific CD8 T cells were adoptively transferred to naïve recipients, it resulted in severe EAE with extensive demyelination (Huseby et al., 2001). More recently, CD8 T cells generated from mice immunized in the traditional way with myelin antigens in CFA also induced a severe EAE when adoptively transferred to naïve recipients, demonstrating the pathogenic role of CD8 T cells in EAE (Abdul-Majid et al., 2003; Ford and Evavold, 2005; Ji and Goverman, 2007; Sun et al., 2001).

B cells and autoantibodies in EAE

Generally EAE is thought to be a T cell-mediated disease. It does not require B cells and antibodies, as B cell-deficient mice develop severe disease (Lyons et al., 1999; Wolf et al., 1996). Antibody titer and disease severity do not directly correlate (Cross et al., 2001). However, the most important diagnostic marker for early MS,

particularly in patients with normal brain scans, is the presence of oligoclonal antibodies and plasma cells in CSF (Paolino et al., 1996). But the heterogeneity of antigen specificity of these antibodies questioned whether there are consequences of MS-related antigen or represent MS-unrelated B cell responses. A very small proportion of these antibodies were found to be against myelin antigens but their contribution to the actual disease process is unknown (Cross et al., 2001; Ziemssen and Ziemssen, 2005).

B cells, plasma cells and myelin-specific antibodies are present in MS plaques and areas of demyelination (Genain et al., 1999). However, evidence that autoantibodies cause demyelination came from observations that administration of antimyelin antibodies enhanced demyelination in rats and non-human primates (Genain et al., 1999; Schluesener et al., 1987). In mice, it was found that B cells are critical in EAE induction with MOG protein but not peptide (Lyons et al., 1999). Even though autoantibodies that recognize many myelin proteins such as MBP and PLP have been identified to promote demyelination and potentiate EAE (Cross et al., 2001; Endoh et al., 1986), antibodies to MOG are considered to be more critical because MOG is expressed on the outer surface of the myelin sheath (Gardinier et al., 1992).

Transgenic mice producing high titers of anti-MOG antibodies did not develop spontaneous EAE but developed an early and exacerbated disease upon induction, indicating that the autoantibodies can modify the disease course and pathogenesis (Litzenburger et al., 1998). Anti-MOG antibodies capable of inducing EAE require glycosylated epitopes on the surface of oligodendrocytes (Marta et al., 2005) and their demyelinating ability depends on the activation of complement cascade rather than direct cell mediated cytotoxicity (Urich et al., 2006). Additionally, B cells function as antigen

presenting cells. The autoantibodies increase myelin opsonization and subsequent phagocytosis by macrophages and microglial cells and thus contribute to demyelination (Jegou et al., 2007; Ziemssen and Ziemssen, 2005).

Genetic susceptibility of EAE

The observation that different strains of mice differ significantly in their susceptibility to EAE was made in the first study of EAE in mice when it was noted that Swiss mice were susceptible to EAE induced by brain-tissue homogenate in Freund's adjuvant, while the Rockefeller Institute strain of mice did not develop the disease (Olitsky and Yager, 1949). Subsequently, a large number of studies analyzing the genetic control of susceptibility and resistance to EAE have been carried out using inbred strains of mice and, to date, a total of 40 quantitative trait loci (QTL) have been identified (Baker et al., 1995; Blankenhorn et al., 2000; Butterfield et al., 1999; Butterfield et al., 1998; Encinas et al., 1996; Encinas et al., 2001; Fillmore et al., 2003; Karlsson et al., 2003; Mazon Pelaez et al., 2005; Sundvall et al., 1995; Teuscher et al., 2006a). A genomic region on chromosome 17 containing MHC genes, like in MS, has been the strongest and consistently linked region in EAE. Also, this was the first QTL to be identified (Fritz et al., 1985).

A large number of non-MHC loci have also been identified to control EAE susceptibility in mice. Among these, in addition to loci that control clinical disease parameters, such as incidence (Baker et al., 1995; Bakker et al., 2002; Butterfield et al., 1998; Encinas et al., 1996; Sundvall et al., 1995), disease onset (Butterfield et al., 1998; Mazon Pelaez et al., 2005) and disease severity (Baker et al., 1995; Butterfield et al., 1998; Mazon Pelaez et al., 2005), genes that control sub-phenotypes of the disease,

such as histopathological lesion-severity either in the brain (Blankenhorn et al., 2000; Butterfield et al., 1999; Karlsson et al., 2003) or spinal cord (Baker et al., 1995; Blankenhorn et al., 2000; Butterfield et al., 1998; Karlsson et al., 2003), weight loss (Encinas et al., 1996; Encinas et al., 2001), demyelination (Blankenhorn et al., 2000), inflammation (Encinas et al., 2001; Mazon Pelaez et al., 2005) and paralysis (Encinas et al., 2001), have been identified. QTLs controlling disease-subtypes, such as acute progressive, remitting-relapsing, chronic non-relapsing and monophasic non-relapsing/non-relapsing EAE (Butterfield et al., 1999; Karlsson et al., 2003), and those controlling electro-pathophysiological changes of neurons that reflect the extent of demyelination (Mazon Pelaez et al., 2005) have been reported.

EAE and MS are sexually dimorphic diseases with more females affected than males. Accordingly, most of the loci identified are gender specific (Butterfield et al., 1999; Fillmore et al., 2004; Fillmore et al., 2003). The effect of the Y-chromosome, reflecting parent-of-origin, has also been documented (Teuscher et al., 2006a). In addition, extrinsic factors such as the physical structure of the antigen-CFA containing particles (on the surface against buried within) of the emulsion (Fillmore et al., 2003), age and season (Fillmore et al., 2004; Teuscher et al., 2006a), use of pertussis toxin (Blankenhorn et al., 2000) have been shown to override genetic checkpoints, demonstrating the role of gene-environmental interactions in the disease susceptibility. Thus different loci are linked to different aspects of the disease development process and may reflect the heterogeneity observed in MS patients. The study of these loci in isolation and their contribution to disease development may help in understanding the inherent heterogeneity of the disease. One such locus is *Bordetella pertussis* induced histamine

sensitization (*Bp_{hs}*), controlling susceptibility to histamine-induced death in PTX sensitized mice (Sudweeks et al., 1993), has been identified to be *Hrh1*, the gene encoding histamine receptor H₁ protein (Ma et al., 2002).

Identification of histamine receptor H₁ as a susceptibility gene in EAE

Anaphylactic-like hypovolemic shock syndromes can be induced in mice by injecting vasoactive amines such as histamine or serotonin or a mixture of both (Bergman and Munoz, 1965, 1968; Harris and Fulton, 1958; Iff and Vaz, 1966). Inbred strains of mice varied in their sensitivity to these agents and the variation was genetically determined (Bergman and Munoz, 1968; Iff and Vaz, 1966; Parfentjev, 1955; Tokuda et al., 1963). Subsequently, it was found that products from *Bordetella pertussis* significantly enhanced this sensitivity to vasoactive amine treatment and that inbred strains of mice differ in their susceptibility to the enhancing effect. The *B. pertussis* product was later identified as PTX (Bergman and Munoz, 1968; Black et al., 1988; Munoz, 1957; Munoz, 1963; Vaz et al., 1977). SJL/J is the prototypic susceptible mouse strain and C3H/HeJ and CBA/J are the prototypic resistant strains of mice to the PTX-induced histamine sensitivity. The susceptibility of inbred strains to the histamine-sensitizing effects of PTX was found to be under the control of a single autosomal dominant gene (Wardlaw, 1970). The strains of mice susceptible for *Bp_{hs}* developed EAE, while the strains resistant to *Bp_{hs}* did not (Linthicum, 1982). However, it is noteworthy that there are some exceptional strains of mice, suggesting that additional genes control the disease susceptibility. *Bp_{hs}* is also associated with susceptibility to experimental allergic orchitis (Teuscher, 1985).

Using microsatellite and random amplified polymorphic DNA (RAPD)

markers and backcross populations of susceptible SJL/J and resistant C3H/HeJ and CBA/J strains, the *Bphs* locus was mapped to a 33 centimorgan (cM) region of mouse chromosome 6 (Sudweeks et al., 1993). The candidate interval was further refined to an interval to include fewer genes (Meeker et al., 1999). For positionally cloning *Bphs*, a panel of interval specific congenic lines was generated by introgressing the susceptible SJL/J allele onto the resistant C3H/HeJ background. Studies of histamine sensitivity in the congenic lines established that *Bphs* resided in a region containing *Hrh1* (Ma et al., 2002). The identity of *Hrh1* as *Bphs* was further confirmed by the complete resistance of histamine receptor H₁ knock out (H1RKO) mice to *Bphs*. Further, H1RKO mice exhibited a reduced severity and delayed onset of EAE compared to the wild type (WT) mice (Ma et al., 2002), indicating that histamine, acting through histamine receptor H₁, regulates EAE.

Histamine and histamine receptor H₁

Histamine [2-(4-imidazole) ethylamine] is a ubiquitously distributed biogenic amine that mediates diverse physiological processes including neurotransmission and brain functions, secretion of pituitary hormones, and regulation of gastrointestinal and circulatory functions (Parsons and Ganellin, 2006). Additionally, histamine is a potent mediator of inflammation and a regulator of innate and adaptive immune responses (Akdis and Simons, 2006).

Mast cells and basophils are the major sources of stored histamine (Code and Mitchell, 1957; Riley and West, 1953). The granule-stored histamine from these cells is rapidly released upon various immunological and non-immunological stimuli. Mast cell-deficient mice were induced to synthesize histamine upon phorbol ester stimulation

(Taguchi et al., 1982). This “nascent” or “inducible” histamine is proposed to be synthesized by the induction of L-histidine decarboxylase (HDC), the rate-limiting enzyme for histamine synthesis in cells such as activated monocytes/macrophages and neutrophils (Ghosh et al., 2002; Kahlson and Rosengren, 1968; Shiraishi et al., 2000; Takamatsu et al., 1996; Tanaka et al., 2004). T cells, B cells and dendritic cells also synthesize “inducible” histamine (Aoi et al., 1989; Kubo and Nakano, 1999; Szeberenyi et al., 2001). As these cells lack storage vesicles, histamine synthesized is immediately released. The HDC activity is modulated by a variety of stimuli during infections and inflammation (Schneider et al., 2002).

Histamine exerts its pleiotropic effect through four receptors that are designated as histamine receptor H₁, H₂, H₃, and H₄, according to the chronological order of their discovery (Hill et al., 1997; Parsons and Ganellin, 2006). H₁R is widely distributed on a variety of tissues and cell types including: mammalian brain; gastrointestinal tract; genitourinary system; cardiovascular system; adrenal medulla; hepatocytes; nerve cells; airway and vascular smooth muscle cells; endothelial cells; eosinophils; monocytes neutrophils; dendritic cells; and lymphocytes (both T and B cells) (Hill et al., 1997; Parsons and Ganellin, 2006; Smit et al., 1999). Biochemical characterization of the H₁R protein using photoaffinity binding studies and gel electrophoresis under reducing conditions has revealed a molecular weight of 56kDa in mice, rats and guinea pig brain (Ruat et al., 1988; Ruat and Schwartz, 1989; Ruat et al., 1990; Smit et al., 1999).

Purification of H₁R protein has not been successful thus far. H₁R was first cloned from bovine adrenal medulla, which yielded an intron-less gene (Yamashita et al., 1991). This enabled subsequent cloning of H₁R from several species including mouse, which

mapped to chromosome 6 (Inoue et al., 1996). The deduced amino acid sequence represented a 488 amino acid protein with calculated molecular weight of 56kDa. Modeling of the protein revealed the presence of seven transmembrane domains, characteristic of G protein coupled receptors (GPCRs). A striking feature of the proposed structure was a very large third intracytoplasmic loop (212 amino acids) and relatively short intracellular C-terminal tail (17 amino acids). The histamine binding pocket is formed between the third (TM3) and fifth (TM5) transmembrane domains (Hill et al., 1997; Jongejan et al., 2005; Smit et al., 1992). Similar to H₁R, H₂R is also expressed on a variety of cell types, while H₃R expression is restricted mostly to neuronal cells in the brain and some peripheral tissues. H₄R is expressed exclusively on cells of hematopoietic origin (Parsons and Ganellin, 2006).

GPCRs transduce the external signal of ligand binding by activating heterotrimeric G proteins, which in turn couple to a variety of second messenger signaling pathways (Fredholm et al., 2007). H₁R couples to second messenger signaling pathways via the activation of G proteins belonging to G $\alpha_{q/11}$ sub-family (Parsons and Ganellin, 2006). Generally, activation of H₁R leads to stimulation of phospholipase C, resulting in the hydrolysis of phosphatidylinositol 4,5-bisphosphate (PIP₂) to form inositol-1,4,5-trisphosphate (IP₃) and diacylglycerol (DAG), which causes calcium mobilization from intracellular stores and activation of protein kinase C (PKC), respectively (Hill et al., 1997). In addition, H₁R signaling also mediates other signaling pathways such as the production of phospholipase A2 and arachidonic acid (Leurs et al., 1994), cGMP and nitric oxide (Hill, 1992; Leurs et al., 1995; Satoh and Inui, 1984; Toda, 1987), and the activation of NF- κ B (Bakker et al., 2001), STAT1 (Sakhalkar et al.,

2005), and STAT4 (Engelhardt, 2006). H₁R-mediated PKC α stimulation activates MAP kinase pathways, particularly MEK1 (Lipnik-Stangelj and Carman-Krzan, 2004; Megson et al., 2001), ERK MAP kinase and p38 MAP kinase (Robinson and Dickenson, 2001; Steffel et al., 2005) (Chapter 2). Even though H₁R is the first histamine receptor to be identified and a large number of studies on histamine and H₁R have been published in the last decade (Simons, 2004), little is known about the cell-type specific H₁R signaling pathways.

H₂R signaling is mediated via the G_{as} subfamily of G proteins and primarily leads to increased cAMP production and calcium mobilization (Alewijjnse et al., 1998; Del Valle and Gantz, 1997; Leurs et al., 1994; Smit et al., 1996). H₃R is coupled to G_{ai/o} subfamily of G proteins and leads to inhibition of cAMP and accumulation of calcium (Krueger et al., 2005). H₄R signaling is also mediated by coupling to G_{ai/o} subfamily of G proteins and induces calcium mobilization, inhibits cAMP production and activates MAP kinases (Buckland et al., 2003; Hofstra et al., 2003; Morse et al., 2001).

In endothelial cells, H₁R-mediated calcium mobilization and PKC activation promotes cytoskeletal changes to induce cell shape change (Lum and Malik, 1994). Additionally, H₁R-mediated signals lead to disassembly of VE-cadherin complexes that regulate endothelial barrier function (Gao et al., 2000; Winter et al., 1999). These effects result in increased vascular permeability. H₁R signaling also increases expression of adhesion molecules such as ICAM-1, VCAM-1 and P-selectin on endothelial cells (Gonzalez-Scarano et al., 1987; Kubes and Kanwar, 1994; Yamaki et al., 1998).

In dendritic cells, H₁R provides positive signals for enhanced antigen presentation capacity by upregulating several co-stimulatory molecules such as CD80 and

CD86 by increasing the production of proinflammatory cytokines such as IL-1, IL-6, IL-8, MCP-1 and MIP-1 α and Th1 priming activity of these cells (Caron et al., 2001; Mazzoni et al., 2001; Meretej et al., 1991). In contrast, H₂R acts as a negative signal for many of these functions. H₁R induces intracellular calcium flux, actin polymerization and chemotaxis by immature dendritic cells (Mazzoni et al., 2001). H₁R is upregulated in monocyte-derived macrophages and leads to calcium mobilization and enhanced IL-8 production (Triggiani et al., 2007). Treatment of macrophages, isolated from lung parenchyma, with H₁R blockers led to lower IL-6 production (Triggiani et al., 2001).

In B cells, H₁R signals enhance anti-IgM mediated proliferation and antibody production against a T cell-independent antigen, TNP-ficoll, indicating that H₁R signals are important in B cell receptor-triggered responses (Banu and Watanabe, 1999). H1RKO mice produce higher ova-specific IgG1 and IgE compared to the WT mice, indicating that H₁R suppresses humoral responses (Banu and Watanabe, 1999; Jutel et al., 2001).

Studies using total splenocytes have shown that H₁R regulates antigen-specific T-cell effector functions and modulates production of the cytokines IFN- γ and IL-4 (Bakker et al., 2002; Banu and Watanabe, 1999; Bryce et al., 2006; Jutel et al., 2001) Chapter two of this thesis will demonstrate that H₁R in purified CD4 T cells regulates IFN- γ and IL-4 production.

Histamine and histamine receptor H₁ in MS and EAE

The first observation of the role of histamine and histamine receptors in EAE came from the use of pharmacological anti-histaminic agents to block the development of the disease (Linthicum, 1982). Subsequently, several studies used these drugs, particularly H₁R blockers, to reduce the pathology of EAE (Chabas et al., 2001;

Dietsch and Hinrichs, 1989; Dimitriadou et al., 2000; El Behi et al., 2007; Pedotti et al., 2003; Waxman et al., 1984). The genetic susceptibility to EAE development was originally thought to be a function of MHC genes and genes controlling hypersensitivity to histamine (Linthicum, 1982). An analysis of CSF from several MS patients showed a 60% higher histamine content than the control group, while histamine-N-methyltransferase, a histamine metabolizing enzyme, was lower than the control group (Tuomisto et al., 1983). Microarray analysis of chronic plaques in MS patients revealed relative overexpression of H₁R transcripts (Dormond et al., 2002). Administration of anti-H₁R agents either reduced the risk of MS (Alonso et al., 2006) or improved the neurological symptoms (Logothetis et al., 2005). H1RKO mice exhibit milder disease than WT mice (Bakker et al., 2002)(chapter 2 and 3). Mice deficient in H₂R also develop an attenuated disease (Teuscher et al., 2004). EAE is significantly enhanced in H₃R-deficient (Teuscher et al., 2007) and H₄R-deficient mice (Teuscher, unpublished data). Mice deficient in histidine decarboxylase, and therefore in histamine, develop more severe disease than WT mice (Musio et al., 2006). All these findings indicate a regulatory role for histamine in the pathogenesis of EAE.

Mast cells and basophils are the major source of histamine in the body (Mekori and Metcalfe, 2000). It has long been known that mast cells accumulate at the site of inflammatory demyelination in the brain and spinal cord both in animal models and in MS patients (Bebo et al., 1996; Brenner et al., 1994; Dietsch and Hinrichs, 1989; Ibrahim et al., 1996; Kermode et al., 1990; Olsson, 1974; Orr, 1988). Mast cell numbers and/or distribution correlated with MS lesion and EAE susceptibility (Brenner et al., 1994). Mast cell-stabilizing drugs have been shown to improve disease symptoms in EAE

(Brosnan and Tansey, 1984; Dietsch and Hinrichs, 1989; Seeldrayers et al., 1989). Mast cell-deficient mice exhibited delayed onset and reduced disease severity compared to the WT mice. The disease was restored upon reconstitution of these mice with bone marrow derived-mast cells (Secor et al., 2000), indicating a pathologic role for mast cells in EAE. Interestingly, reconstituted mast cells were present only in peripheral tissues but not in the brain and spinal cord, an observation confirmed by another independent study (Tanzola et al., 2003). The number of reconstituted mast cells in the spleen decreased with increased disease severity. While no mast cells were detected in the lymph node of naïve reconstituted animals, a large number of them were present in the draining inguinal lymph node in diseased animals (Tanzola et al., 2003). These findings suggest that mast cells act in the periphery, rather than the CNS, and therefore influence EAE during the induction phase rather than the effector phase. In addition, immunized mast cell-deficient mice had lower frequency of IFN- γ positive cells in the draining lymph node than WT mice. *Ex-vivo* stimulated T cells from these mice produced significantly lower IFN- γ and IL-4 than WT mice (Secor et al., 2000) (Tanzola et al., 2003). These results suggest that mast cells, and therefore histamine, provide a permissible microenvironment for the optimal induction of autoreactive T cells in the secondary lymphoid organs.

Due to its activity in multiple cell types including endothelial cells, antigen presenting cells and T cells, histamine acting through H₁R can function at several critical checkpoints during both induction and effector phases of EAE. In Chapter 2, it is demonstrated that H₁R exerts its effects during the induction of encephalitogenic T cells and that expression of H₁R in T cells is sufficient to restore clinical disease severity and cytokine production in H1RKO mice to the WT levels, independent of its actions in

other cell types important in the disease process. Further, in Chapter 3, it is established that even though the resistant allele of H₁R differs only by three amino acids from the susceptible allele, it confers resistance to disease due to lack of cell surface expression.

In endothelial cells, as described before, H₁R signaling leads to vasodilation, increased vascular permeability and thus affects BBB integrity. H₁R signaling also acts as a secretagogue for the regulated release of the stored factors from endothelial-specific storage vesicles called Weibel-Palade bodies (WPBs) (Hattori et al., 1989). The WPBs contain several vasoactive factors such as von Willebrand factor, P-selectin, and IL-8, the syntheses of which are induced by inflammatory signals including PTX (Rondaij et al., 2006). When these factors are released, they act on the endothelial cells in an autocrine fashion. The direct vasodilatory effects of histamine combined with the autocrine effects of the WPB contents are likely to result in shock and the death observed during the effector phase of Bphs. However, in Appendix A, it is shown that the release of WPB contents do not mediate the shock observed during the Bphs.

CHAPTER 2: HISTAMINE RECEPTOR H₁ IS REQUIRED FOR TCR MEDIATED p38 MAP KINASE ACTIVATION AND IFN-GAMMA PRODUCTION

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Abstract

Histamine H₁ receptor (H₁R) is a shared susceptibility gene in experimental allergic encephalomyelitis (EAE) and orchitis (EAO), two classical T-cell mediated models of organ-specific autoimmune diseases. Here we show that expression of H₁R in CD4 T cells is required for IFN γ production but is dispensable for proliferation. H₁R ligation is necessary for TCR-mediated activation of p38 MAP kinase, a known regulator of IFN γ expression. Importantly, selective expression of H₁R in CD4 T cells fully complements both IFN γ production and EAE susceptibility of H₁R deficient mice. Thus, the presence of H₁R in CD4 T cells and its interaction with histamine regulates early TCR signals that lead to Th1 differentiation and autoimmune disease.

Introduction

Histamine [2-(4-imidazole) ethylamine] is a ubiquitous mediator of diverse physiological processes including neurotransmission and brain functions, secretion of pituitary hormones, and regulation of gastrointestinal and circulatory functions (Parsons and Ganellin, 2006). Additionally, histamine is a potent mediator of inflammation and a regulator of innate and adaptive immune responses (Akdis and Simons, 2006). Histamine exerts its effect through four receptors that belong to the seven-transmembrane G protein-coupled receptor family and are designated histamine H₁, H₂, H₃, and H₄ receptor, according to the chronological order of their discovery (1, 3).

H₁R couples to second messenger signaling pathways via the activation of heterotrimeric G $\alpha_{q/11}$ family of G proteins (Parsons and Ganellin, 2006). Generally, activation of H₁R leads to stimulation of phospholipase C, resulting in the hydrolysis of phosphatidylinositol 4,5-bisphosphate (PIP₂) to form inositol-1,4,5-trisphosphate (IP₃) and diacylglycerol (DAG), which causes calcium mobilization from intracellular stores and activation of protein kinase C (PKC), respectively (Hill et al., 1997). In addition, H₁R signaling also mediates other signaling pathways such as the production of cGMP, arachidonic acid and nitric oxide (Leurs et al., 1995), and the activation of NF- κ B (Bakker et al., 2001), STAT1 (Sakhalkar et al., 2005), STAT4 (Engelhardt, 2006) and MAP kinase pathway (Lipnik-Stangelj and Carman-Krzan, 2004; Megson et al., 2001; Robinson and Dickenson, 2001). However, even though H₁R is the first histamine receptor to be identified and a large number of studies on histamine and H₁R have been published in the last decade (Simons, 2004), little is known about the cell-type specific H₁R signaling pathways.

In the immune system, histamine has been reported to be a potent modulator of innate and adaptive immune responses. Histamine, acting through H₁R, affects the maturation of dendritic cells and alters their T cell-polarizing activity (Caron et al., 2001). It regulates antigen-specific T-cell effector functions and the related antibody isotype response (Banu and Watanabe, 1999). H₁R signaling in splenocytes has been reported to modulate cytokine secretion by these cells (Bakker et al., 2002; Banu and Watanabe, 1999; Bryce et al., 2006; Jutel et al., 2001) but no study has addressed the role of H₁R in purified CD4 T cells.

We have previously demonstrated that *Hrh1* (encoding the mouse H₁R protein) is a shared susceptibility gene in experimental allergic orchitis (EAO) and encephalomyelitis (EAE), the autoimmune model of multiple sclerosis (MS) (Bakker et al., 2002). In both MS and EAE, CD4 T cells secreting IFN γ (Th1) (Baron et al., 1993) and/or IL-17 (Th17) (Krueger et al., 2005) are necessary and sufficient for eliciting EAE pathology and clinical signs. The relative contributions of each of these cytokines to the development of EAE *in vivo* are debated, because conflicting evidence exists on the importance of IFN γ vs. IL-17. On the one hand, the importance of IL-17 is established in studies showing that EAE is diminished in IL-23-deficient but not IL-12-deficient animals (with no expression of the Th17-promoting or Th1-promoting cytokines, respectively) (Cua et al., 2003), and severe EAE is observed in IFN γ knockout mice and IFN γ R knockout mice (Ferber et al., 1996; Willenborg et al., 1996). These findings contrast with studies showing that either CD4 Th1 cells (Baron et al., 1993) or CD4 Th17 cells (Langrish et al., 2005) can transfer EAE to naïve recipients. Recent studies reporting the predominant presence of a pre-Th1, IFN γ ⁺/IL-17⁺ CD4 T cell subtype, early

after induction of EAE with encephalitogenic myelin oligodendrocyte glycoprotein 35-55 (MOG₃₅₋₅₅) peptide (Suryani and Sutton, 2007) may help resolve these apparent inconsistencies. Nevertheless, IFN γ alone or in conjunction with IL-17, is well-established as a cytokine of relevance in EAE immunopathology.

We have previously shown that H₁R deficient (H1RKO) mice exhibit a significant delay in the onset of EAE and a reduction in the severity of the clinical signs compared to wild-type (WT) mice (Bakker et al., 2002). This phenotype is associated with an immune deviation of the elicited CD4 T cell population from a Th1 response to a Th2 response with no detectable difference in IL-17 secretion, suggesting that the CD4 Th1 cells and the IFN γ produced by them play an important role in the pathology of the disease. In this report, we have studied the mechanism underlying the immune deviation, and show that it is directly due to H₁R regulation of cytokine responses in CD4 T cells, and not to H₁R expression in antigen presenting cells (APCs). In this study, we also show that H₁R is expressed in unstimulated CD4 T cells but is rapidly downregulated upon activation. H₁R is required for the activation of the p38 MAP kinase signaling pathway and for IFN γ production in response to TCR stimulation in CD4 T cells. Finally, H₁R mediated signaling in CD4 T cells, independent of APCs, regulates the encephalitogenic Th1 effector cell response in EAE.

Results

H₁R expression is required for IFN γ production by CD4 T cells

MOG₃₅₋₅₅ peptide-immunized H1RKO splenocytes produce less IFN γ and more IL-4 than the splenocytes from immunized WT mice (Bakker et al., 2002). However, it is not clear whether this immune deviation is due to the lack of H₁R signaling in CD4 T cells or in APCs. To investigate the role of H₁R in regulating IFN γ production and Th1 differentiation, CD4 T cells were purified from WT and H1RKO mice and activated with anti-CD3 and anti-CD28 monoclonal antibodies (mAbs) in the presence of recombinant IL-12 and neutralizing anti-IL-4 mAb. After 4 days, Th1 effector cells were extensively washed, counted and equal number of cells were re-stimulated with anti-CD3 mAb for 24 hours. Th1 effector cells from H1RKO mice produced considerably less IFN γ than WT Th1 cells (Fig. 1A). We also examined the production of IL-4 upon re-stimulation of Th2 effector cells generated in presence of IL-4 and anti-IFN γ mAb. A marginal increase in IL-4 production was observed in cells from H1RKO mice compared to cells from WT mice (Fig. 1B). Recent studies have established IL-17 as an important cytokine in EAE (20). Consequently, we examined IL-17 production by Th17 cells generated in the presence of IL-6 and TGF- β and anti-IFN γ and anti-IL-4 mAbs. There was no difference in IL-17 production by Th17 differentiated cells from H1RKO and WT mice (Fig. 1C). Moreover, we examined the role of H₁R in non-polarized effector cells, generated by stimulating cells in the absence of exogenous cytokines for 4 days. Effector cells were then re-stimulated with anti-CD3 mAb for 24 hours. CD4 T effector cells from H1RKO mice produced significantly less IFN γ than those from WT mice (Fig. 1D). Thus, under

these conditions, IFN γ production in H1RKO effector CD4 T cells is impaired.

IFN γ production by CD4 T cells contributes to their differentiation into Th1 effector cells (Robinson and O'Garra, 2002). To examine the role that H₁R signaling plays in this process, purified CD4 T cells from H1RKO and WT mice were stimulated with anti-CD3 and anti-CD28 mAbs for different periods of time and IFN γ production was quantified. CD4 T cells from H1RKO mice produced significantly lower IFN γ than those from WT mice at all time points examined (Fig. 1E). In contrast, no difference in IL-2 production between WT and H1RKO CD4 T cells was observed (Fig. 1F). Furthermore, proliferation was comparable between WT and H1RKO CD4 T cells (Fig. 1G). Taken together, these results demonstrate that H₁R expression in CD4 T cells plays a critical role in regulating IFN γ production during the activation and differentiation of these cells.

H₁R gene expression is downregulated early upon TCR activation

In order to demonstrate that the reduced secretion of IFN γ by CD4 T cells is due to the absence of a functional H₁R in these cells, we carried out H₁R complementation in to H1RKO CD4 T cells by retroviral transduction. We generated a retroviral construct using the pEGZ-HA vector where H₁R was subcloned downstream of a hemagglutinin (HA) tag and upstream of IRES-EGFP. To confirm that the HA-H₁R could be properly expressed we transiently transfected HEK293T cells with the pEGZ-HA-H₁R construct and examined its expression by Western blot analysis using anti-HA mAb. A band corresponding to the HA-H₁R size (~55 kDa) was present only in HA-H₁R transfected cells (Fig. 2A). To demonstrate that the HA-H₁R was expressed on the cytoplasmic membrane, the HA-H₁R transfected HEK293T cells were stained using anti-

HA mAb and examined by confocal microscopy. HA-H₁R was expressed on the cytoplasmic membrane only in HA-H₁R transfected cells (Fig. 2B).

H₁R coupling to second messenger pathways is primarily via G $\alpha_{q/11}$ (Parsons and Ganellin, 2006). The ability of the transfected HA-H₁R to activate G α_{11} was tested in a [³⁵S] GTP γ S binding assay. When membrane fractions from transfected HEK293 cells were used in the [³⁵S] GTP γ S binding assay, HA-H₁R was capable of activating G α_{11} in response to histamine (Fig. 2C). Taken together, these results show that HA-H₁R is properly expressed and is functional.

To perform retroviral transduction, CD4 T cells were isolated from H1RKO and WT mice, activated with anti-CD3 and anti-CD28 mAbs for 16 hours and transduced with either pEGZ or pEGZ-HA-H₁R retroviruses. Expression of HA-H₁R in transduced CD4 T cells was confirmed by confocal microscopy and flow cytometry (data not shown). After 2 days, transduced CD4 T cells were isolated by cell sorting based on EGFP expression and equal numbers of cells were activated with anti-CD3 mAb for an additional 24 hours. Both pEGZ and pEGZ-HA-H₁R transduced CD4 T cells from H1RKO mice produced significantly lower levels of IFN γ than those from WT mice (Fig. 3A). These results indicate that the expression of H₁R in activated CD4 T cells does not restore the IFN γ production in H₁R deficient cells.

Retroviral transduction requires prior activation of CD4 T cells for at least 16 hours to induce cell cycling. Thus, if H₁R is normally required during the early phase of activation concomitant with TCR engagement, the retroviral transduction would not rescue the H1R deficiency. Our results above (Fig.1C) indicated that the IFN γ production was already reduced at 36 hours in H1RKO CD4 T cells compared to the WT cells.

We therefore examined IFN γ production by H1RKO CD4 T cells earlier during the activation with anti-CD3 and anti-CD28 mAbs. Although lower levels of IFN γ were present in WT CD4 T cells at 24 hours of activation, H1RKO CD4 T cells still produced significantly less IFN γ (Fig. 3B) indicating that H₁R plays a role early during the activation of CD4 T cells.

H₁R expression during mouse T cell activation has not been investigated. We therefore analyzed the H₁R gene expression in WT CD4 T cells stimulated for different periods of time with anti-CD3 and anti-CD28 mAbs. Relative levels of H₁R mRNA were examined by conventional and quantitative real time RT-PCR analysis. CD4 T cells markedly downregulated H₁R mRNA expression by 24 hours after activation (Fig. 3C and 3D), further indicating that H₁R plays a role early (< 24 hours) after TCR engagement and that it is not required for IFN γ production by CD4 T cells once they are activated.

Selective H₁R expression in T cells in transgenic mice restores IFN γ production

To examine the role of H₁R during the initial activation of CD4 T cells, we generated transgenic mice expressing H₁R under the control of distal *lck* promoter, which drives expression in T cells (Wildin et al., 1991). Transgenic mice were generated directly on the C57BL/6J background. Two transgenic founders were identified and crossed to H1RKO mice to obtain H1RKO mice expressing H₁R selectively in T cells (H1RKO-Tg mice). The expression of the transgene in CD4 T cells from two lines (H1RKO-Tg-1 and H1RKO-Tg-3) was confirmed by RT-PCR using transgene-specific primers (Fig. 4A). We examined the surface expression of the transgene in CD4 T cells by immuno-staining using anti-HA mAb and confocal microscopy (Fig. 4B). The

transgene was expressed in CD4 T cells from both transgenic lines. No differences in the total numbers or distribution of T cell subpopulations in the thymus and peripheral lymphoid tissues were observed among WT, H1RKO and either of the H1RKO-Tg lines (data not shown).

We then examined whether the expression of H₁R in H1RKO CD4 T cells restored IFN γ production. CD4 T cells from WT, H1RKO and H1RKO-Tg mice were stimulated with anti-CD3 and anti-CD28 mAbs and IFN γ levels quantified. The levels of IFN γ secreted by CD4 T cells from H1RKO-Tg-3 were comparable to WT CD4 T cells and those from H1RKO-Tg-1 remained slightly lower than the WT CD4 T cells but significantly higher than the levels in H1RKO CD4 T cells (Fig. 4C). Analyses at different periods of time after activation confirmed that the transgenic expression of H₁R in H1RKO CD4 T cells fully restores IFN γ production (Fig. 4D).

We also studied the IFN γ production from Th1 polarized and non-polarized effector cells from H1RKO-Tg mice. CD4 T cells from WT, H1RKO and H1RKO-Tg mice were differentiated in the absence of exogenous cytokines (non-polarized) or in the presence of recombinant IL-12 and anti IL-4 mAb (Th1). After 4 days, effector cells were re-stimulated with anti-CD3 mAb for 24 hours and IFN γ production was measured. Both Th1 polarized (Fig. 4E) and non-polarized CD4 effector T cells (Fig. 4F) from H1RKO-Tg mice produced significantly more IFN γ than the H1RKO effectors. Furthermore, the levels of IFN γ in H1RKO-Tg cells were comparable to those in WT CD4 T cells. Together, these data demonstrate that the presence of H₁R at the time of activation of CD4 T cells under both polarizing and non-polarizing conditions regulates IFN γ

production and Th1 differentiation.

Impaired activation of p38 MAP kinase by TCR ligation in H1RKO CD4 T cells

In order to dissect the molecular mechanism of H₁R signaling in regulating IFN γ production by CD4 T cells, we examined the signaling pathways that have been previously associated with H₁R in other cell types. NF- κ B has been shown to be activated through H₁R in green monkey kidney cells (Bakker et al., 2001) and has been associated with regulation of IFN γ expression in CD4 T cells (Aronica et al., 1999). Therefore, we performed an electrophoretic mobility shift assay (EMSA) to examine NF- κ B DNA binding. CD4 T cells from WT and H1RKO mice were stimulated with anti-CD3 and anti-CD28 mAbs for different periods of time. There was no difference in NF- κ B activation between WT and H1RKO CD4 T cells (Fig. 5A). STAT1 is also known to regulate IFN γ expression in CD4 T cells (Ramana et al., 2002) and it has recently been shown that H₁R signaling regulates STAT1 phosphorylation in splenocytes (Sakhalkar et al., 2005). Therefore we examined activation of STAT1 by Western blot analysis in stimulated CD4 T cells. STAT1 phosphorylation was undetected at early time points up to 3 hours of activation in both WT and H1RKO cells (data not shown). Phospho-STAT1 was detected after 3 hours of activation but there was no difference in STAT-1 phosphorylation between WT and H1RKO CD4 T cells (Fig. 5B). Although H₁R signaling has also been reported to regulate STAT4 phosphorylation in splenocytes (Engelhardt, 2006), phospho-STAT4 was not detected in WT and H1RKO CD4 T cells after activation with anti-CD3 and anti-CD28 mAbs (data not shown).

H₁R ligation has recently been shown to lead to the phosphorylation of p38 MAP kinase in DDT₁MF-2 cells (Robinson and Dickenson, 2001) and in human aortic

endothelial cells (Steffel et al., 2005). Activation of p38 MAP kinase pathway is required for IFN γ production and Th1 differentiation (Rincon et al., 1998). We therefore examined the activation of p38 MAP kinase by Western blot analysis. CD4 T cells from WT and H1RKO mice were stimulated with anti-CD3 and anti-CD28 mAbs for different periods of time. p38 MAP kinase was activated in WT CD4 T cells but was markedly impaired in H1RKO CD4 T cells (Fig. 5C). In contrast, no difference in ERK MAP kinase activation was observed between WT and H1RKO CD4 T cells (Fig. 5D). As has been reported by us previously (Weiss et al., 2000), activation of JNK MAP kinase could not be detected at the earlier time points in both WT and H1RKO CD4 T cells stimulated with anti-CD3 and anti-CD28 mAbs (data not shown). We further examined the activation of p38 MAP kinase by TCR ligation in H1RKO-Tg CD4 T cells. Unlike H1RKO CD4 T cells, the levels of phospho p38 MAP kinase in H1RKO-Tg CD4 T cells were equivalent to those in the WT CD4 T cells (Fig. 5E). Thus, TCR mediated activation of p38 MAP kinase required the presence of H₁R in CD4 T cells.

Activation of p38 MAP kinase by TCR is mediated by histamine/H₁R binding

To understand the mechanism by which H₁R could regulate TCR mediated p38 MAP kinase activation, we examined if histamine itself could activate the p38 MAP kinase in CD4 T cells. Histamine is already present at low concentrations (about 10⁻⁷M) in the serum used for the culture medium. Therefore, we assessed p38 MAP kinase phosphorylation in response to histamine using a medium prepared with previously dialyzed serum to deplete histamine (Banu and Watanabe, 1999). CD4 T cells from WT and H1RKO mice were resuspended in the histamine-free medium and treated with histamine. p38 MAP kinase was activated by histamine in WT CD4 T cells but not

in H1RKO CD4 T cells (Fig. 6A), indicating that histamine activates this pathway in CD4 T cells through H₁R.

Since histamine was present in the normal medium used to activate CD4 T cells with anti-CD3 and anti-CD28 mAbs (Fig. 5C and 5E), it was possible that the activation of p38 MAP kinase by TCR ligation was co-dependent upon histamine signaling through the H₁R. To test this possibility, we examined p38 MAP kinase activation upon anti-CD3 and anti-CD28 mAb stimulation in histamine-free medium. TCR ligation failed to activate p38 MAP kinase in both WT and H1RKO CD4 T cells in histamine-free medium (Fig. 6B). In contrast, the absence of histamine did not affect TCR-mediated ERK activation (Fig. 8) or the intracellular calcium mobilization (data not shown) in WT CD4 T cells. To further demonstrate the selective requirement for histamine in TCR-mediated p38 MAP kinase activation, WT and H1RKO CD4 T cells were stimulated in histamine-free medium with anti-CD3 and anti-CD28 mAbs in the presence of histamine. TCR-mediated p38 MAP kinase activation was restored by histamine in WT CD4 T cells but not in H1RKO CD4 T cells (Fig. 6C), indicating that binding of histamine to H₁R was required for activation of p38 MAP kinase upon TCR ligation. Interestingly, the levels of phospho-p38 MAP kinase in WT CD4 T cells treated anti-CD3 and anti-CD28 mAbs and histamine were similar to the levels obtained when the cells were treated with histamine alone (Fig. 6C). The inability of TCR to activate p38 MAP kinase in H₁R deficient cells in normal medium (Fig. 5C), the inability of TCR ligation to activate p38 MAP kinase in the histamine-free medium (Fig. 6B) and the inability of TCR to further increase p38 MAP kinase activation when histamine was added to the histamine free medium strongly suggest that the activation of p38 MAP kinase observed upon TCR ligation is dependent

upon concomitant H₁R signaling.

Although the precise mechanism by which p38 MAP kinase regulates IFN γ production in CD4 T cells remains unclear, recent studies have suggested that the activation of the this MAP kinase pathway is required for T-bet expression (Engelhardt, 2006; Jones et al., 2003) and T-bet regulates IFN γ production (Szabo et al., 2000). We therefore examined T-bet expression by Western blot analysis during activation of WT and H1RKO CD4 T cells. T-bet levels were lower in activated H1RKO CD4 T cells compared to the WT CD4 T cells (Fig. 6D). Thus, the impairment in p38 MAP kinase activation in the absence of H₁R reduces the T-bet expression and thereby IFN γ production by CD4 T cells during TCR activation.

In order to demonstrate that the reduced p38 MAP kinase activation in H1RKO CD4 T cells is responsible for the lower IFN γ production by these cells, we crossed H1RKO mice with the previously described distal MKK6_{Glu}-Tg mice (Rincon et al., 1998). These mice express a constitutively active form of MKK6, a specific upstream activator of p38 MAP kinase, under the control of *dlck* promoter to drive the expression in T cell lineage. Thus p38 MAP kinase is constitutively and selectively active in T cells in these mice. Anti-CD3 and anti-CD28 mAb stimulated CD4 T cells from H1RKO-MKK6_{Glu}-Tg mice produced significantly more IFN γ than CD4 T cells from littermate H1RKO mice (Fig. 6E), indicating that the diminished activation of p38 MAP kinase in H1RKO CD4 T cells is responsible for the reduced IFN γ production by these cells.

H₁R signaling directly in CD4 T cells regulates encephalitogenic Th1 effector responses

As a shared autoimmune disease susceptibility gene, *Hrh1* has been shown to control numerous disease associated subphenotypes, including blood brain barrier permeability, antigen presentation and delayed type hypersensitivity responses (Caron et al., 2001; Gao et al., 2003). To assess whether or not H₁R signaling in CD4 T cells influences EAE by regulating encephalitogenic Th1 responses, we examined the susceptibility of H1RKO and H1RKO-Tg mice to EAE using the classical MOG₃₅₋₅₅+CFA+PTX model and the 2× MOG₃₅₋₅₅+CFA model (Teuscher et al., 2006a), which does not use PTX as an ancillary adjuvant. Regression analysis (Teuscher et al., 2006a) revealed that the clinical disease courses elicited by both induction protocols fit a Sigmoidal curve and that compared to H1RKO mice the clinical course of EAE is significantly more severe in the transgenic mice [MOG₃₅₋₅₅+CFA+PTX model: (overall F = 66.1; p < 0.0001) with WT (F = 132.1; p < 0.0001), H1RKO-Tg-1 (F = 127.5; p < 0.0001), and H1RKO-Tg-3 (F = 83.3; p < 0.0001) mice significantly greater than H1RKO mice; 2× MOG₃₅₋₅₅+CFA model: (overall F = 8.9; p < 0.0001) with WT (F = 226.9; p < 0.0001), H1RKO-Tg-1 (F = 134.0; p < 0.0001) and H1RKO-Tg-3 (F = 215.8; p < 0.0001) mice significantly greater than H1RKO mice].

An analysis of EAE associated clinical quantitative trait variables (Butterfield et al., 1998) revealed that the mean day of onset (DO), cumulative disease score (CDS), number of days affected (DA), overall severity index (SI) and the peak score (PS) were significantly different among the strains immunized with either MOG₃₅₋₅₅+CFA+PTX (Table 1) or 2× MOG₃₅₋₅₅+CFA (Table 2). Post hoc multiple comparisons of each

trait variable revealed that WT = H1RKO-Tg-1 = H1RKO-Tg-3 > H1RKO. Additionally, compared to H1RKO mice both MOG₃₅₋₅₅+CFA+PTX (Fig. 7C) and 2× MOG₃₅₋₅₅+CFA (Fig. 7D) immunized H1RKO-Tg-1 and H1RKO-Tg-3 mice exhibited significantly more severe overall CNS pathology (Blankenhorn et al., 2000) which was equivalent in severity to that seen in WT mice. Therefore, H₁R expression in CD4 T cells alone is capable of complementing EAE susceptibility in H₁R deficient animals.

We also examined cytokine production following *ex-vivo* stimulation of splenocytes from mice immunized with MOG₃₅₋₅₅+CFA+PTX and 2× MOG₃₅₋₅₅+CFA. The H₁R transgene fully complemented IFN γ production by H1RKO CD4 T cells and restored IL-4 production to WT levels (Fig. 7E and 7F). In contrast, no significant differences in TNF α or IL-17 production were detected among WT, H1RKO and H1RKO-Tg mice. Together, these data indicate that H₁R signaling in CD4 T cells complements EAE severity independently of TNF α and IL-17 production.

Discussion

Although H₁R has been previously shown to play a role in regulating encephalitogenic Th1 immune response in EAE (Bakker et al., 2002), it was unclear whether this was caused by the deficiency of H₁R in CD4 T cells or APCs. In this study, we show that the presence of H₁R in CD4 T cells is essential for the activation of p38 MAP kinase and IFN γ production by these cells and the lack of H₁R in CD4 T cells is responsible for the increased EAE resistance of H1RKO mice. These findings also explain the likely cause of the Th2 deviation and aberrant IL-4 production seen in the H1RKO (Bakker et al., 2002), a result we confirmed in the present study. This deviation could logically be due to the impairment in p38 MAP kinase activation that reduces the T-bet expression and thereby IFN γ production by CD4 T cells during TCR activation. Without H₁R, naïve T cells cannot be driven into the full Th1 developmental pathway, and the result is an unbalanced immune repertoire that is generally thought to be protected from signs of EAE (Shaw et al., 1997).

Even though the expression of H₁R in CD4 T cells has been reported (Sachs et al., 2000) it was unknown how H₁R is regulated during the activation phase of CD4 T cells. Here we show, for the first time, that the H₁R gene expression is silenced early after the activation of CD4 T cells. Modulation of H₁R signaling, like other GPCRs, is complex and includes receptor desensitization, internalization and the subsequent down-regulation (McCreath et al., 1994; Smit et al., 1996). Desensitization of H₁R is induced by both agonist specific (homologous) and agonist non-specific (heterologous) pathways, mainly involving PKC-mediated phosphorylation of H₁R (Fujimoto et al., 1999; Miyoshi et al., 2004). PKC activation has been shown to inhibit H₁R both at the protein level as

well as at the gene expression level (Miyoshi et al., 2006; Pype et al., 1998; Yoshimura et al., 2005). Because TCR ligation leads to potent activation of PKC (Acuto and Cantrell, 2000), silencing of H₁R expression in activated CD4 T cells may be a consequence of PKC activation. Although the transcriptional regulation of H₁R promoter is not well understood, H₁R-mediated signaling has been shown to be necessary for continued H₁R expression (Miyoshi et al., 2006; Yoshimura et al., 2005). Thus, the loss of H₁R gene expression in activated CD4 T cells in mice may be a mechanism to turn off possible subsequent histamine signals in these cells. In humans, H₁R expression is reported to increase in Th1 differentiated cells (Jutel et al., 2001). However, H₁R mRNA was rapidly downregulated even during the Th1 differentiation of mouse CD4 T cells (data not shown). These apparently contradictory results may be explained by the different origin of the T cells (mouse *vs.* human) or by other differences in the culture conditions used.

H₁R has been previously implicated in the regulation of IFN γ production. H₁R-deficient splenocytes have been shown to produce lower IFN γ when activated by anti-CD3 and-CD28 mAbs or by specific antigen (Bakker et al., 2002; Banu and Watanabe, 1999; Bryce et al., 2006; Jutel et al., 2001) but no studies have addressed the role of H₁R in isolated CD4 T cells. Here we show that H₁R expression in CD4 cells is essential specifically for IFN γ production by these cells but not for IL-2 production or proliferation. A previous report showed hypoproliferation of total splenocytes from H₁R deficient mice in response to anti-CD3 mAb (Banu and Watanabe, 1999). However, the low proliferative response could be due to the H₁R deficiency in cells other than CD4 T cells, such as antigen presenting cells (e.g. macrophages or dendritic cells) that also express H₁R. Although CD4 T cells also express H₂R and H₄R, in addition to H₁R,

the selective restoration of the IFN γ response in CD4 T cells from H1RKO-Tg mice clearly demonstrates that signaling through H₁R is necessary for regulation of IFN γ production in these cells.

Several studies have shown that p38 MAP kinase is activated in CD4 T cells or total T cells upon TCR activation. Co-stimulatory molecules (such as CD28, 4-1BB, ICOS, CD30) also contribute to the activation of p38 MAP kinase during activation (Dodeller and Schulze-Koops, 2006). While most studies agree on the role of p38 MAP kinase on IFN γ production and Th1 differentiation, recent studies have questioned the requirement of TCR-mediated p38 MAP kinase activation. Instead, they propose that activation of this pathway by cytokines such as IL-12 or IL-18 is probably more relevant (Berenson et al., 2006). To date, the effect of other components also present in the milieu during TCR activation has not been addressed. Here we show, for the first time, that activation of p38 MAP kinase by TCR/CD28 ligation is dependent on the presence of histamine and its binding to H₁R. A previous study has shown the requirement of H₁R for ZAP-70 activation in H1RKO total splenocytes in conjunction with the hypoproliferative defect in these cells (Banu and Watanabe, 1999). However, here we show that in CD4 T cells, H₁R is not required for other key signaling pathways such as ERK activation (Fig.8), NF- κ B activation (Fig. 5A) or calcium mobilization (data not shown), as well as for IL-2 production and proliferation. Thus, deficiency of H₁R in CD4 T cells appears to selectively impair the activation of the p38 MAP kinase pathway, but the mechanism remains to be investigated further. p38 MAP kinase is normally activated through the upstream MAPKK, MKK3 and MKK6 (and MKK4 in response to some stimuli) (Kyriakis and Avruch, 2001). It has been shown that GADD45 proteins interact

with MEKK4, an upstream kinase of MKK3 and MKK6 and thus activate p38 MAP kinase (Takekawa and Saito, 1998). An alternative pathway for activation of p38 MAP kinase through its autophosphorylation has also been recently proposed (Salvador et al., 2005). H₁R signaling is mediated by G $\alpha_{q/11}$ protein, which is also associated with TCR signaling through CD3 ϵ (Stanners et al., 1995). Thus, it is possible the H₁R through G $\alpha_{q/11}$ could regulate GADD45 members (α , β and γ) and lead to p38 MAP kinase activation through either the classical or alternative pathway in CD4 T cells.

Epidemiological data indicate that the use of sedating H₁R antagonists is associated with decreased MS risk (Alonso et al., 2006); and in a small pilot study, patients with relapsing-remitting or relapsing-progressive MS given the H₁R antagonist hydroxyzine remained stable or improved neurologically (Logothetis et al., 2005). Additionally, microarray analysis revealed that the H₁R is overexpressed in the chronic plaques of MS patients (Dormond et al., 2002). Historically, the role of histamine in autoimmune inflammatory disease of the CNS has been viewed as a mediator of the effector or inflammatory phase of the disease (Bebo et al., 1996). However, recent data showing that EAE and neuroantigen specific T effector cell responses are significantly different in histamine- and histamine receptor-deficient mice compared to WT mice revealed that histamine plays a role during the induction phase and priming of autoreactive effector T cells (Bakker et al., 2002; Fillmore et al., 2004; Musio et al., 2006). In this regard, our results show that H₁R signaling in T cells regulates Th1 effector functions, but not Th17 effector functions, and EAE severity, independent of APCs and other hematopoietically-derived cells. Moreover, our results demonstrate that H₁R signaling in CD4 T cells regulates the encephalitogenic Th1 effector responses

during the priming of naïve antigen-specific CD4 T cells. Taken together, this suggests that pharmacological targeting of the H₁R may be useful early in the treatment of MS and other autoimmune inflammatory diseases in which molecular mimicry, bystander activation (with or without epitope spreading), and viral persistence play a role in perpetuating immunopathology as a consequence of continual priming of pathogenic adaptive immune responses (Fujinami et al., 2006).

Materials and methods

Mice

C57BL/6J mice were purchased from the Jackson Laboratory (Bar Harbor, ME). B6.129P-*Hrh1^{tm1Wat}* (H1RKO) (Banu and Watanabe, 1999) mice were maintained in the animal facility at the University of Vermont (Burlington, VT). The experimental procedures used in this study were approved by the Animal Care and Use Committee of the University of Vermont.

For transgenic mouse generation, an HA-H₁R construct was made by deleting the methionine of the Bphs-susceptible H₁R allele (Bakker et al., 2002) and adding an HA tag at the N-terminus using TOPO cloning vector (Invitrogen, Carlsbad, CA). The HA-H₁R was then subcloned downstream of the distal *lck* promoter (Wildin *et al.*, 1991). The linear DNA fragment containing the distal *lck* promoter, the HA-H₁R gene and the human growth hormone (hGH) intron and polyadenylation signal was injected directly into fertilized C57BL/6J eggs at the University of Vermont transgenic/knockout facility. Mice were screened by DNA slot blot using a *Bam*HI–*Sac*I 0.5 kb fragment from the *hGH* gene as a probe. Two founders were generated and were crossed to H1RKO mice to establish transgenic mouse lines in H1RKO background (H1RKO-Tg mice). Distal *lck* MKK6_{Glu} transgenic mice (Rincon et al., 1998) were crossed to H1RKO mice to generate H1RKO-MKK6_{Glu} transgenic mice.

Cell preparation and culture conditions

CD4 T cells were isolated from spleen and lymph nodes by negative selection for CD8-, MHC class II-, NK1.1- and CD11b-positive cells using magnetic beads from Qiagen, Valencia, CA, as previously described (Rincon et al., 1998). Purified

CD4 T cells were stimulated with plate bound anti-CD3 (5 µg/ml) and soluble anti-CD28 (1 µg/ml) monoclonal antibodies (mAbs) from BD Pharmingen (Franklin Lakes, NJ). Th1 polarized CD4 effector T cells were generated by culturing the CD4 T cells (1×10^6 cells/ml) with anti-CD3 and anti-CD28 mAbs in presence of 4 ng/ml of recombinant IL-12 (R&D systems, Minneapolis, MN) and 10 µg/ml of anti IL-4 mAb (BD Pharmingen, San Diego, CA). Th2 polarized CD4 effector T cells were generated by activating cells (1×10^6 /ml) with anti-CD3 and anti-CD28 mAbs in presence of 30 ng/ml of recombinant IL-4 (R&D systems, Minneapolis, MN) and 10 µg/ml of anti IFN γ -4 mAb. Effector Th17 CD4 T cells were generated by activating CD4 T cells (1×10^6 cells/ml) with anti-CD3 and anti-CD28 mAbs in presence of 1 ng/ml of TGF β (Peprotech Inc, Rocky Hill, NJ) and 30 ng/ml of IL-6 (R&D systems, Minneapolis, MN) and 10 µg/ml of anti-IFN γ and 10 µg/ml of anti IL-4 mAbs. After 4 days, the cells were extensively washed, counted and equal number of cells were restimulated with anti-CD3 mAb. After 24 hours, the supernatants were collected and IFN γ , IL-4 and IL-17 were analyzed by ELISA. Non-polarized effector cells were generated by culturing CD4 T cells with anti-CD3 and anti-CD28 mAbs in the absence of exogenous cytokines for four days. The cells were then extensively washed, counted and equal numbers of cells were restimulated with anti-CD3 mAb. After 24 hours, the supernatants were collected and IFN γ was analyzed by ELISA.

Histamine dihydrochloride was obtained from Sigma-Aldrich (St. Louis, MO). RPMI prepared with 10% Fetalclone © bovine serum (Hyclone, Logan, UT), serum dialyzed twice with 10,000 kDa molecular cutoff, was used as histamine free medium.

Cytokine production

ELISAs were performed on the cell culture supernatants as described previously (Fillmore et al., 2004), using the primary antibodies: anti-IFN γ , anti-IL-2, anti-IL-4 and anti-IL17 mAbs and their corresponding biotinylated mAbs (BD 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 , IL-4 and IL-2 (R&D Systems, Minneapolis, MN) used as standards.

For cytokine analysis in ex-vivo stimulated splenocytes from mice immunized with the classical MOG₃₅₋₅₅+CFA+PTX model and the 2x MOG₃₅₋₅₅+CFA model, single cell suspensions were prepared @ 1×10^6 cells/ml in RPMI medium and stimulated with 50 μ g/ml of MOG₃₅₋₅₅. Cell culture supernatants were recovered at 72 hours and cytokine levels were measured by ELISA using anti-IFN γ , anti-IL-4 and anti-IL17 mAbs and their corresponding biotinylated mAbs (BD Pharmingen, San Diego, CA). TNF α ELISA kit was from (BD Pharmingen, San Diego, CA).

Proliferation Assays

CD4 T cells (2.5×10^5 cells/well) were activated with anti-CD3 and anti-CD28 mAbs for 72 h and proliferation was determined by 3 [H]-thymidine incorporation during the last 18 h of culture.

Quantitative Real-Time Polymerase Chain Reaction (RT-PCR)

Total RNA was extracted from CD4 T cells using RNeasy RNA isolation reagent (Qiagen, Valencia, CA) as recommended by the manufacturer. cDNA generated from 1 μ g total RNA was used in quantitative real time RT-PCR using the SYBR green

method. The sequences of *Hrh1* primers used were F: 5'-CCAGAGCTTCGGGAAGATAA-3' and R: 5'ACCACAGCATGAGCAAAGTG-5'. β -2-microglobulin was used as reference gene and relative mRNA levels were calculated using comparative C_T method. For conventional RT-PCR, the cDNA was amplified by PCR and visualized on 1% gel. The primers mentioned above were used for *Hrh1* and the primers used for *Hprt1* were F: 5'-GTTGGATACAGGCCAGACTTTGTTG-3' and R: 5'-GAGGGTAGGCTGCCTATAGGCT-3'. To study the transgene expression in HIRKO-Tg mice, the cDNA prepared as explained above was amplified using a forward primer in *Hrh1* (5'-CTCCCGGACCACAGACTCAGA-3') and a reverse primer in the 3rd exon of *hGH* (5'-GACGGAGGTCTGGGGGTTCTG) and the PCR product was visualized on 1% agarose gel.

Retroviral transduction experiments

The retroviral vector plasmid pEGZ-HA was a generous gift from Dr. Ingolf Berberich (University of Wurzburg, Wurzburg, Germany) and packaging vectors pHIT123 and pHIT 60 were generous gifts from Dr. Alan Klingsman (Oxford University, Oxford, UK). Two restriction sites, *BamHI* and *EcoRI* were inserted into the mouse H_1R cDNA by PCR and cloned such that the second codon is in frame with the HA tag of pEGZ generating an HA- H_1R fusion protein. pEGZ is a bicistronic system with IRES-EGFP. EGFP served as a marker for transfected cells.

The retroviral vector plasmids, pEGZ-HA- H_1R or the empty pEGZ and the packaging vectors pHIT60 and pHIT123 were transiently transfected into human embryonic kidney fibroblasts expressing the SV40 large T antigen (HEK293T) cells using the calcium phosphate method. After two days, the retrovirus containing

supernatants were used to transduce (by centrifugation at 800g for 3 hours at 32⁰C) CD4 T cells previously activated with anti-CD3 and anti-CD28 mAbs for 16 hours. The transduced CD4 T cells were cultured in presence of 50 U/ml of IL-2 for two days and were sorted using a FACSAria instrument (BD Pharmingen, San Diego, CA), based on their EGFP expression. Equal numbers of EGFP positive cells were restimulated with anti-CD3 mAb and 24 hours later IFN γ was measured in the supernatant by ELISA.

Confocal microscopy

HEK293T cells were transfected with pEGA-HA-H₁R or empty pEGZ control vector (5 μ g total DNA) using the calcium phosphate method. Cells were fixed, permeabilized and stained using an anti-HA mAb (Cell Signaling Technologies, Danvers, MA) followed by an incubation with Alexa-568 anti-mouse antibody (Molecular Probes, Eugene, Oregon). TOPRO-3 nuclear stain (Molecular Probes, Eugene, Oregon) was used as a nuclear marker. Cells were examined by confocal microscopy using Zeiss LSM 510 META Confocal Laser Scanning Imaging System (Carl Zeiss Microimaging Inc, Thronwood, NY)

Cell lysates and Western blotting

Whole-cell lysates were prepared from 1x10⁶-5x10⁶ cells in Triton lysis buffer and were then separated via sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred to nitrocellulose membranes as described previously (Farley et al., 2006). Primary antibodies used for Western blot analysis include anti-HA (Abcam Inc. Cambridge, MA), anti-p38, anti-phospho-p38, anti-phospho-STAT1, anti-phospho-STAT4, anti-phospho-ERK, anti-ERK, anti-phospho-JNK, anti-JNK (Cell Signaling Technologies. Danvers, MA), anti-T-bet (a gift from Dr. L. Glimcher, Harvard

University School of Public Health, Boston, MA) and anti-actin (Santa Cruz Biotechnology, Santa Cruz, CA).

[³⁵S]GTP γ S binding assay

The HA-H₁R cDNA was subcloned into pcDNA3 using restriction sites *EcoRI/BamHI*. The [³⁵S]GTP γ S binding experiments were initiated by the addition of 50 fmols of receptor to an assay buffer (20mM HEPES (pH 7.4), 3mM MgCl₂, 100mM NaCl, 1 μ M GDP, 0.2mM ascorbic acid, and 100nCi [³⁵S]GTP γ S) containing 100 μ M histamine. Non-specific binding was determined in the above condition with the addition of 100 μ M GTP γ S. Reactions were incubated for 15 min at 30⁰C and were terminated by the addition of 500 μ l of ice-cold buffer containing 20mM HEPES (pH 7.4), 3mM MgCl₂, 100mM NaCl and 0.2mM ascorbic acid. The samples were centrifuged at 16,000 x g for 10 minutes at 4⁰C. The resulting pellets were re-suspended in solubilization buffer (100mM Tris, 200mM NaCl, 1mM EDTA, and 1.25% Nonidet P-40) plus 0.2% SDS. Samples were precleared with Pansorbin for 1 hour, followed by immunoprecipitation with C-terminal G α_{11} antiserum. Finally, the immunocomplexes were washed with solubilization buffer and bound [³⁵S]GTP γ S was estimated by liquid scintillation-spectrometry.

Electrophoretic mobility shift assay (EMSA)

Nuclear extracts were prepared from anti-CD3 and anti-CD28 mAbs treated CD4 T cells as previously described (Berenson et al., 2006). Binding reactions for electrophoretic gel mobility shift assay were carried out at room temperature using 2 μ g nuclear proteins and [³²P]dCTP-end labeled double-stranded oligonucleotide probes containing NF- κ B binding site from the mouse κ intron enhancer (Sense 5'-

GATCAGAGGGGACTTTCCGAGGGAT-3' and anti-sense 5'-GATCCCTCGGAAAGTCCCCTCTGAT-3'). Samples were separated by electrophoresis under non-denaturing conditions and exposed to film for autoradiography.

Induction and Evaluation of EAE

Mice were immunized for the induction of EAE using either the MOG₃₅₋₅₅-complete Freund's adjuvant (CFA) double-inoculation (Butterfield et al., 1998) or the MOG₃₅₋₅₅-CFA+PTX single-inoculation protocols (Teuscher et al., 2006a). For the double-injection protocol mice were injected subcutaneously with an emulsion of 100 µg of MOG₃₅₋₅₅ and an equal volume of CFA containing 200 µg of *Mycobacterium tuberculosis* H37RA (Difco Laboratories, Detroit, MI) in the posterior right and left flank; one week later all mice were similarly injected at two sites on the right and left flank anterior of the initial injection sites. Animals immunized using the MOG₃₅₋₅₅-CFA+PTX single-inoculation protocol received an emulsion of 200 µg MOG₃₅₋₅₅ and equal volume of CFA containing 200 µg of *Mycobacterium tuberculosis* H37RA by subcutaneous injections distributed equally in the posterior right and left flank and scruff of the neck. Immediately thereafter, each animal received 200 ng PTX (List Biological Laboratories, Campbell, CA) by intravenous injection. Mice were scored daily starting at day 5 post-injection as previously described (Teuscher et al., 2006a). Clinical quantitative trait variables including disease incidence and mean day of onset (DO), cumulative disease score (CDS), number of days affected (DA), overall severity index (SI) and the peak score (PS) were generated as previously described (Butterfield et al., 1998).

Brains and SC were dissected from calvaria and vertebral columns, respectively, and fixed by immersion in 10% phosphate-buffered formalin (pH 7.2). Following

adequate fixation, brain and SC were trimmed and representative transverse section embedded in paraffin, sectioned at 5 μm , and mounted on glass slides. Sections were stained with hematoxylin and eosin for routine evaluation and Luxol fast blue-periodic acid Schiff for demyelination. Sections from representative areas of the brain and SC were scored in a semi-quantitative fashion for the various histopathologic parameters as previously described (Blankenhorn et al., 2000). An overall CNS pathology index (PI) for each lesions was obtained by calculating the average scores for the lesions observed in the brain and spinal cord.

Statistical analysis

The statistical analyses, as indicated in the figure legends, were performed using GraphPad Prism 4 software (GraphPad software Inc, San Diego, CA).

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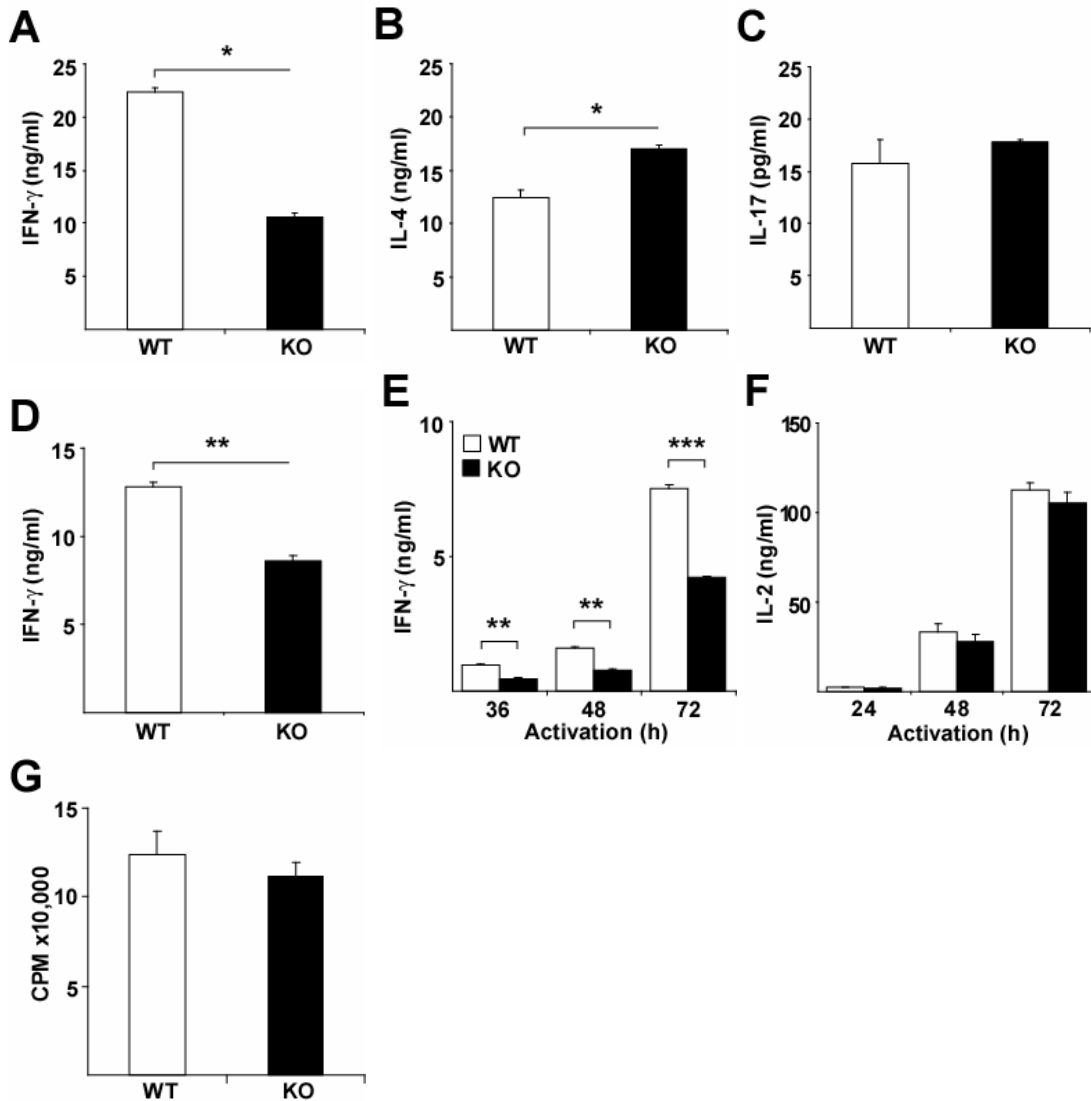


Figure 1. H₁R is required for IFN γ production by CD4 T cells.

Purified CD4 T cells from WT and H1RKO mice were activated with anti-CD3 (5 μ g/ml) and anti-CD28 (1 μ g/ml) mAbs either in presence of IL-12 (4ng/ml) and anti-IL-4 mAb (10 μ g/ml) (A), or IL-4 (30ng/ml) and anti-IFN γ mAb (10 μ g/ml) (B) or TGF- β (1ng/ml), IL-6 (30ng/ml) and anti-IFN γ (10 μ g/ml) and anti-IL4 mAbs (10 μ g/ml) (C). After 4 days, cells were restimulated with anti-CD3 mAb (5 μ g/ml) for 24h. IFN γ (A), IL-4 (B) or IL-17 (C) production was determined by ELISA in triplicate. *, $p < 0.05$, compared with H1RKO cells (Student's t-test). (D) CD4 T cells were activated with anti-CD3 (5 μ g/ml) and anti-CD28 (1 μ g/ml) mAbs. After 4 days, cells were restimulated with anti-CD3 mAb (5 μ g/ml) for 24h and IFN γ production was determined by ELISA. **, $p = 0.002$ compared with H1RKO cells (Student's t-test). (E and F) CD4 T cells were stimulated as in (D) for the indicated periods of time. Supernatants were analyzed for IFN γ (E) and IL-2 (F) by ELISA. Significance of differences in cytokine production were assessed by two-way ANOVA ($F = 168.8$; $p < 0.0001$) followed by post-hoc comparisons using one-way ANOVA (** $p < 0.01$; *** $p < 0.001$). (G) CD4 T cells from WT and H1RKO mice were stimulated as in (E) and 18h ^3H -thymidine incorporation measured in total 72h culture. All the data are representative of at least two independent experiments.

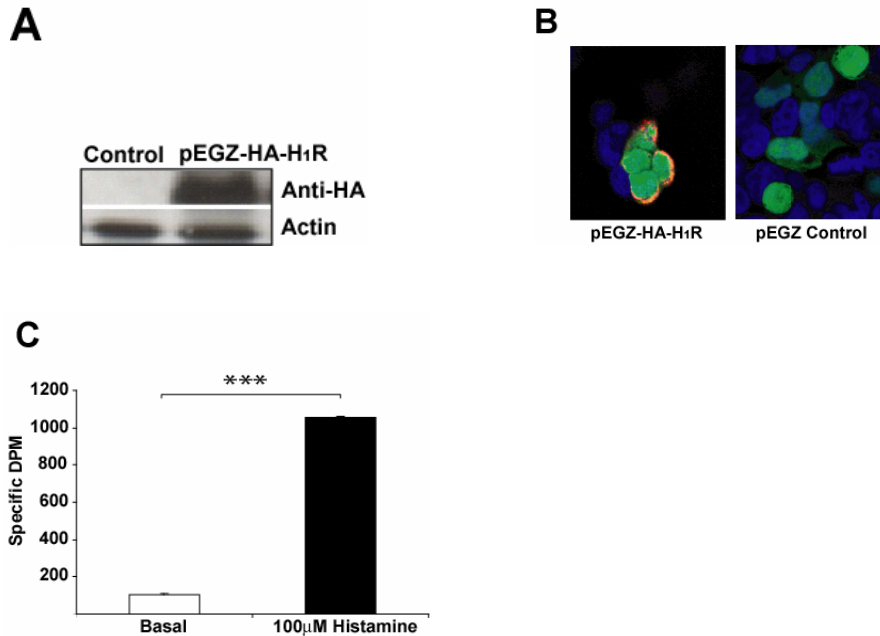


Figure 2. Expression and function of HA-H₁R in HEK293T cells.

(A) HEK293T cells were transfected with empty pEGZ (control) and pEGZ-HA-H₁R plasmids and the expression of HA-H₁R was determined by Western blot using an anti-HA mAb. The data is representative of at least three independent experiments. (B) HEK293T cells were transfected as in (A), fixed, permeabilized and stained with an anti-HA mAb (red) and Topro-nuclear dye (blue). EGFP expression (green) represents transfected cells. Cells were visualized by confocal microscopy. The data are representative of at least three independent experiments. (C) HEK293 cells were transfected with pHA-H₁R-G_{α11} fusion construct, membrane fractions generated and were used in absence (basal) or presence of 10⁻⁴M histamine in [³⁵S] GTPγS binding assay. Samples were then used in immuno-precipitation using G_{α11} antiserum and the bound [³⁵S] GTPγS was measured by liquid-scintillation spectrometry.

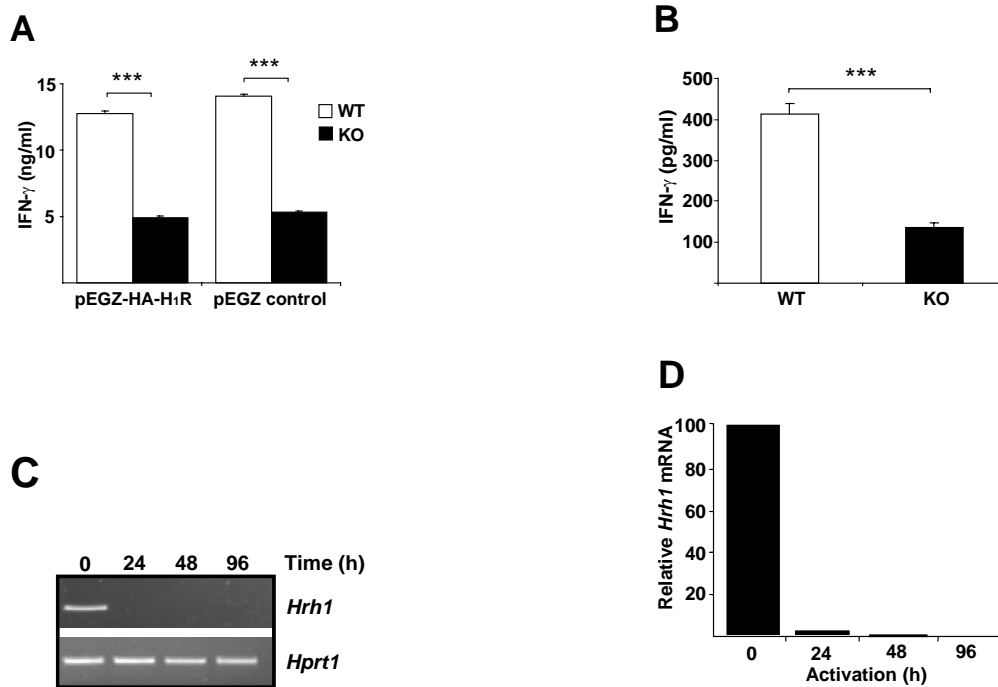


Figure 3. H₁R expression is downregulated upon activation in CD4 T cells.

(A) CD4 T cells from WT and H1RKO mice were stimulated in the presence of anti-CD3 and anti-CD28 mAbs for 16h and then retrovirally transduced with pEGZ-HA-H₁R or with empty pEGZ control plasmids. Transduced, sorted EGFP⁺ cells were then re-stimulated with anti-CD3 mAb and 24h later the supernatants were harvested for determination of IFN γ by ELISA in triplicate. The data presented is representative of two independent experiments. ***, $p < 0.0001$ compared with H1RKO cells (Student's t-test). (B) Freshly isolated CD4 T cells from WT and H1RKO were activated with anti-CD3 and anti-CD28 mAbs. After 24h, IFN γ production was determined by ELISA. The results shown are representative of at least three independent experiments. ***, $p < 0.001$ compared with H1RKO cells (Student's t-test). (C and D) CD4 T cells were isolated from WT mice and stimulated with anti-CD3 and anti-CD28 mAbs. Cells were harvested at the indicated time point, total RNA was isolated and used to examine H₁R expression by conventional RT-PCR with HPRT as the endogenous control (C) and by quantitative real time RT-PCR relative to β 2-microglobulin as the endogenous control (D). Data presented as expression relative to the unstimulated CD4 T cells. The data are representative of at least three independent experiments.

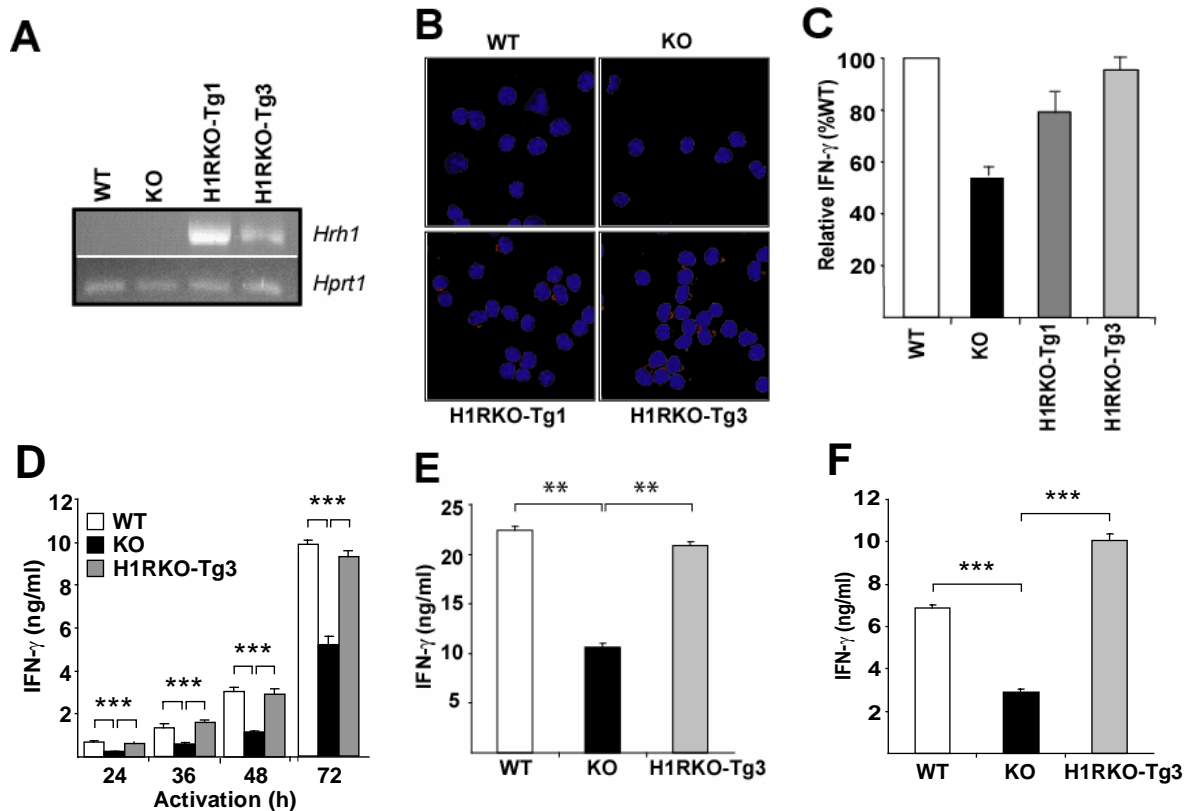


Figure 4. Transgenic expression of H₁R in H1RKO CD4 T cells complements IFN- γ production.

(A) H₁R transgene expression was analyzed by RT-PCR in CD4 T cells from WT, H1RKO mice and the two independent lines of H₁R transgenic mice crossed with H1RKO mice (H1RKO-Tg-1 and H1RKO-Tg-3). (B) CD4 T cells were stained with anti-HA mAb (red) and visualized by confocal microscopy. Nuclear stain Topro (blue) is shown. (C) CD4 T cells were activated with anti-CD3 and anti-CD28 mAbs for 72 h and IFN γ was determined by ELISA. Data are expressed as IFN γ production relative to that by WT cells (set as 100%). (D) CD4 T cells from WT, H1RKO and H1RKO-Tg-3 were stimulated as in (C) for the indicated periods of time and IFN γ was determined by ELISA. Statistical analysis using two-way ANOVA ($F=55.1$; $p<0.0001$) followed by post-hoc comparisons using one-way ANOVA was performed (**, $p<0.01$; ***, $p<0.001$). (E) CD4 T cells were activated with anti-CD3 and anti-CD28 mAbs in presence of IL-12 (4ng/ml) and anti-IL-4 mAb (10 μ g/ml). After 4 days, cells were restimulated and IFN γ production was determined. Statistical analysis using one-way ANOVA ($F=25.4$; $p<0.001$) followed by Bonferroni's post-hoc comparisons with H1RKO cells was performed (**, $p<0.01$). (F) CD4 T cells were activated with anti-CD3 and anti-CD28 mAbs. After 4 days, cells were restimulated with anti-CD3 mAb for 24h and IFN γ production was determined by ELISA. Significance of differences was determined as in (E) (***, $p < 0.001$). The data presented are representative of at least three independent experiments.

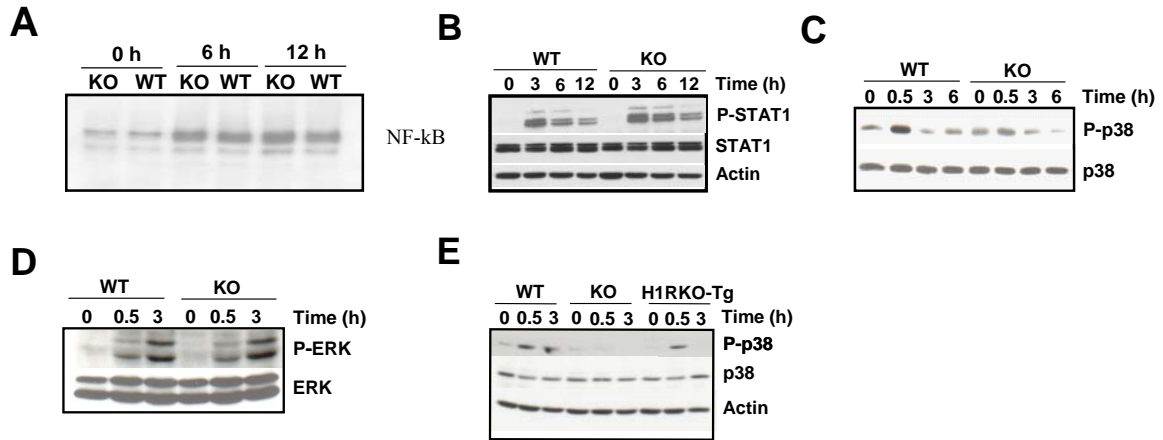
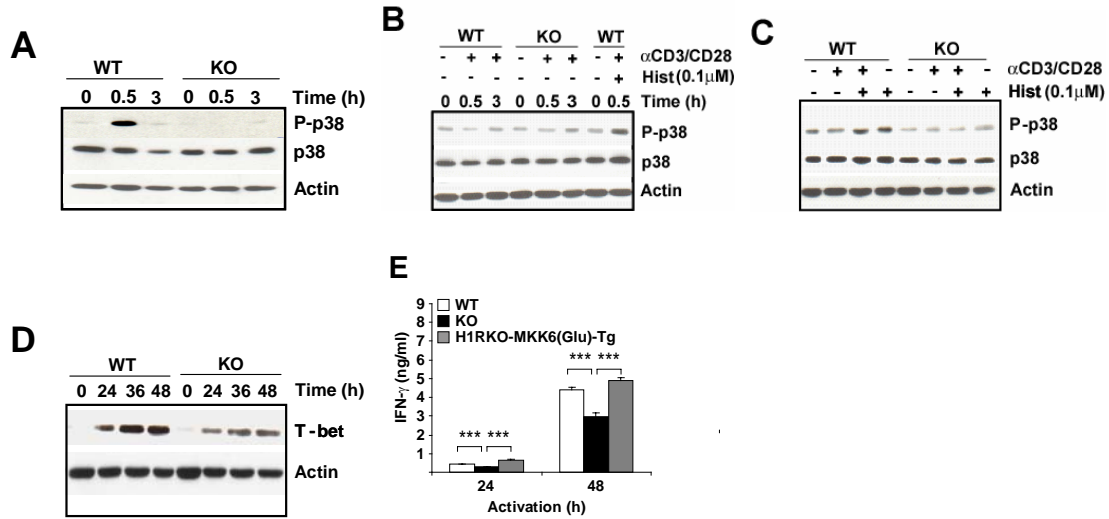


Figure 5. Activation of p38 MAP kinase by TCR ligation requires H₁R signals.

(A) Purified CD4 T cells from WT and H1RKO mice were stimulated with anti-CD3 and anti-CD28 mAbs for the indicated periods of time, nuclear extracts were prepared and analyzed for NF- κ B DNA binding by EMSA. (B) CD4 T cells from WT and H1RKO mice were stimulated with anti-CD3 and anti-CD28 mAbs for the indicated periods of time, whole cell lysates were prepared and analyzed for phospho-STAT1 (P-STAT1) and total STAT1 by Western blot analysis. Actin was used as loading control. (C) CD4 T cells from WT and H1RKO were treated with anti-CD3 and anti-CD28 mAbs for the indicated periods of time, whole cell lysates were prepared and analyzed for phospho-p38 MAP kinase and total p38 by Western blot analysis. (D) CD4 T cells from WT and H1RKO were activated with anti-CD3 and anti-CD28 mAbs for the indicated periods of time, whole cell lysates were prepared and analyzed for phospho-ERK and total ERK by Western blot analysis. (E) CD4 T cells from WT, H1RKO and H1RKO-Tg-3 mice were stimulated with anti-CD3 and anti-CD28 mAbs for the indicated periods of time and whole cell lysates were analyzed for phospho-p38, total p38 and actin by Western blotting. All the results presented are representative of at least two independent experiments.

Figure 6. Activation of p38 MAP kinase by TCR ligation is mediated by histamine/H₁R binding.



(A) CD4 T cells from WT and H1RKO mice were treated with histamine (10^{-7} M) for the indicated periods of time in the histamine-free medium. Whole cell extracts were used to analyze phospho-p38, total p38 and actin by Western blotting. (B) CD4 T cells were isolated from WT and H1RKO mice and stimulated with anti-CD3 and anti-CD28 mAbs in the histamine free-medium for the indicated periods of time. CD4 T cells stimulated in 10^{-7} M histamine (Hist) containing medium are shown as positive control for p38 MAP kinase activation. Phospho-p38, total p38 and actin are shown. (C) CD4 T cells from WT and H1RKO were incubated with anti-CD3 and anti-CD28 mAbs, 10^{-7} M histamine or both in the histamine-free medium for 30 minutes and whole cell lysates were analyzed for phospho-p38, total p-38 and actin by Western blotting. (D) CD4 T cells from WT and H1RKO mice were stimulated with anti-CD3 and anti-CD28 mAbs for the indicated periods of time and whole cell lysates were analyzed for T-bet expression by Western blot. Actin is shown as loading control. (E) Purified CD4 T cells from WT, H1RKO and H1RKO-MKK6_{Glu} transgenic mice were stimulated with anti-CD3 and anti-CD28 mAbs for the indicated periods of time and supernatants were analyzed for IFN γ production by ELISA in triplicate. Significance of differences were determined by Student's t-test (***) ($p < 0.001$). All the data are representative of at least two independent experiments.

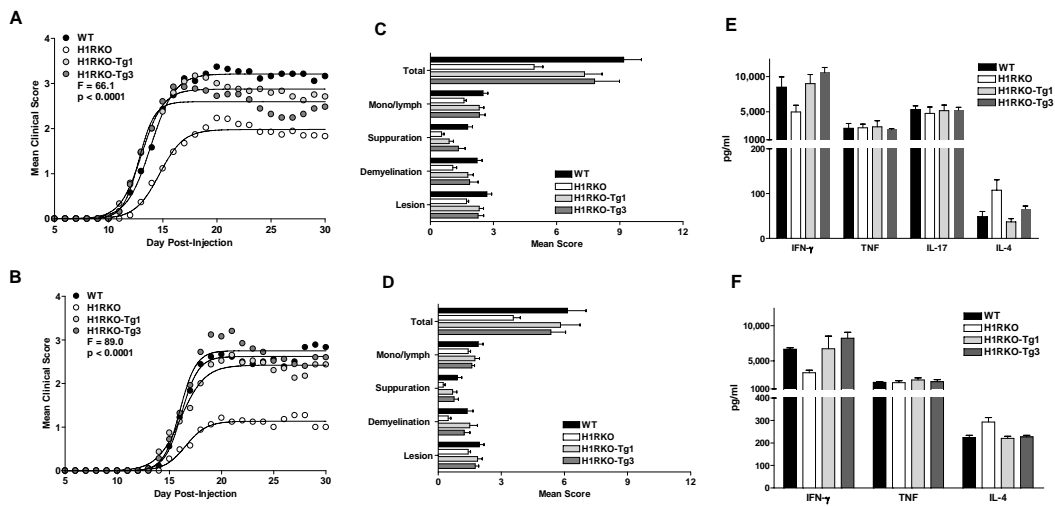


Figure 7. H₁R signaling directly in CD4 T cells regulates encephalitogenic Th1 effector responses.

Clinical EAE course, severity of CNS pathology and *ex-vivo* cytokine responses of WT, HIRKO and HIRKO-Tg mice were compared following immunization with MOG₃₅₋₅₅+CFA+PTX (A, C and E) and 2× MOG₃₅₋₅₅+CFA (B, D and F). Cytokine production was assessed by stimulating splenocytes with MOG₃₅₋₅₅ on D10 post-injection, supernatants collected and quantified by ELISA in triplicate. The significance of differences in the course of clinical disease, clinical disease traits, CNS pathology indices (PI) and cytokine responses were assessed by regression analysis (63), Chi-square test, or ANOVA followed by post hoc multiple comparisons. With the exception of disease incidence, and TNF- α and IL-17 production, significant differences among the strains were detected for all parameters at p < 0.0001 with C57BL/6J = HIRKO Tg-1 = HIRKO Tg-3 > HIRKO.

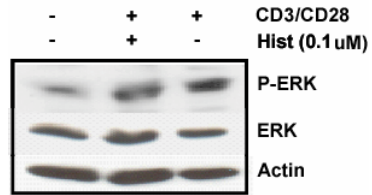


Figure 8. Absence of histamine does not affect TCR-mediated ERK activation.

WT CD4 T cells were activated with anti-CD3 and anti-CD28 mAbs for 30 min in presence or absence of 10^{-7} M histamine and whole cell lysates were analyzed for phospho-ERK, total ERK and actin by Western blotting.

Strain	Incidence	Day of onset	Cumulative disease score	Days affected	Severity index	Peak score
C57BL/6J	19/19	13.1±0.3	56.2±4.6	18.0±0.3	3.1±0.2	3.9±0.3
H1RKO	55/56	15.7±0.4	32.1±1.4	15.0±0.4	2.1±0.1	3.0±0.1
Tg-1	24/24	12.9±0.4	50.0±3.7	17.8±0.5	2.8±0.2	3.6±0.2
Tg-3	23/25	12.1±0.1	50.0±3.2	18.7±0.2	2.7±0.2	3.6±0.2
$\chi^2 = 4.5$ $F = 20.6$ 18.1 32.5 11.7 8.1 $p = 0.2$ $p < 0.0001$ < 0.0001 < 0.0001 < 0.0001 < 0.0001 C57BL/6J = H1RKO-Tg-1 = H1RKO-Tg-3 > H1RKO						

Table 1: Clinical disease parameters in MOG₃₅₋₅₅+CFA+PTX immunized mice

Strain	Incidence	Day of onset	Cumulative disease score	Days affected	Severity index	Peak score
C57BL/6J	18/18	16.6±0.7	37.6±2.9	14.2±0.7	2.6±0.1	3.2±0.2
H1RKO	26/33	17.1±0.5	20.0±1.8	9.8±0.9	1.6±0.1	2.2±0.1
Tg-1	22/23	16.2±0.6	36.4±3.8	13.3±0.8	2.5±0.2	3.2±0.2
Tg-3	23/25	15.7±0.4	46.1±4.0	14.0±0.9	2.7±0.2	3.6±0.2
$\chi^2 = 7.5$ $F = 1.5$ 9.5 5.1 11.2 12.2 $p = 0.06$ $p = 0.051$ < 0.0001 0.0025 < 0.0001 < 0.0001 C57BL/6J = H1RKO-Tg-1 = H1RKO-Tg-3 > H1RKO						

Table 2: Clinical disease parameters in 2x (MOG₃₅₋₅₅+CFA) immunized mice

CHAPTER 3: POLYMORPHISMS IN MURINE HISTAMINE RECEPTOR H₁ LEAD TO DIFFERENTIAL CELL SURFACE EXPRESSION AND INFLUENCE AUTOIMMUNE DISEASE PROGRESSION

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ABSTRACT

Structural polymorphisms (L263P, M313V and S331P) in the third intracellular loop of the murine histamine receptor H₁ (H₁R) are candidates for *Bphs*, a shared autoimmune disease locus in experimental allergic encephalomyelitis (EAE) and experimental allergic orchitis. The P-V-P haplotype is associated with increased disease susceptibility (H₁R^S) whereas the L-M-S haplotype is associated with less severe disease (H₁R^R). Here we show that selective reexpression of the H₁R^S allele in T cells fully complements EAE susceptibility and the production of disease associated cytokines while selective reexpression of the H₁R^R allele does not. Mechanistically, we show that the two H₁R alleles exhibit differential cell surface expression and altered intracellular trafficking, with the H₁R^R allele being retained within the endoplasmic reticulum (ER). Moreover, we show that all three residues (L-M-S) comprising the H₁R^R haplotype are required for altered expression. These data are the first to demonstrate that structural polymorphisms influencing cell surface expression of a G-protein coupled receptor in T cells regulates immune functions and autoimmune disease susceptibility.

INTRODUCTION

Multiple sclerosis (MS) is the major demyelinating disease of the central nervous system (CNS) in humans, affecting more than 2.5 million people worldwide (Greenstein, 2007). Both environmental and genetic factors contribute to the immunopathologic etiology of the disease. A genetic component in disease susceptibility is supported by the 20-30% concordance rate among monozygotic twins and 3-5% for dizygotic twins. Compared to the general population, MS is 20-40 times more common in first degree relatives and there is no excess risk in adopted relatives of patients with MS (Hafler et al., 2005). Evidence of an environmental etiology in MS comes primarily from migration studies and geographic distribution data. Migration studies indicate that individuals moving from high-risk areas before puberty tend to adopt the lower risk of the native population and vice versa (Kantarci and Wingerchuk, 2006). Thus, susceptibility to MS is likely the result of environmental triggers acting on a susceptible genetic background at the population level.

Experimental allergic encephalomyelitis (EAE), the primary animal model of MS, is also a genetically determined inflammatory disease of the CNS (Gold et al., 2000). EAE can be actively induced in genetically susceptible animals by immunization with either whole spinal cord homogenate or encephalitogenic proteins/peptides and adjuvants (Kuchroo et al., 2002). EAE, like MS, is a complex polygenic disease (Andersson and Karlsson, 2004), with multiple genes exerting a modest effect, thus making it difficult to study the contribution of individual loci to overall disease pathogenesis. However, reduction of complex disease states into intermediate or subphenotypes that are

under the control of a single locus has the potential to facilitate mechanistic studies and gene identification (Andersson and Karlsson, 2004). One such phenotype associated with EAE is *Bordetella pertussis* toxin-induced histamine sensitization, which is controlled by the single autosomal dominant locus known as *Bphs* (Ma et al., 2002). Previously, we identified *Hrh1*/ H_1R as the gene underlying *Bphs* (Ma et al., 2002) and as a shared autoimmune disease susceptibility gene in EAE (Linthicum and Frelinger, 1982) and experimental allergic orchitis (EAO) (Teuscher, 1985). H_1R is a seven-transmembrane spanning, G protein coupled receptor (GPCR). Generally, ligation of H_1R with histamine is believed to couple to second messenger signaling pathways via the activation of the heterotrimeric $G\alpha_{q/11}$ family of G proteins and leads to a variety of signaling cascades depending on the cell type involved (Parsons and Ganellin, 2006).

Compared to wild-type (WT) mice, H_1R deficient (H_1RKO) mice exhibit significantly reduced EAE susceptibility (Ma et al., 2002). As a disease susceptibility gene, *Hrh1*/ H_1R can exert its effect in multiple cell types involved in the disease process including endothelial cells, antigen presenting cells and T cells. Moreover, H_1R may function at critical check points during both the induction and effector phases of the disease. In this regard, we recently demonstrated that selective reexpression of the H_1R^S allele in T cells is sufficient to complement EAE in H_1RKO mice and that H_1R signals are important during priming of naïve T cells rather than during the effector phase of the disease (Noubade et al., 2007).

Hrh1/ H_1R -susceptible ($Hrh1^S/H_1R^S$) and –resistant ($Hrh1^R/H_1R^R$) alleles differ by three amino acids in their coding sequences (Ma et al., 2002). The H_1R^R haplotype possesses a L²⁶³, M³¹³ and S³³¹ whereas the H_1R^S haplotype is characterized by P²⁶³,

V³¹³ and P³³¹ (Ma et al., 2002). The mechanism whereby these polymorphic residues influence EAE susceptibility is unknown but it was hypothesized to be the result of differential coupling to second messenger signaling pathways, because the three residues reside within the third intracytoplasmic domain associated with G $\alpha_{q/11}$ activation (Tan et al., 2004). Here we show that, unlike the H₁R^S allele (Noubade et al., 2007), expression of the H₁R^R allele in T cells does not complement EAE in HIRKO mice and that the polymorphic residues of the H₁R^R allele affect intracellular trafficking and retention in the ER rather than the inherent capacity to signal. Moreover, we show that all three residues (L-M-S) comprising the H₁R^R haplotype are required for altered cell surface expression. These data are the first to demonstrate that structural polymorphisms influencing differential cell surface expression of a GPCR in T cells can regulate immune functions and susceptibility to autoimmune disease.

RESULTS

Expression of H₁R^R does not complement EAE in H₁R deficient mice

Using transgenic complementation, we recently showed that expression of the H₁R^S allele only in T cells of H1RKO mice was sufficient to restore EAE severity to WT levels in these mice (Noubade et al., 2007). To understand if the H₁R^R allele would also complement EAE in H1RKO mice, we generated transgenic mice expressing the N-terminus hemagglutinin (HA)-tagged H₁R^R allele under the control of the distal *lck* promoter, which drives expression in peripheral T cells (Wildin et al., 1991). The transgenic founders were generated directly on the C57BL/6J background and were crossed to H1RKO mice to obtain H1RKO mice expressing the H₁R^R allele selectively in T cells. The expression of the transgene in CD4 T cells was assessed by RT-PCR using transgene-specific primers (Fig. 1A) and by real time RT-PCR using primers that recognize H₁R (Fig. 1B). The two established lines of H₁R^R (H1RKO-Tg^{R1} and H1RKO-Tg^{R2}) expressed the transgene mRNA at levels comparable to one of the H₁R^S allele transgenic mice (H1RKO-Tg^S) that we reported previously (Noubade et al., 2007).

We then examined the susceptibility of these transgenic mice to myelin oligodendrocyte glycoprotein peptide 35-55 (MOG₃₅₋₅₅) induced EAE. We used two protocols to induce disease, one using MOG₃₅₋₅₅ plus complete Freund's adjuvant (CFA) and pertussis toxin (PTX) (MOG₃₅₋₅₅-CFA plus PTX) (Fig. 1C) and the other using two injections of MOG₃₅₋₅₅ plus CFA (2× MOG₃₅₋₅₅-CFA) (Fig. 1D), which does not use PTX as an ancillary adjuvant. Regression analysis revealed that the clinical disease courses elicited by both induction protocols fit a Sigmoidal curve and that the clinical

course of disease in two independent lines of H1RKO-Tg^R mice was not different from that in H1RKO mice. However, as reported previously (Noubade et al., 2007), the clinical course of EAE in H1RKO-Tg^S mice was significantly more severe than that of H1RKO mice and was equivalent to the disease course observed in WT mice. These results indicate that, unlike the H₁R^S allele, expression of the H₁R^R allele by H1RKO T cells does not complement EAE susceptibility.

An analysis of EAE-associated clinical quantitative trait variables from the two transgenic cohorts revealed that the mean day of onset (DO), cumulative disease score (CDS), overall severity index (SI) and the peak score (PS) were significantly different among the strains immunized with either MOG₃₅₋₅₅-CFA plus PTX or 2× MOG₃₅₋₅₅-CFA (Table 1). *Post hoc* multiple comparisons of each trait variable revealed that H1RKO-Tg^S mice were equivalent to WT mice while H1RKO-Tg^R mice were equivalent to H1RKO mice. Furthermore, for each trait, H1RKO-Tg^S and WT mice were significantly greater than H1RKO-Tg^R and H1RKO mice.

We next analyzed the *ex vivo* MOG₃₅₋₅₅ specific proliferative response of spleen and draining lymph node (DLN) cells from mice immunized with 2× MOG₃₅₋₅₅-CFA. Significant differences in proliferative responses were not detected among WT, H1RKO, H1RKO-Tg^S and H1RKO-Tg^R mice (data not shown). Since MOG₃₅₋₅₅-stimulated splenocytes from immunized-H1RKO mice exhibit an immune deviation from Th1 to Th2 response in *ex vivo* recall assays (Ma et al., 2002), we analyzed cytokine production by MOG₃₅₋₅₅-stimulated spleen and DLN cells from mice immunized with both EAE-induction protocols. With the classical MOG₃₅₋₅₅-CFA plus PTX protocol, as we observed previously (Noubade et al., 2007), antigen-stimulated spleen and DLN cells

from H1RKO-Tg^S mice produced significantly greater amounts of IFN- γ compared to H1RKO mice and at levels comparable to WT mice (Fig. 2A). In contrast, the levels of IFN- γ produced by antigen-stimulated spleen and DLN cells from the two lines of H1RKO-Tg^R mice were equivalent to those produced by H1RKO mice. Similarly, antigen-stimulated spleen and DLN cells from H1RKO-Tg^S mice produced IL-4 at levels comparable to WT mice while those from H1RKO-Tg^R mice were similar to H1RKO mice (Fig. 2B). Similar results for IFN- γ (Fig. 2D) and IL-4 (Fig. 2E) were observed for 2 \times MOG₃₅₋₅₅-CFA immunized mice.

Because IL-17 is considered to be an important effector cytokine in EAE (Furuzawa-Carballeda et al., 2007), we examined IL-17 production by spleen and DLN cells following *ex vivo* stimulation with MOG₃₅₋₅₅. IL-17 production by WT, H1RKO, H1RKO-Tg^S and H1RKO-Tg^R mice immunized with MOG₃₅₋₅₅-CFA and PTX was not significantly different (Fig. 2C) among strains. In contrast, IL-17 production by MOG₃₅₋₅₅ stimulated spleen and DLN cells from animals immunized with 2 \times MOG₃₅₋₅₅-CFA differed significantly among the strains (Fig. 2F). Compared to WT mice, H1RKO mice produced significantly less IL-17, indicating that H₁R signaling regulates IL-17 production by T cells. Moreover, production of IL-17 by H1RKO-Tg^S mice was not significantly different from WT mice and IL-17 production by H1RKO-Tg^R mice was not significantly different from H1RKO mice (Fig. 2F). Taken together, like EAE, H₁R^R expression in H1RKO T cells does not complement cytokine production by these cells.

H₁R alleles activate G α_q and G α_{11} equally well *in vitro*

The above results suggest that the H₁R^R allele is not functional relative to the H₁R^S allele. To understand the mechanism by which the polymorphic residues of the

H₁R^S and H₁R^R alleles influence H₁R function, we examined the predicted structural location for the three residues within H₁R. The three polymorphic residues reside within the third intracytoplasmic loop of H₁R (Fig 3A), which is the region frequently associated with recruitment and activation of downstream G proteins (Tan et al., 2004). We, therefore, examined whether the polymorphic residues distinguishing the H₁R^S and H₁R^R alleles might result in significant alterations in G protein activation. Since H₁R is normally coupled to G_{αq} and/or G_{α11} proteins, we generated fusion proteins of the two H₁R alleles with both G_{αq} and G_{α11} by linking in-frame the N-terminus of G_{αq/11} with the C-terminal tail of H₁R^R or H₁R^S.

HEK293 cells were transfected with the H₁R^S-G_{αq/11} or H₁R^R-G_{αq/11} fusion proteins, lysed and membrane fractions prepared from these cells. These were used initially to measure the levels of expression of each construct via the specific binding of the H₁R antagonist [³H]mepyramine. There were no differences in the levels of specific binding of [³H]mepyramine between the various constructs, indicating that the polymorphisms did not alter total protein expression. Also, the binding affinity of [³H]mepyramine was not different between the two alleles (Fig 3B). To study their differential capacity to activate G_{αq} and G_{α11}, membrane amounts containing exactly the same number of copies of each construct were employed in [³⁵S]GTPγS binding assays. A maximally effective concentration of histamine stimulated binding of [³⁵S]GTPγS equally to G_{αq} or G_{α11} when each G protein was linked to either the H₁R^S or H₁R^R variants (Fig. 3C, Fig. 3D). The dose-response curves to histamine indicated that the potency of histamine is equivalent for each receptor variant (data not shown). These data indicate that the H₁R^S and H₁R^R alleles can activate these G proteins equally well and

that the phenotypic difference associated with the H₁R alleles is not inherently a function of differential capability to activate G α_q or G α_{11} .

H₁R alleles are differentially expressed on the cell surface

Specific mutations in the signaling domain of several GPCRs (e.g. vasopressin V2 receptor, rhodopsin) can interfere with their cell surface expression and are associated with disease (Tao, 2006). To determine if the polymorphisms in H₁R influence cell surface expression of the receptor, HA-H₁R^S or HA-H₁R^R expression vectors were used to transfect HEK293T cells. The expression of these receptors at the cell surface was then examined by Flow cytometric analysis using an anti-HA mAb. HA-H₁R^S was expressed at higher levels than HA-H₁R^R (Fig. 4A). The number of H₁R^S-positive cells (Fig. 4B) and the mean fluorescence intensity of H₁R^S were considerably higher than those of H₁R^R, (Fig. 4C) indicating that the two H₁R alleles are differentially expressed on the cell surface. We observed similar results when the H₁R^S and H₁R^R constructs were transfected into 721.221 B cells (data not shown).

In parallel, we examined the cell surface expression of H₁R^S and H₁R^R by confocal microscopy using anti-HA mAb in cells stained prior to permeabilization. The results confirmed higher expression of H₁R^S on the surface than H₁R^R (Fig. 4D). However, Western blot analysis of H₁R^S and H₁R^R expression in lysates of transfected HEK293T cells showed no difference in the amount of total protein present (Fig. 4E). Taken together, these data indicate that the polymorphic residues associated with the H₁R^S and H₁R^R haplotypes result in differential translocation of the receptor to the cell surface.

H₁R^R is retained in the endoplasmic reticulum

The Western blot results described above (Fig. 4E) suggest that the H₁R^S and H₁R^R alleles are expressed at similar levels but that the H₁R^R allele is largely retained in intracellular compartments instead of being trafficked to the cell surface. To investigate this possibility, HEK293T cells were transfected with HA-H₁R^S or HA-H₁R^R constructs. After 24 h cells were fixed, permeabilized, stained with anti-HA mAb and observed by confocal microscopy. A predominantly plasma membrane staining pattern was observed for the H₁R^S allele (Fig. 5A). In contrast, a large fraction of the H₁R^R allele appeared to localize intracellularly (Fig. 5B) indicating that H₁R^R is retained in the intracellular compartments and fails to traffic efficiently to the cell surface. The network-like intracellular distribution of H₁R^R throughout the cell (Fig. 5B, right panel) resembled that of endoplasmic reticulum (ER). Therefore, to determine if the H₁R^R allele is retained in this compartment, we transiently co-transfected HEK293T cells with H₁R^S or H₁R^R constructs and a plasmid expressing the dsRed fluorescent protein that targets the ER. Co-localization of the two proteins was examined by confocal microscopy following staining the cells for HA-H₁R. The majority of H₁R^R was again expressed intracellularly and co-localized with the dsRed protein, while minimal colocalization of H₁R^S with the ER-targeted dsRed protein was observed (Fig. 5B). Using LSM5 image browser software, we quantified the number of pixels that express both dsRed protein and HA-H₁R in multiple cells that were imaged under exactly the same settings. The results showed a significant difference in the co-localization of the H₁R^S and H₁R^R alleles in ER (Fig. 5C), suggesting that the H₁R^R L-M-S haplotype leads to its sequestration and retention in ER.

Retention of H₁R^R in the ER requires the L-M-S haplotype

To understand which of the three amino acids comprising the H₁R^R L-M-S haplotype is responsible for the observed differential cell surface expression of the allele we generated single H₁R^S mutants, replacing each of the H₁R^S haplotype associated residues with the corresponding H₁R^R allele (P263L, V312M, and P330S), by site directed mutagenesis. HEK293T cells were transfected with H₁R^S, H₁R^R and each of the three H₁R^S mutant constructs. Cells were stained with anti-HA mAb, without permeabilization, and cell surface expression of H₁R analyzed by Flow- cytometry. Each of the single H₁R^S mutants was expressed at higher levels on the cell surface than the H₁R^R allele (Fig. 6A) with the levels comparable to those observed with the H₁R^S allele. This indicates that the presence of a single H₁R^R polymorphism is not sufficient to induce its intracellular retention. We also generated double mutants of the H₁R^S allele wherein we replaced two residues of the H₁R^S haplotype with the corresponding residues of the H₁R^R allele (P263L and V312M, P263L and P330S, V312M and P330S). Similar to the single H₁R^S mutants, the double H₁R^S mutants were expressed on the cell surface at levels comparable to the H₁R^S and at significantly higher levels than the H₁R^R allele (Fig. 6B). We observed similar results in 721.221 B cells following transient transfection with H₁R^S, H₁R^S mutants and H₁R^R constructs (data not shown). Furthermore, when HEK293T cells were co-transfected with double H₁R^S mutants and the dsRed plasmid, each of the mutants showed a typical plasma membrane expression pattern with very little co-localization with the ER-targeted dsRed protein (Fig. 6C). Quantification of the number of pixels expressing dsRed- protein and HA-H₁R confirmed that each of the double H₁R^S mutants behaved like H₁R^S and only H₁R^R was retained in ER (Fig. 6D),

confirming the flow cytometry data that all the polymorphic residues are required for differential cell surface expression of the H₁R alleles. Taken together, these data indicate that all three residues of the H₁R^R L-M-S haplotype are required for its intracellular sequestration. Interestingly, we sequenced the H₁R alleles from more than 100 different inbred laboratory and wild-derived mouse strains and did not identify any recombinant haplotypes (Table 2), suggesting that the two alleles are evolutionarily conserved and have been selected for functionally.

DISCUSSION

To date, *Hrh1*/H₁R is the only murine EAE and EAO susceptibility gene that has been positionally cloned (Ma et al., 2002). In this study, using transgenic mouse models, we show that polymorphic variants in H₁R regulate cytokine production by T cells thereby influencing susceptibility to EAE. Furthermore, using HEK293T cells, we show that the polymorphisms in H₁R affect its functions by modulating cell surface expression rather than inherently altering the capacity of the receptor to generate intracellular signals.

Hrh1/H₁R has long been implicated in EAE susceptibility (Linthicum and Frelinger, 1982; Ma et al., 2002). As H₁R is widely expressed (Parsons and Ganellin, 2006), this suggested that it might act in different cell types and at multiple checkpoints. We recently showed, however, that H₁R expression in T cells is sufficient to complement EAE severity in H1RKO mice. In this study, we show that the polymorphic residues of the H₁R^R allele interfere with its ability to complement EAE in H1RKO mice. This is in accordance with genetic complementation studies in F1 hybrids between H1RKO and strains of mice expressing the H₁R^S or H₁R^R alleles. Susceptibility to histamine sensitivity could be restored in F1 hybrids of H1RKO and SJL/J, 129X1/SvJ or C57BL/6J that express H₁R^S allele but not in F1 hybrids between H1RKO and C3H/HeJ or CBA/J mice that express H₁R^R (Ma et al., 2002).

Hrh1/H₁R also controls delayed type hypersensitivity (DTH) responses when PTX is used as an adjuvant. The DTH response is mediated by CD4 T cells that produce large amounts of IFN- γ (Sewell et al., 1987; Sewell et al., 1984; Sewell et al., 1983). Using C3H.*Bphs*^S congenic mice expressing the H₁R^S allele from SJL/J mice on the

resistant C3H/HeJ background, Gao et al., (Gao et al., 2003) showed that polymorphisms in H₁R regulate ovalbumin-specific DTH response elicited in mice immunized with ovalbumin in CFA and PTX, indicating that the polymorphisms in H₁R regulate IFN γ production by CD4 T cells. This study confirms the role of H₁R polymorphisms in regulating IFN- γ production by these cells. Further, the complementation of IFN- γ production by splenocytes immunized using the 2 \times MOG₃₅₋₅₅ model suggests that H₁R regulation of IFN γ production by T cells does not require PTX.

Recently, IL-17-producing Th17 CD4 T cells have been considered more pathogenic in EAE (Furuzawa-Carballeda et al., 2007). We show here, for the first time, that H₁R signaling regulates IL-17 production and that H₁R polymorphisms influence IL-17 production by T cells. However, it is noteworthy that we did not observe differences in IL-17 production between WT and H1RKO mice immunized with MOG₃₅₋₅₅-CFA plus PTX, nor in Th17 cells differentiated *in vitro* in the presence of excessive amounts of IL-6. PTX promotes the generation of Th17 cells, by inducing IL-6 production (Chen et al., 2007). Thus, it is possible that immunization with PTX (*in vivo*) or addition of exogenous IL-6 (*in vitro*) enables CD4 T cells to overcome the absence of H₁R signals required for the optimal IL-6 production and generation of Th17 cells. Even though we observed significant differences in IL-17 production by spleen and DLN cells from transgenic mice selectively expressing either H₁R^S or H₁R^R in T cells, we believe, based on *in vitro* differentiation data, that the H₁R regulation of IL-6 and IL-17 is independent of H₁R signals in T cells. In this regard, compared to WT macrophages H1RKO macrophages produce significantly less IL-6 (unpublished data) and treatment of lung parenchymal macrophages with H₁R blockers results in decreased IL-6 production (Triggiani et

al., 2001). Further studies are being carried out to elucidate the role of H₁R in the generation of Th17 CD4 T cells.

GPCRs, in spite of the diversity of their polypeptide sequences, as a family retain enough structural information to allow them to be properly folded in the ER and adopt their highly conserved seven transmembrane confirmation (Spiegel and Weinstein, 2004). Several studies have identified critical residues and motifs important in many of the functions of GPCRs including ligand binding, G protein coupling, internalization, downregulation and intracellular trafficking (Duvernay et al., 2005). However, the three polymorphic residues distinguishing the H₁R^S and H₁R^R alleles are located in the third intracytoplasmic loop and do not constitute any known motif. Even though the exact PXXP motif is not present, it is worth noting that two of the three polymorphic residues associated with the H₁R^S haplotype are prolines, and that proline rich-motifs are known to mediate protein-protein interactions with Src homology SH3 domains (Sparks et al., 1996). In this regard, polymorphic residues containing polyproline motifs in the third intracytoplasmic loop of the dopamine D4 receptor and β 1-adrenergic receptor have been shown to interact with multiple SH3 domain-containing proteins (Oldenhof et al., 1998) and affect the trafficking of these receptors. However, at this point, we do not have any evidence to suggest that H₁R interacts with any of the known SH3 domain-containing proteins or that such interactions differ between H₁R^S and H₁R^R alleles. Future studies will address this issue.

GPCRs interact with numerous proteins that play a role in their cellular trafficking (Tan et al., 2004). H₁R has an unusually long third intracytoplasmic loop, suggesting that the polymorphic residues may result in improper folding of the receptor to a non-

native conformation in ER, which is then recognized by the quality control machinery of molecular chaperones and excluded from ER export. Several chaperone proteins [such as Nina (Schneuwly et al., 1989; Shieh et al., 1989), ODR-4 (Dwyer et al., 1998; Gimelbrant et al., 2001) and a variety of receptor activity modifying proteins (RAMPs) (Christopoulos et al., 2003; McLatchie et al., 1998)] that support the trafficking of a range of GPCRs to their target site have been identified. Therefore, it is possible that polymorphic residue-induced misfolding of H₁R^R could hinder its interaction with an essential chaperone thereby affecting its trafficking.

Proper cell surface expression of GPCRs is required to access the requisite ligands and signal transduction machinery (Tan et al., 2004). The functional importance of proper GPCR localization is emphasized by several human diseases that result from receptor mutation and mislocalization, including X-linked nephrogenic diabetes, retinitis pigmentosa and hypogonadotropic hypogonadism, which result from intracellular accumulation of mutant V2 vasopressin receptor, rhodopsin and gonadotropin releasing hormone receptor, respectively (Tao, 2006). In fact, mutations that lead to intracellular accumulation comprise the largest class of mutations in GPCRs that result in human diseases (Tan et al., 2004). Accordingly, our results are the first to demonstrate that structural polymorphisms influencing differential trafficking and cell surface expression of a GPCR in T cells can regulate immune functions and susceptibility to autoimmune disease.

MATERIALS AND METHODS

Mice

C57BL/6J mice were purchased from the Jackson Laboratory (Bar Harbor, ME). B6.129P-*Hrh1*^{tm1Wat} (H1RKO) (Banu and Watanabe, 1999) mice were maintained in the animal facility at the University of Vermont (Burlington, VT). The experimental procedures used in this study were approved by the Animal Care and Use Committee of the University of Vermont.

For transgenic mouse generation, the HA-H₁R^S or HA-H₁R^R constructs were made by deleting the methionine of the *Bphs*-susceptible H₁R allele from SJL/J and *Bphs*-resistant C3H/HeJ mice, respectively (Ma et al., 2002), and adding an HA tag at the N-terminus using TOPO cloning vector (Invitrogen, Carlsbad, CA). The HA-H₁R was then subcloned downstream of the distal *lck* promoter (Wildin et al., 1991). The linear DNA fragment containing the distal *lck* promoter, the HA-H₁R gene and the human growth hormone (hGH) intron and polyadenylation signal was injected directly into fertilized C57BL/6J eggs at the University of Vermont transgenic/knockout facility. Mice were screened by DNA slot blot testing using a *Bam*HI–*Sac*I 0.5 kb fragment from the *hGH* gene as a probe. Two founders were generated for both the H₁R^S and H₁R^R alleles and each was crossed to H1RKO mice to establish transgenic mouse lines on the H1RKO background (H1RKO-Tg^S1 and H1RKO-Tg^S2 and H1RKO-Tg^R1 and H1RKO-Tg^R2 mice). Mice from the H1RKO-Tg^S1 line expressed the transgene at comparable levels to the two lines expressing the H₁R^R allele, so it was used in all the experiments in this study.

Cytokine production

For cytokine analysis spleen and lymph nodes were obtained from mice immunized ten days earlier with either MOG₃₅₋₅₅-CFA plus PTX or 2× MOG₃₅₋₅₅-CFA model, single cell suspensions prepared at a concentration of 1×10^6 cells/ml in RPMI medium and stimulated with 50 µg/ml of MOG₃₅₋₅₅. Cell culture supernatants were recovered at 72 h and cytokine levels measured by ELISA using anti-IFN- γ , anti-IL-4 and anti-IL17 mAbs and their corresponding biotinylated mAbs (BD Pharmingen, San Diego, CA). TNF- α ELISA kit was from (BD Pharmingen, San Diego, CA).

Proliferation Assays

Mice were immunized with the 2× MOG₃₅₋₅₅-CFA protocol: single cell suspensions were prepared at 2.5×10^5 cells/well in RPMI medium and stimulated in a 96 well plate with different concentrations (0, 2, 10 and 50 µg/ml) of MOG₃₅₋₅₅ for 72 h and proliferation was determined by [³H]-thymidine incorporation during the last 18 h of culture.

Cell surface expression studies

The pEGZ-HA vector plasmid was a generous gift from Dr. Ingolf Berberich (University of Wurzburg, Wurzburg, Germany). Two restriction sites, *Bam*HI and *Eco*RI were inserted into H₁R^S or H₁R^R cDNA by PCR and cloned such that the second codon is in-frame with the HA tag of pEGZ generating an HA-H₁R fusion protein. pEGZ is a bicistronic system with IRES-EGFP. EGFP served as a marker for transfected cells.

HEK293T cells were plated at 1.25×10^6 cells/plate and cultured in DMEM-F12 containing 10% FBS. When the cells were about 50-80% confluent, they were transfected with 5 µg of pEGZ-HA-H₁R^S, pEGZ-HA- H₁R^R or the empty pEGZ vector using

calcium phosphate method. After 16-24 h, cells were scraped off the plate by rigorous pipetting with 1% Calf serum in PBS and stained with anti-HA mAb conjugated to PE (Miltenyi Biotech, Auburn, CA) according to the manufacturer's guidelines. Cells were analyzed by Flow cytometry using FACSAria instrument (BD Pharmingen, San Diego, CA) and the data were further analyzed using FlowJo flow cytometry analysis software (Tree star Inc, Ashland, OR).

Confocal microscopy

HEK293T cells were transfected with pEGA-HA-H₁R^S, pEGZ-HA-H₁R^R or empty pEGZ control vector (5 µg total DNA) using the calcium phosphate method. Cells were fixed, permeabilized and stained using an anti-HA mAb (Cell Signaling Technologies, Danvers, MA) followed by an incubation with Alexa-568 anti-mouse antibody (Molecular Probes, Eugene, Oregon). TOPRO-3 nuclear stain (Molecular Probes, Eugene, Oregon) was used as a nuclear marker. For non-permeabilized cells, the transfected HEK293T cells were stained with the anti-HA mAb and were then fixed. Cells were examined by confocal microscopy using Zeiss LSM 510 META Confocal Laser Scanning Imaging System (Carl Ziess Microimaging Inc, Thronwood, NY).

Cell lysates and Western blotting

Whole-cell lysates were prepared from HEK293T cells transfected with various pEGZ constructs in Triton lysis buffer and were then separated via sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred to nitrocellulose membranes as described previously (Noubade et al., 2007). Anti-HA mAb (Abcam Inc. Cambridge, MA) was used as primary antibody. Anti-actin (Santa Cruz Biotechnology, Santa Cruz, CA) was used as a loading control.

[³H]mepyramine binding studies

[³H]mepyramine binding studies were conducted as described (Bakker et al., 2004) and were used to measure expression levels of H₁R variants and the H₁R^S-Gα_{q/11} and H₁R^R-Gα_{q/11} fusion proteins.

[³⁵S]GTPγS binding Assay

[³⁵S]GTPγS binding experiments to assess the capacity of H₁R variants to cause activation of Gα_{q/11} were initiated by the addition of cell membranes containing 50 fmols of H₁R variant constructs to assay buffer (20mM HEPES (pH 7.4), 3mM MgCl₂, 100mM NaCl, 1μM GDP, 0.2mM ascorbic acid, and 100nCi [³⁵S]GTPγS) containing 100μM histamine. Non-specific binding was determined in the above condition with the addition of 100μM GTPγS. Reactions were incubated for 15 min at 30⁰ C and were terminated by the addition of 500μl of ice-cold buffer containing 20mM HEPES (pH 7.4), 3mM MgCl₂, 100mM NaCl and 0.2mM ascorbic acid. The samples were centrifuged at 16,000 × g for 10 min at 4⁰ C. The resulting pellets were re-suspended in solubilization buffer (100mM Tris, 200mM NaCl, 1mM EDTA, and 1.25% Nonidet P-40) plus 0.2% SDS. Samples were precleared with Pansorbin for 1 h, followed by immunoprecipitation with a C-terminal anti- Gα_q/Gα₁₁ antiserum (Mitchell et al., 1991). Finally, the immunocomplexes were washed with solubilization buffer and bound [³⁵S]GTPγS was estimated by liquid scintillation-spectrometry.

Site directed mutagenesis

pEGZ-HA-H₁R^S was used as template to generate single H₁R^S mutants with each of the polymorphic residues replaced with the corresponding residue of the H₁R^R allele using the Quickchange (Stratagene) site directed mutagenesis kit, according to the manufacturer's guidelines. The forward primers used for the mutagenesis were: for P263L 5'- GGGGGTCCAGAAGAGG**CCG**TCAAGAGACCCTACTGG-3', for V312M 5'- CATGCAGACACAGCC**TGT**TGCCTGAGGGAGATGCCAGG-3', for P330S 5'- CCAGACCTTGAGCC**AGC**CCAAAATGGATGAGCAGAGC-3'. The reverse primers were the complementary sequences of these primers. The altered nucleotides are shown in bold and underlined. The mutants were sequence confirmed and were used as template for the generation of different combinations of double H₁R^S mutants.

Conventional and Quantitative Real-Time Polymerase Chain Reaction (RT-PCR)

Total RNA was extracted from CD4 T cells using RNeasy RNA isolation reagent (Qiagen, Valencia, CA) as recommended by the manufacturer. cDNA generated from 1 µg total RNA was used in conventional and quantitative real-time RT-PCR as described earlier (11).

Induction and Evaluation of EAE

Mice were immunized for the induction of EAE using either the MOG₃₅₋₅₅-complete Freund's adjuvant (CFA) double-inoculation (2× MOG₃₅₋₅₅-CFA) (Butterfield et al., 1998) or the MOG₃₅₋₅₅-CFA plus PTX single-inoculation (MOG₃₅₋₅₅-CFA plus PTX) protocols (Teuscher et al., 2006b). For the 2× MOG₃₅₋₅₅-CFA induction protocol mice are injected subcutaneously with an emulsion of 100 µg of MOG₃₅₋₅₅ and an equal

volume of CFA containing 200 µg of *Mycobacterium tuberculosis* H37RA (Difco Laboratories, Detroit, MI) in the posterior right and left flank; one week later all mice were similarly injected at two sites on the right and left flank anterior of the initial injection sites. Animals immunized using the MOG₃₅₋₅₅-CFA plus PTX single-inoculation protocol received an emulsion of 200 µg MOG₃₅₋₅₅ and equal volume of CFA containing 200 µg of *Mycobacterium tuberculosis* H37RA by subcutaneous injections distributed equally in the posterior right and left flank and scruff of the neck. Immediately thereafter, each animal received 200 ng PTX (List Biological Laboratories, Campbell, CA) by intravenous injection. Mice were scored daily starting at day 5 post-injection as previously described (Teuscher et al., 2006b). Clinical quantitative trait variables including disease incidence and mean day of onset (DO), cumulative disease score (CDS), number of days affected (DA), overall severity index (SI) and the peak score (PS) were generated as previously described (Butterfield et al., 1998).

Statistical analysis

Statistical analyses, as detailed in the figure legends, were performed using GraphPad Prism 4 software (GraphPad software Inc, San Diego, CA). A P value of 0.05 or less was considered significant.

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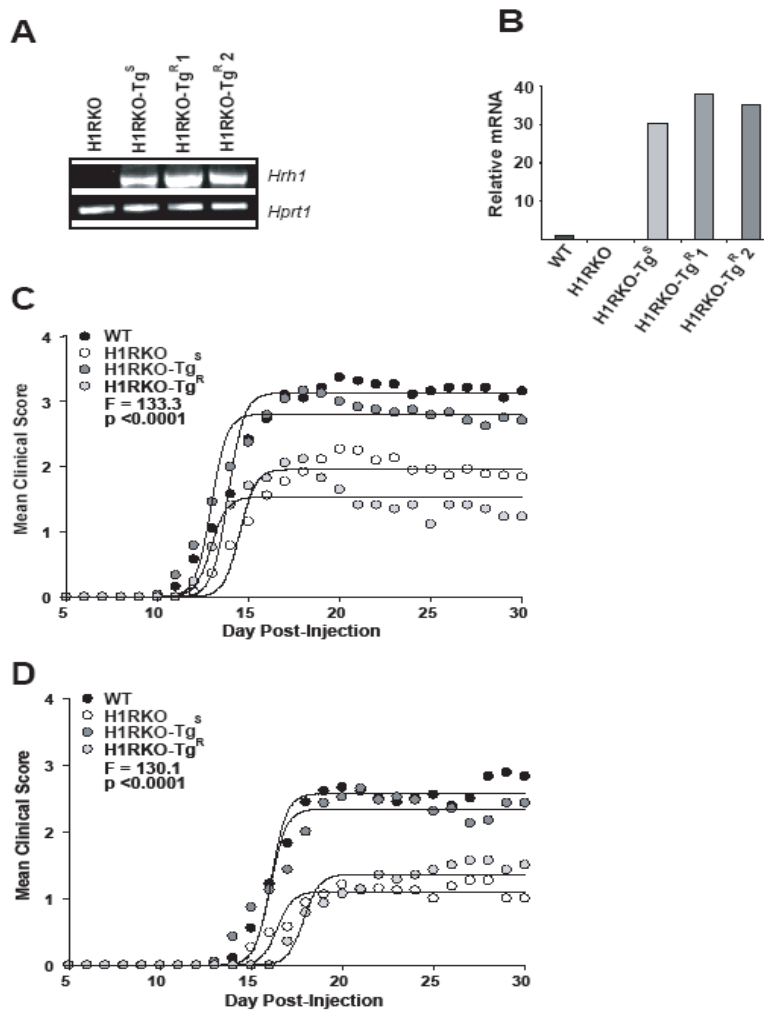


Figure 1. Transgenic expression of H₁R^R in H1RKO T cells fails to complement EAE in H1RKO mice.

H₁R transgene expression was analyzed by (A) RT-PCR and (B) quantitative RT-PCR of H₁R mRNA expression from CD4 T cells from H1RKO mice and the transgenic mice expressing H₁R^S or H₁R^R that were crossed with H1RKO mice (H1RKO-Tg^S, H1RKO-Tg^{R1} and H1RKO-Tg^{R2}). H1RKO-TgR1 and H1RKO-TgR2 represent two independent lines. (C) Clinical EAE in WT (n = 19), H1RKO (n = 56), H1RKO-Tg^S (n = 24), and H1RKO-Tg^R (n = 25) mice that were immunized with MOG₃₅₋₅₅+CFA+PTX. Mice were scored daily starting at D5. Regression analysis revealed that the disease course elicited fits a Sigmoidal curve and that the clinical disease course of the animals was significantly different among the strains (F = 66.1; p < 0.0001) and that WT (F = 132.1; p < 0.0001) and H1RKO-Tg^S (F = 127.5; p < 0.0001) mice were significantly different from H1RKO-Tg^R and H1RKO mice. (D) WT (n = 18), H1RKO (n = 33), H1RKO-Tg^S (n = 23), and H1RKO-Tg^R (n = 25) mice were immunized 2× with MOG₃₅₋₅₅+CFA. EAE severity was significantly different among the strains (F = 8.9; p < 0.0001) with WT (F = 226.9; p < 0.0001), and H1RKO-Tg^S (F = 134.0; p < 0.0001) mice being significantly different from H1RKO-Tg^R (F = 215.8; p < 0.0001) H1RKO mice.

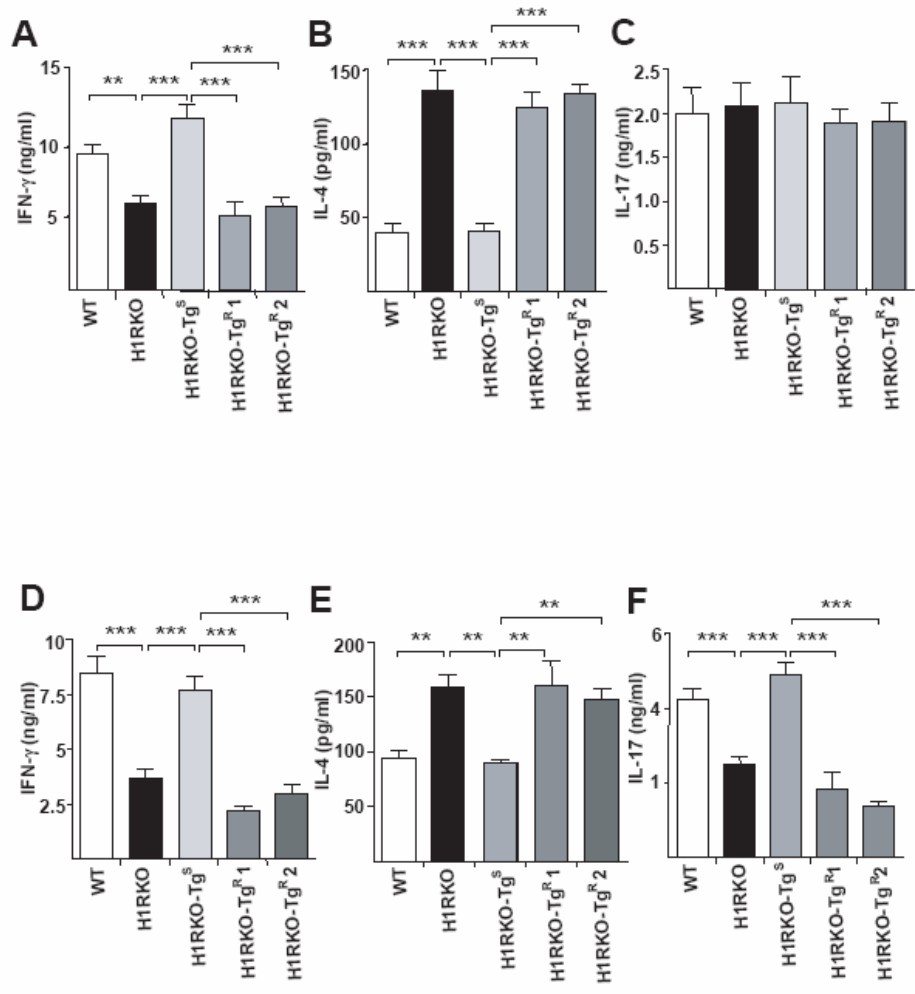


Figure 2. Transgenic expression of H₁R^R in H1RKO T cells fails to complement cytokine production by H1RKO mice.

(A-C) Spleen and draining lymph node (DLN) cells isolated from MOG35-55 plus CFA plus PTX-immunized WT, H1RKO, H1RKO-Tg^S and H1RKO-Tg^R mice 10 days post immunization and stimulated with the indicated 50mg/ml of MOG₃₅₋₅₅ for 72h. Supernatants were collected and analyzed for the production of IFN-g (A), IL-4 (B) and IL-17 (C). Significance of differences in cytokine production were assessed by one-way ANOVA (F = 14.89; p < 0.001 for IFN γ , F = 28.93; p < 0.001 for IL-4, p > 0.5 for IL-17) followed by Benfeorroni's post-hoc comparisons. Except for IL-17, WT = H1RKO-Tg^S > H1RKO-Tg^{R1} = H1RKO-Tg^{R2} = H1RKO mice. (D-F) Spleen and DLN cells from 2x MOG₃₅₋₅₅ plus CFA immunized mice were collected on day 10 post immunization and were activated with 50 μ g/ml of MOG₃₅₋₅₅ for 72h, supernatants were collected and analyzed for IFN γ (D), IL-4 (E) and IL-17 (F) by ELISA in triplicate. Significance of differences in cytokine production were assessed by one-way ANOVA (F = 28.92; p < 0.0001 for IFN γ , F = 3.766; p < 0.0001 for IL-4, F = 10.29; p < 0.0001 for IL-17) followed by Benfeorroni's post-hoc comparisons. For all the cytokines tested WT = H1RKO-Tg^S > H1RKO-Tg^{R1} = H1RKO-Tg^{R2} = H1RKO mice.

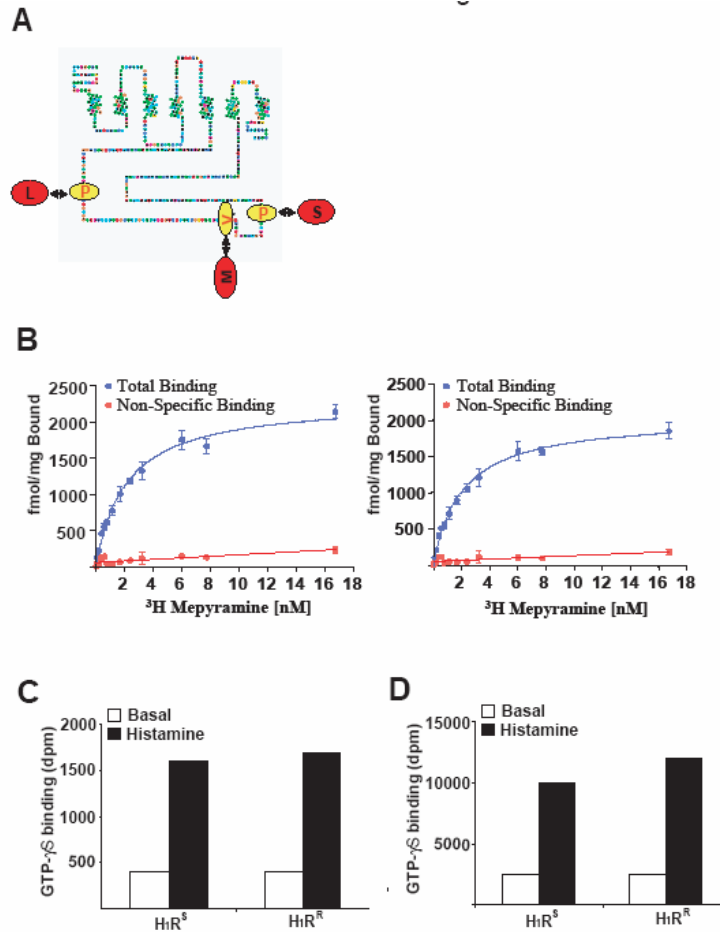


Figure 3. H_1R^S and H_1R^R activate $G\alpha_{q/11}$ G proteins equally well.

(A) The amino acid sequence of the mouse histamine H_1 receptor is displayed with differences between the H_1R^R allele (red) and the H_1R^S allele (yellow) highlighted. Each of the sites of variation is within the long, third intracellular loop. (B) Saturation [3H]mepyramine binding studies were performed on membranes of HEK293T cells transfected to express a H_1R^R - $G\alpha_q$ fusion protein (H_1R^R -left panel, H_1R^S -right panel). Non-specific binding (shown in red) was determined in the same manner but with the additional presence of $1\mu M$ mianserin. These studies provided quantitation of construct expression levels. (C & D) Membranes containing 50 fmol of H_1R^S or H_1R^R linked to either $G\alpha_q$ (C) or $G\alpha_{11}$ (D) were used in [^{35}S]GTP γ S binding studies conducted in the absence (basal, open bars) or presence (histamine, filled bars) of $100\mu M$ histamine to assess the capability of the two variants to activate the G proteins. H_1R^S and H_1R^R were equi-effective in causing activation of each G protein. Representative data are shown.

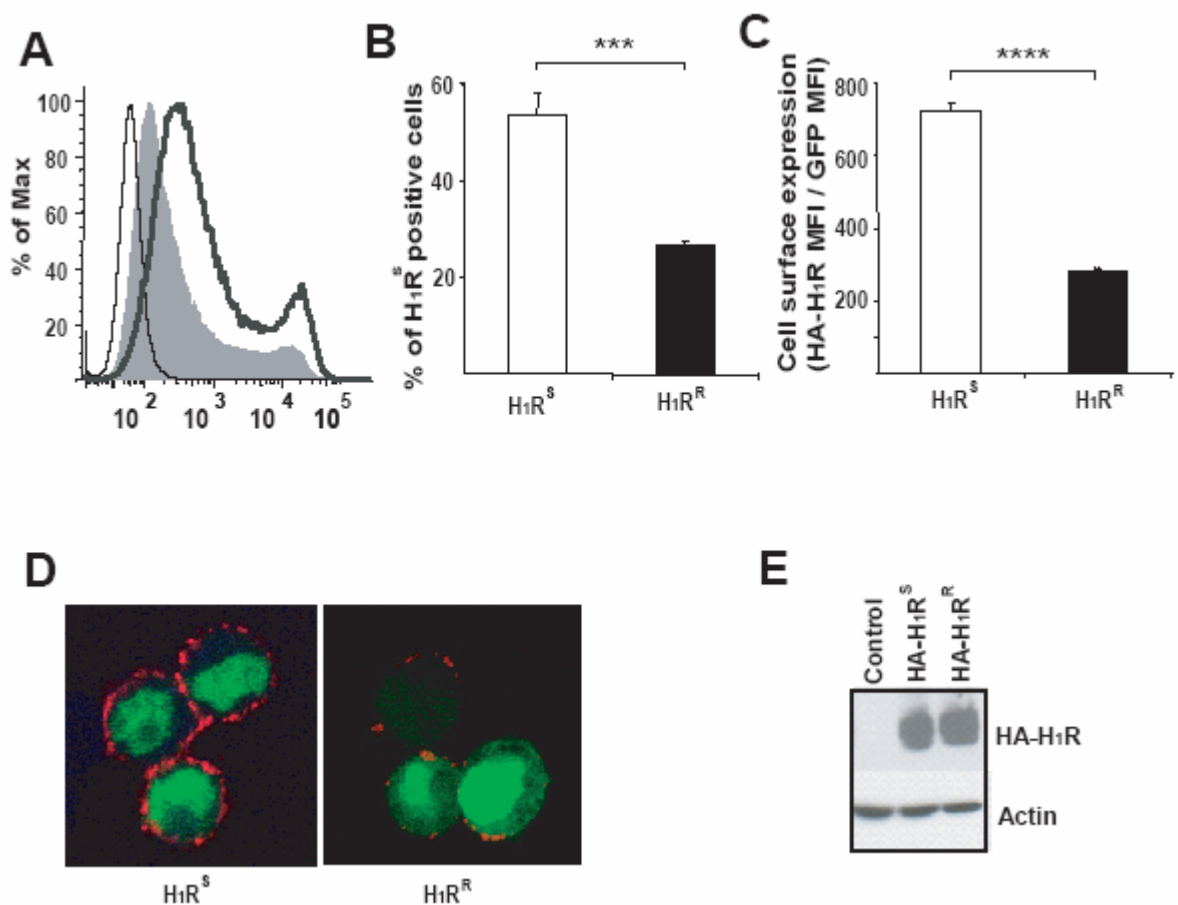


Figure 4. H_1R^S and H_1R^R are differentially expressed on the cell surface.

(A) HEK293T cells were transfected with empty pEGZ, pEGZ-HA- H_1R^S or pEGZ-HA- H_1R^R plasmids in triplicate cultures. Cells were collected 16-24h later without trypsinization, stained with anti-HA mAb and analyzed by Flow cytometry. Thin line represents cells transfected with empty pEGZ, thick line represents cells transfected with HA- H_1R^S and the filled area represents cells transfected with HA- H_1R^R . (B & C) HEK293T cells were analyzed as in (A) and the percentage (B) and the mean fluorescence intensity of anti-HA on H_1R^S positive cells (C) were determined (n=3). (D) HEK293T cells transfected with HA- H_1R^S or HA- H_1R^R plasmids and 24 h later cells were stained with anti-HA mAb (red) without permeabilization. Cells were visualized by confocal microscopy. GFP (green) is shown as a marker of transfected cells. (E). HEK293T cells were transfected as in (A), whole cell lysates prepared and analyzed by Western blotting using anti-HA mAb. Actin is shown as loading control.

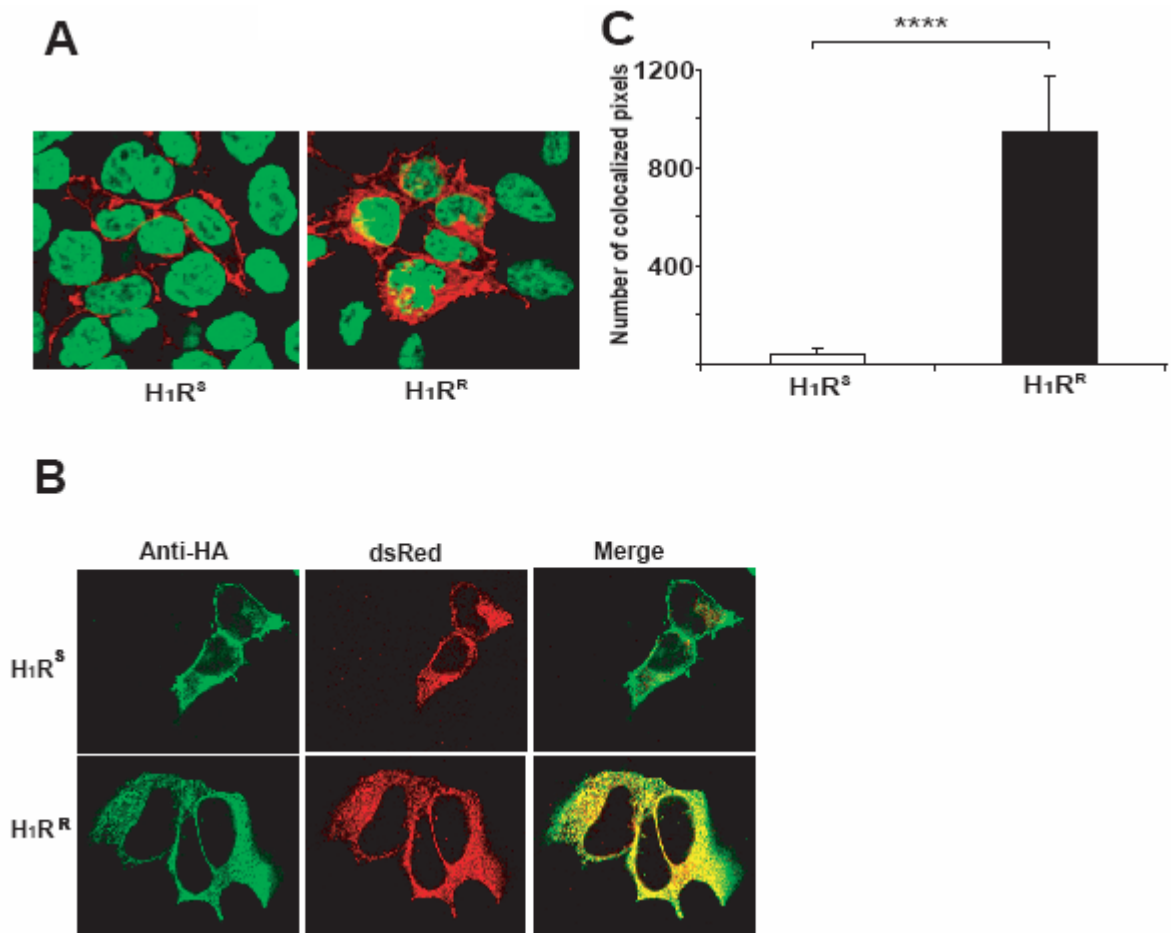


Figure 5. H₁R^R is retained in endoplasmic reticulum.

(A) HEK293T cells were transfected with HA-H₁R^S or HA-H₁R^R plasmids. 24h later, cells were fixed, permeabilized, stained with anti-HA mAb (red) and TOPRO-3 nuclear stain (green) and visualized by confocal microscopy. (B) HEK293T cells were co-transfected with pdsRed plasmid that express ER targeted fluorescent dsRed protein (red) and HA-H₁R^S or HA-H₁R^R. 24h later cells were fixed, permeabilized, stained with anti-HA mAb (green) and the co-localization of HA-H₁R with dsRed was visualized by confocal microscopy. Yellow color represents the co-localization of red and green colors. (C) Quantification of HA-H₁R colocalization with dsRed protein. Using Zeiss LSM 510 META Confocal imaging software the number of pixels expressing both colors were determined in a number of cells (n=36) and the data are presented as the average number of pixels that co-express dsRed and HA-H₁R. Error bars indicate SEM.

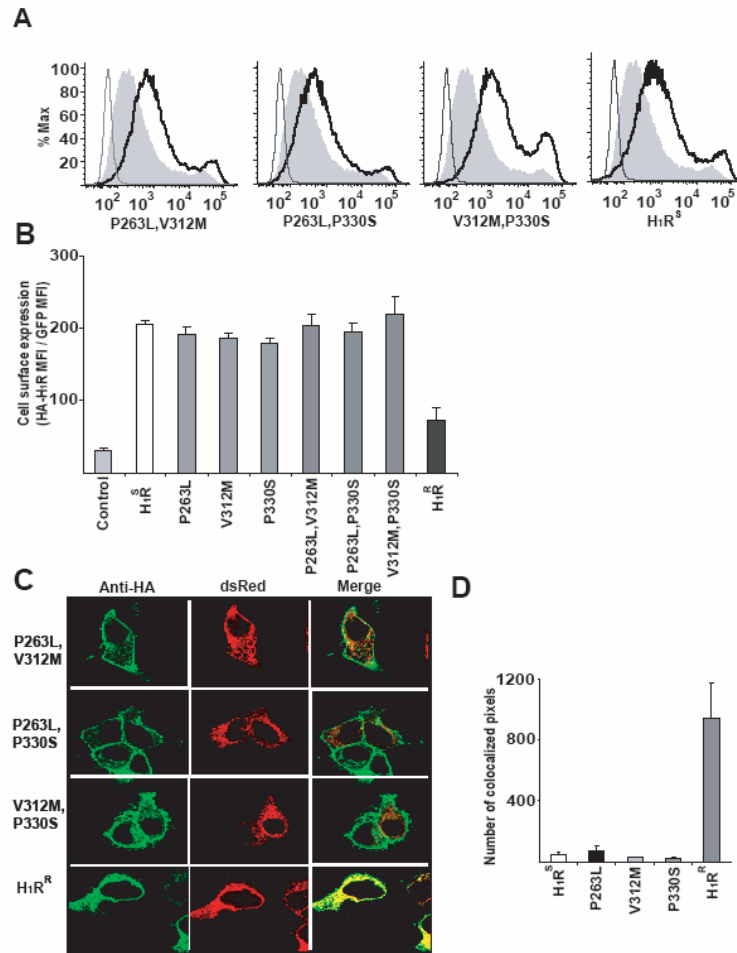


Figure 6. ER retention of H₁R^R requires all of its three polymorphic residues.

(A) HEK293T cells were transfected with empty control, HA-H₁R^S, single HA-H₁R^S mutants or HA-H₁R^R plasmids. Cells were collected 16-24 h later without trypsinization, stained with anti-HA mAb and analyzed by flow cytometry. Thin line represents cells transfected with empty pEGZ, thick line represents cells transfected with HA-H₁R^S and the filled area represents cells transfected with HA-H₁R^R. (B) HEK293T cells were analyzed as in (A) and the mean fluorescence intensity of anti-HA on H₁R^S positive cells was determined. The data presented is the average of triplicate transfections. (C) HEK293T cells were co-transfected with pdsRed plasmid that express ER targeted dsRed protein (red) and HA-H₁R^S, mutants of HA-H₁R^S or HA-H₁R^R. 24h later, cells were fixed, permeabilized, stained with anti-HA mAb (green) and the co-localization of HA-H₁R with dsRed (red) was visualized by confocal microscopy. Yellow color represents the co-localization of red and green colors. (D) Quantification of HA-H₁R colocalization with dsRed protein. Using Zeiss LSM 510 META Confocal imaging software the number of pixels expressing both the colors was determined in a number of cells (n≥16) and the data is presented as the average of number of pixels that co-express dsRed and HA-H₁R. Error bars indicate SEM.

(A)

Strain	Incidence	Day of onset	Cumulative disease score	Severity index	Peak score
C57BL/6J	19/19	13.1±0.3	56.2±4.6	3.1±0.2	3.9±0.3
H1RKO	55/56	15.7±0.4	32.1±1.4	2.1±0.1	3.0±0.1
H1RKO-Tg ^S	24/24	12.9±0.4	50.0±3.7	2.8±0.2	3.6±0.2
H1RKO-Tg ^R	16/17	13.3±0.3	50.0±3.2	2.7±0.2	3.6±0.2
$\chi^2 = 2.5$ F = 13.5 21.2 19.2 14.4 $p = 0.5$ $p < 0.0001$ < 0.0001 < 0.0001 < 0.0001 C57BL/6J = H1RKO-Tg ^S ≠ H1RKO-Tg ^R = H1RKO					

(B)

Strain	Incidence	Day of onset	Cumulative disease score	Severity index	Peak score
C57BL/6J	18/18	16.6±0.7	37.6±2.9	2.6±0.1	3.2±0.2
H1RKO	26/33	17.1±0.5	20.0±1.8	1.6±0.1	2.2±0.1
H1RKO-Tg ^S	22/23	16.2±0.6	36.4±3.8	2.5±0.2	3.2±0.2
H1RKO-Tg ^R	13/14	18.7±0.6	18.6±3.1	1.6±0.2	1.9±0.2
$\chi^2 = 7.4$ F = 2.8 11.6 15.2 14.0 $p = 0.06$ $p = 0.05$ < 0.0001 < 0.0001 < 0.0001 C57BL/6J = H1RKO-Tg ^S ≠ H1RKO-Tg ^R = H1RKO					

Table 1. Clinical disease traits following immunization of mice with (A) MOG₃₅₋₅₅+CFA + PTX and (B) 2x (MOG₃₅₋₅₅+CFA)

H₁R^S		H₁R^R
129 / SvJ	LEWES/EiJ	AKR/J
129S1/SvImJ	LG/J	BPL/1J
129T2/SvEmsJ	LP/J	C3H/HeJ
A/J	Ma/MyJ	CASA/RkJ
A/WySnJ	MOR/RkJ	CAST/EiJ
ALR/LtJ	NOD/LtJ	CBA/J
ALS/LtJ	NON/LtJ	CZECHI/EiJ
B10.S/DvTe	NOR/LtJ	CZECHI/EiJ
BALB / cByJ	NZO/HILtJ	I/LnJ
BALB/ cJ	P/J	JF1/Ms
BDP/J	PANCEVO/EiJ	MOLC/RkJ
BPH/2J	PERA/EiJ	MOLD/RkJ
BPL/1J	PERC/EiJ	MOLF/Eij
BPN/3J	PL/J	MRL/MpJ
BTBR T+ tf/J	RBF/DnJ	MSM/Ms
BXSB/MpJ	RIIS/J	PWK/PhJ
C57BL/10J	SB/LeJ	RF/J
C57BL/10SnJ	SEA/GnJ	SF/CamEiJ
C57BL/6ByJ	SEC/1ReJ	SKIVE/EiJ
C57BL/6J	SENCARA/PtJ	
C57BLKS/J	SENCARB/PtJ	
C57BR/cdJ	SENCARC/PtJ	
C57L/J	SJL/J	
C58/J	SJL/Bm	
CALB/RkJ	SM/J	
CE/J	SPRET/EiJ	
DBA/1J	ST/bj	
DBA/2J	SWR/ J	
DDY/JclSidSeyFrkJ	SWXL-4/TyJ	
EL/SuzSeyFrkJ	TIRANO/EiJ	
FVB/NCr	WSB/EiJ	
IS/CamRkJ	YBR/EiJ	
KK/HIJ	ZALENDE/EiJ	

Table 2. The P-V-P and L-M-S haplotypes of H₁R are evolutionarily conserved in mice.

CHAPTER 4: CONCLUSIONS AND FUTURE DIRECTIONS

Complex diseases such as MS and EAE are governed by multiple susceptibility genes and the risk conferred by polymorphisms in their alleles. Identifying such “risk alleles” and gaining mechanistic understanding of their contribution in the disease development will yield newer targets for therapeutic intervention in ameliorating these diseases. Even though more than 40 QTLs (Becanovic et al., 2006) in EAE and polymorphisms in many of their candidate genes, such as IL-2 (Encinas et al., 1999), MCP-1 and MCP-5 (Butterfield et al., 1999), and Ncf-1 (Becanovic et al., 2006) have been identified, no study has systematically elaborated the pathways of their mechanisms. To date, only one QTL, originally identified as *Idd5.1* and encompassing the gene coding for costimulatory molecule ICOS-1, has been shown to modulate EAE. This is through the differential expression of ICOS-1 in activated CD4 T cells, with higher expression in the resistant NOD/J mice than the congenic mice expressing ICOS-1 from the susceptible C57BL/6J mice (Greve et al., 2004). Our laboratory had previously identified polymorphisms in *Hrh1*/H₁R and shown that it is a susceptibility gene in EAE (Ma et al., 2002). In this study, the role of these polymorphisms was delineated and shows that they affect H₁R functions by differential cell surface expression. Further, the molecular pathways, through which H₁R contributes to the pathogenesis of EAE were identified and demonstrate that H₁R influences EAE by regulating proinflammatory cytokine production by T cells.

H₁R is one of the widely expressed GPCRs and is present on multiple cells types involved in EAE pathogenesis (Parsons and Ganellin, 2006). This study demonstrates that H₁R expression in T cells is important and sufficient to influence the

susceptibility to EAE. Re-expressing the susceptible allele of H₁R (H₁R^S) in T cells of H1RKO mice complemented EAE severity and disease-associated cytokine production by these mice, but the resistant allele of H₁R (H₁R^R) failed to do so. This clearly shows that the H₁R polymorphisms affect its ability to influence EAE pathogenesis and suggests that H₁R^R is not a functional receptor.

A functional GPCR such as H₁R, once synthesized, adopts a “native” structure that enables the receptor to pass through the quality control machinery of the endoplasmic reticulum (ER) and traffics to its target site, the cell surface (Spiegel and Weinstein, 2004). In transfected 293T cells, the polymorphisms in H₁R regulated the trafficking of the receptor with H₁R^R failing to reach its final compartment and being retained in ER. In contrast H₁R^S was efficiently trafficked and expressed on the cell surface. Thus, polymorphisms in H₁R^R join the group of a number of examples in which polymorphisms and mutations in GPCRs lead to their mislocalization and in many cases are associated with pathologies.

This study provides evidence that the polymorphisms in H₁R are evolutionarily conserved as haplotype blocks among several inbred strains of mice. The natural evolutionary history of the common house mouse suggests that, about a million years ago, its ancestors evolved into at least three well-developed subspecies that dominated different parts of the world (Wade and Daly, 2005). These include *M. m. domesticus* in Western Europe, *M. m. musculus* in Russia, Northern China and Eastern Europe and *M. m. castaneus* in West Asia, Southeast Asia and Southern China (Beck et al., 2000; Paigen, 2003). However, it is still unclear if the three subspecies diverged simultaneously or *M. m. musculus* and *M. m. castaneus* diverged from a common ancestor shortly after

the divergence of *M. m. domesticus* (Yang et al., 2007). Several thousand years ago, the Asian *M. m. musculus* and *M. m. castaneus* made their way to the Japanese Islands forming a new subspecies known as *M. m. molossinus* (Paigen, 2003). Because of their close cohabitation, hundreds of years ago, humans noted spontaneously arising coat colors in mice in Europe, China and Japan and domesticated several varieties as pets. Europeans even imported what were considered fancier coat colors from Asian regions and bred them with local mice to create few pools of mice. Some of these fancy mice were prized and even traded throughout Europe. With the rediscovery of Mendel's laws of inheritance, in the early twentieth century, geneticists such as Cuenot, Castle and Little started studying the discrete inheritance of the coat colors in mice. They received their animals from a large mice-breeding farm owned by Abbie Lathrop, whose colonies originated from European and Asian fancy mice. Castle and Little recognized the value of homozygous mice and established inbred strains of mice by brother x sister matings. DBA (having the coat color allele, dilute, brown and non-agouti) was the first inbred mouse strain developed in 1909. Since then, more than 450 inbred strains of mice have been established (Beck et al., 2000; Paigen, 2003). Therefore, most of the inbred laboratory mouse strains originated from a mixed, restricted number of founders. Based on this, the genomes of the common inbred mice strains were proposed to represent a mosaic of regions originating from different subspecies. *M. m. domesticus* is the major contributor while *M. m. musculus* and *M. m. castaneus* are the minor contributors to the genetic background of these mice (Wade and Daly, 2005). This hypothesis was strengthened by the observations that the mitochondrial DNA in many inbred strains of mice was derived from *M. m. domesticus* while the Y-chromosome was derived from *M.*

m. musculus (Bishop et al., 1985; Ferris et al., 1982). Further, it was noted that the musculus-type Y-chromosome originated from *M. m. molossinus* males (Nagamine et al., 1992). However, strains with Y-chromosome from *M. m. domesticus* have also been identified (Yang et al., 2007). Recently, the fine structure of this mosaic variation of the mouse genome is described (Wade et al., 2002; Yang et al., 2007). Strain-to-strain comparisons of single nucleotide polymorphisms (SNPs) revealed a long interspersed regions of high and low sequence identities. The segments genome with extremely high SNP variation is indicative of different subspecies origin and spanned only one-third of the genome. The segments of the genome covered with extremely low variation represent similar subspecies (*M. m. domesticus*) origin and spanned two thirds of the genome (Yang et al., 2007). However, another study reported a predominant introgression of *M. m. domesticus* segments at exceptionally high levels (86 to 96%) in the genomes of common laboratory strains while *M. m. musculus* contributed about 1-8 % and *M. m. castaneus* contributed only 1-2 % (Yang et al., 2007). Further, high-density sequence based studies identified three distinct genetic variation patterns indicative of the evolutionary origin; large monomorphic haplotypes representing a common ancestor, large polymorphic blocks representing recombination of two ancestor genomes, and large fragmented haplotype blocks representing greater complexity and multiple ancestor origin (Frazer et al., 2004; Sakai et al., 2005; Zhang et al., 2005). This study herein found that the H₁R alleles are conserved among several inbred strains of mice, including the wild-derived inbred strains, suggesting that the two haplotypes have evolutionarily co-evolved over a long period of time and reflect evolutionarily conserved functional differences. Future studies are necessary to ascertain the subspecies origin of the H₁R

haplotype block and examine if the haplotype block encompasses even a larger region of chromosome 6.

Traditionally, histamine was considered to be a mediator of the effector phase of EAE rather than the priming of autoreactive T cells (Bebo et al., 1996; Linthicum, 1982). This study exhibits that *Hrh1*/H₁R is expressed in unstimulated CD4 T cells but downregulated upon activation. Complementation of H₁R in naïve, but not in activated, H1RKO CD4 T was able to restore the ability of these cells to produce IFN- γ to the levels of WT CD4 T cells. These observations, along with the findings that mast cells exert their effect outside the CNS in EAE (Tanzola et al., 2003), suggests that histamine interaction with H₁R is important during the initial induction and priming of the naïve antigen-specific CD4 T cells in EAE pathogenesis.

H₁R has been previously implicated in the regulation of IFN- γ production (Banu and Watanabe, 1999; Bryce et al., 2006; Ma et al., 2002). In this study, it is evidenced that H₁R regulates IFN- γ by modulating activation of p38MAP kinase and T-bet. Further, it was found that histamine interaction with H₁R is required for p38 MAP kinase activation in TCR-stimulated CD4 T cells. However, how H1R activates p38 MAP kinase is unknown. p38 MAP kinase is normally activated through the upstream MAPKK, MKK3 and MKK6 (and MKK4 in response to some stimuli) (Kyriakis and Avruch, 2001). It has been documented that GADD45 proteins interact with MEKK4, an upstream kinase of MKK3 and MKK6 and thus activate p38 MAP kinase (Takekawa and Saito, 1998). Whether H₁R associates with GADD45 members and activates p38 MAP kinase needs to be investigated.

Overall, the results presented herein demonstrate the importance of

histamine and its interaction with H₁R as a significant immunomodulatory factor in EAE. *Hrh1*/H₁R is a shared susceptibility gene in EAE and experimental allergic orchitis (Ma et al., 2002). A shared genetic basis among different autoimmune diseases has been proposed and non-MHC candidate loci of several autoimmune or inflammatory disease are present as clusters in humans and in animal models (Becker et al., 1998). This suggests common susceptibility genes or tightly linked loci in multi-gene families. Thus, studying the role of H₁R in other autoimmune diseases may shed a light on its role as a common autoimmune modifier. Further, even though polymorphisms in human H₁R have not yet been reported, a syntenic region has been identified as a major risk factor in MS patients. Administration of antihistaminics in MS patients stabilized the disease progression (Dimitriadou et al., 2000). A retrospective epidemiological study found that the use of H₁R blockers reduced the risk of MS (Alonso et al., 2006). Together, all these observations suggest that pharmacological targeting of the H₁R may be useful early in the treatment of MS and other autoimmune inflammatory diseases.

APPNEDIX A: WEIBEL PALADE BODIES NEGATIVELY REGULATE BLOOD BRAIN BARRIER PERMEABILITY

AND BRAIN INFLAMMATION IN EXPERIMENTAL ALLERGIC ENCEPHALOMYELITIS

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Abbreviations: BBB, blood brain barrier; CFA, complete Freund's adjuvant; CNS, central nervous system; EAE, experimental allergic encephalomyelitis; HA, histamine; VWF, von-Willebrand factor; VWFKO, von Willebrand factor knockout; WPB, Weibel-Palade bodies; MS, multiple sclerosis; MOG₃₅₋₅₅, myelin oligodendrocyte glycoprotein peptide-(35-55); PTX, pertussis toxin; SC, spinal cord; WT, wild-type.

Abstract

Weibel-Palade bodies (WPB) within endothelial cells (EC) are secretory granules that release von Willebrand Factor (VWF), P-selectin, chemokines and other stored molecules following exposure to histamine (HA). Mice with a disrupted VWF gene (VWFKO) have EC that are deficient in WPB. These mice were used to evaluate the role of this organelle in *Bordetella pertussis* toxin induced hypersensitivity to HA (Bphs), an intermediate phenotype associated with susceptibility to experimental allergic encephalomyelitis (EAE), the principal autoimmune model of multiple sclerosis. No significant differences in susceptibility to Bphs between wild-type and VWFKO mice were detected at three days; however, in VWFKO mice HA sensitivity persists significantly longer. Correspondingly, the onset of EAE was earlier, disease was more severe and blood brain barrier (BBB) permeability significantly increased in VWFKO mice compared to wild-type mice. Moreover, inflammation was selectively increased in the brains and not in the spinal cords of VWFKO mice compared to wild-type mice. Early increases in BBB permeability in VWFKO mice were not due to increased encephalitogenic T-cell activity because BBB permeability was significantly greater in adjuvant treated VWFKO mice compared to littermate mice immunized with encephalitogenic peptide plus adjuvants. Taken together, these data indicate that VWF and/or WPBs negatively regulate BBB permeability changes and autoimmune inflammatory lesion formation within the brain elicited by peripheral inflammatory stimuli.

Introduction

Pertussis toxin (PTX) is a major virulence factor of *Bordetella pertussis*, the causative agent of whooping cough (Bordet and Gengou, 1906). The holotoxin is a hexameric protein that conforms to the A/B model of bacterial exotoxins (Rappouli and Pizza, 1991). The A-subunit is an ADP-ribosyl transferase which affects signal transduction by ribosylation of the α -subunit of trimeric Gi/o proteins, and the β -oligomer of PTX binds cell surface receptors on a variety of mammalian cells (Kaslow and Burns, 1992). Intoxication with PTX elicits an array of physiological responses *in vivo* including increased blood brain barrier (BBB) permeability and sensitization of the vascular endothelium to vasoactive agents such as histamine (HA) (Locht, 1999; Munoz, 1985). Inbred strains of mice differ in susceptibility to challenge with vasoactive agents following sensitization with PTX in that genetically susceptible strains succumb to hypotensive and hypovolemic shock while resistant strains do not (Wardlaw, 1970). Additionally, the genetic control of susceptibility to lethal shock is agent specific (Gao et al., 2003). For example, PTX-induced vascular endothelial sensitization, controlled by *Bphs* (*Bordetella pertussis* induced HA sensitization), is detected by HA challenge, but not by serotonin challenge. *Bphs* is an autosomal dominant locus that we recently identified as the histamine H₁ receptor (*Hrh1/H1R*) (Kantarci et al., 2002). Importantly, susceptibility to experimental allergic encephalomyelitis (EAE), the principal autoimmune model of multiple sclerosis (MS) (Musio et al., 2006), is also controlled by *Bphs/Hrh1* (Kantarci et al., 2002; Linthicum, 1982), underscoring the role of genetic factors in regulating BBB permeability and susceptibility to inflammatory demyelinating diseases of the CNS.

The mechanism whereby PTX sensitizes the vascular endothelium to HA is unknown, but it is consistent with a two-step process: an induction phase, characterized by a 2- to 3-day latent period following intoxication, and an effector phase, manifest by rapid onset of lethal shock that usually occurs within ten minutes of HA challenge (Bergman and Munoz, 1968),(Munoz et al., 1981). Bphs is also characterized by a protracted period of sensitivity that persists upwards of 30 days (Munoz et al., 1981). The fact that sensitization of the vascular endothelium continues well beyond the likely half-life of the toxin *in vivo* suggests that the induction phase may be associated with the synthesis and storage of additional vasoactive factors within endothelial cells (ECs) that are released by exposure to HA during the effector phase. In this regard, it is known that following inflammation preformed KC (IL-8 homologue), eotaxin-3, von Willebrand Factor (VWF), P-selectin, CD63/lamp3, angiopoietin 2, endothelin-1, endothelin converting enzyme, tissue-type plasminogen activator (t-PA), factor XIIa and/or α 1,3-fucosyltransferase VI can be stored in EC Weibel Palade bodies (WPBs) (Rondaij et al., 2006), and that HA is a secretagogue for the release of these agents (Hattori et al., 1989). Under a hypothetical two-step model, lethal shock would be due to the direct vasodilatory activity of HA combined with the effects of the stored products released from WPBs. In the absence of exposure to PTX, the ECs must be able to compensate for the effects of subsequently administered HA because most mice do not succumb following HA challenge alone. In contrast, EC would not be able to compensate for the increase in synergistic second messenger signaling arising from exposure to both HA and PTX-induced stored vasoactive factors. In this study, mice with a disrupted VWF gene (VWFKO) and a consequent deficiency in WPBs (Denis et al., 1998) were used to

directly test this hypothesis and to evaluate the role of WPBs in regulating BBB permeability and susceptibility to EAE. We report that, contrary to this model, WPBs suppress Bphs and adjuvant-induced alterations in BBB function associated with actively induced EAE.

Results

Bphs in VWFKO mice

The role of WPBs in Bphs was evaluated by i.v. sensitization of B6 and VWFKO mice with 200 ng PTX on day 0. Three days later HA sensitivity was assessed in a dose response fashion by i.v. challenge with HA and deaths were recorded at 30 min. A significant difference in the LD₅₀ values between the two strains was not detected (B6 = 1.65 ± 0.05 mg/kg vs. VWFKO = 1.41 ± 0.08 mg/kg; $F = 0.55$, $p = 0.46$), indicating that neither VWF nor WPBs are required for Bphs susceptibility. Given the role of WPBs in vascular function, we nevertheless assessed their effect on the persistence of HA sensitivity. Compared to B6 mice, HA sensitivity persistent longer in VWFKO mice at all challenge doses studied ($F = 38.25$; $p < 0.0001$) (Fig. 1). The half-life of sensitization was 64.8 days in VWFKO mice compared 34.4 days in B6 mice at 100 mg/kg HA challenge. Similarly, the sensitization half-lives were 66.0 and 63.3 days in VWFKO mice at 50 mg/kg and 25mg/kg of HA respectively while the corresponding sensitization half-lives in WT mice were 34.2 and 30.7 days. Taken together, these data demonstrate that WPBs and/or VWF ordinarily act to shorten the longevity of HA sensitivity elicited by *in vivo* intoxication with PTX.

EAE in VWFKO mice

Because VWFKO mice exhibited significantly prolonged sensitivity to HA, and because *Bphs* is an EAE susceptibility gene (Kantarci et al., 2002), we studied the role of WPBs in regulating EAE induced by immunization with MOG₃₅₋₅₅+CFA+PTX. Compared to B6 mice, VWFKO mice developed significantly more severe clinical signs of EAE (Fig. 2). Clinical signs of EAE in VWFKO mice were notably enhanced

during the acute-early phase (D7 through D18 postimmunization) compared to the chronic late-phase of the disease (day 20-30) (Polanczyk et al., 2004). The mean day of disease onset in VWFKO mice was 14.1 ± 2.0 vs. 16.4 ± 3.2 ($p = 0.01$) in B6 mice. The acute-early phase cumulative disease score in VWFKO mice was 22.6 ± 11.1 vs. 13.3 ± 11.9 ($p = 0.008$) in B6 mice.

Histological analysis of CNS samples obtained during the acute-early phase of the disease revealed that VWFKO mice exhibited significantly greater pathology in the brain than did B6 mice (Fig. 3A-3E). VWFKO mice had a higher overall pathology index with significantly greater lesion scores, more severe demyelination, more severe suppuration, and more extensive mononuclear cell infiltrates compared to B6 mice. In contrast, however, no difference in the overall severity of the lesions between VWFKO and B6 mice was observed in the spinal cord (Fig. 3F). These results demonstrate that the absence of WPB and/or VWF selectively promotes lesion formation in the brain, compared to the spinal cord-dominant disease seen in mice with intact VWF and WPBs.

We examined a number of T cell parameters in B6 and VWFKO mice following sensitization with MOG₃₅₋₅₅+CFA+PTX in order to evaluate the encephalitogenic T cell response elicited in each strain. No difference in the proliferative response of spleen cells to MOG₃₅₋₅₅ at day 10 p.i. was observed between B6 and VWFKO mice (Fig. 4A). Similarly, no significant differences in cytokine and chemokine expression following *ex vivo* restimulation with MOG₃₅₋₅₅, were detected between B6 and VWFKO animals (Fig. 4B, C). Taken together, these results indicate that the more severe acute-early phase disease seen in VWFKO mice is unlikely to be due to a direct effect of the absence of VWF or WPBs on T cell effector responses.

Increased BBB permeability in VWFKO mice during EAE

To delineate the mechanisms underlying the more severe acute-early phase of EAE in VWFKO mice, we analyzed EC function by measuring BBB permeability. A BBB permeability index (BBB-PI) was determined by measuring the traverse of systemically injected FITC-labelled bovine serum albumin (BSA) into the cerebrospinal fluid of EAE-induced mice at 8, 10 and 12 days p.i. (Fig. 5). BBB-PIs were not significantly different between unmanipulated B6 and VWFKO mice; however, BBB-PIs were significantly elevated in both mouse strains ($p = 0.01$ for B6 and $p < 0.001$ for VWFKO) following immunization with MOG₃₅₋₅₅+CFA+PTX. Moreover, the test of the main effect of group (mouse strain) showed a significant difference ($p = 0.02$) between the two strains over time, with the BBB-PI being greater in VWFKO mice compared to B6 mice.

The significant difference in clinical signs and brain pathology between B6 and VWFKO mice during the acute-early phase of the disease, despite the absence of detectable differences in encephalitogenic T cell effector responses, point to a potential role for WPBs in regulating the interface between the circulation and the brain. We therefore compared the integrity of the BBB in B6 and VWFKO mice at various time points after injection with MOG₃₅₋₅₅+CFA+PTX or CFA+PTX. Immunization with CFA+PTX alone lead to increased BBB permeability in B6 mice (Fig. 6A) to an extent that was not different from that seen following immunization with MOG₃₅₋₅₅+CFA+PTX ($p = 0.45$). The change in BBB permeability over time was also not significant in B6 mice (Fig. 6B) ($p = 0.08$). Similarly, immunization with CFA+PTX alone significantly increased the BBB permeability in VWFKO mice but again, there was no difference in

the BBB-PIs between the animals immunized with or without the encephalitogen ($p = 0.47$). This indicates that in both B6 and VWFKO mice, antigen-specific encephalitogenic T cells are not responsible for eliciting increased BBB permeability across the time points studied. Because the BBB-PIs between the animals immunized with or without MOG₃₅₋₅₅ were not different, they were pooled and reanalyzed. The results revealed that the BBB-PI in VWFKO mice was significantly greater than the BBB-PI in B6 mice ($p = 0.001$) (Fig. 6C) when CFA and PTX are used as adjuvants, and that this difference is encephalitogen-independent.

To understand which component of the adjuvants (CFA or PTX) is responsible for increased BBB permeability, we determined the BBB-PIs in B6 and VWFKO mice injected with either CFA or PTX alone. Immunization with CFA alone increased BBB permeability in both B6 and VWFKO mice compared to unimmunized mice ($p < 0.001$ for both B6 and VWFKO) (Fig. 7A). The BBB-PI for CFA-immunized mice was significantly greater in VWFKO than in B6 mice ($p = 0.03$). Interestingly, the effect of CFA on BBB permeability was greater on day 8 and decreased over time, reaching almost basal levels both in B6 and VWFKO mice, indicating that ECs can overcome the CFA-induced inflammatory signals that compromise BBB integrity. Importantly, the decrease in CFA-induced BBB permeability over time was significant ($p < 0.0001$), but the rate of change was not different between strains.

PTX alone also independently increased BBB permeability in both B6 and VWFKO mice compared to untreated mice ($p = 0.0001$ for both B6 and VWFKO) (Fig. 7B). However, the effect of PTX on BBB permeability was different than that of CFA. BBB permeability changes induced by PTX did not vary over time ($p = 0.67$) and

remained elevated at each of the time points examined. However, as with CFA, the BBB-PI elicited by *in vivo* intoxication with PTX alone was significantly greater in VWFKO than in B6 mice ($p = 0.02$). These data suggest that BBB compromise and repair by ECs differs depending on the peripheral inflammatory stimulus. Therefore in order to assess if the ECs responses elicited independently by CFA and PTX are capable of cross regulating each other when administered simultaneously (CFA+PTX), we compared the BBB-PIs from animals receiving CFA and PTX alone with those from animals that received CFA+PTX. When CFA+PTX were injected at the same time, the BBB-PIs in both B6 (Fig. 8A) and VWFKO (Fig. 8B) were significantly lower compared to the BBB-PIs elicited by these agents separately. Although the CFA-induced increase in BBB permeability was greater at day 8 and decreased to basal levels by day 12 (conditions under which PTX-induced changes remain relatively constant), when the two agents were used together, the vascular permeability was, in contrast, lowest on day 8 with the BBB-PIs increasing to the PTX levels by day 12. These data support the concept that changes in BBB permeability elicited by CFA and PTX alone occur via different pathways and that the two pathways cross regulate each other with the overall differences in BBB permeability reflecting their integration over time. Moreover, these data indicate that WPBs and/or VWF protect against the vascular permeability changes induced by these inflammatory agents.

Discussion

In this study we show that the absence of WPBs and/or VWF leads to increased BBB permeability and, in appropriately immunized mice, concomitantly more severe EAE. The disruption of BBB integrity is due to adjuvants alone; and although the mechanism(s) by which CFA and PTX act to increase BBB permeability is unknown, these processes are independent of encephalitogenic T cell responses. Moreover, our study indicates that ECs respond differently to CFA and PTX with the outcome of simultaneous exposure being the integration of the different pathways over time. This is in agreement with previous studies examining the effects of inflammatory pain elicited by formalin, CFA and λ -carrageenan on BBB permeability (Brooks et al., 2005; Brooks et al., 2006). BBB permeability changes elicited by these stimuli were associated with unique alterations in the temporal expression of tight junctional proteins as well as disruption of the interaction between tight junctional complexes and the cytoskeleton. It is unclear what the mechanism(s) for tight junctional alterations following peripheral inflammation might be, but both CFA and PTX are known to lead to increased levels of IL-1 β , TNF- α , and/or IL-6 within the periphery and CNS rapidly after exposure (Armstrong et al., 2003; Donnelly et al., 2001; Loscher et al., 2000; Raghavendra et al., 2004; Samad et al., 2001). Within the CNS the increase in IL-1 β expression is associated with widespread changes in neuronal activity, including Cox-2 expression in CNS neurons leading to elevated prostaglandin E2 levels in the CSF (Ek et al., 2001). Consequently, alterations in BBB permeability might be subject to modulation via both peripheral and centrally mediated responses to inflammatory stimuli. In fact, we recently demonstrated that neurogenic control of BBB permeability is negatively

regulated by central histamine H₃ receptor signaling (Teuscher et al., 2007).

Alterations in BBB permeability can occur in a variety of different situations (Brooks et al., 2005), some of which relate directly to MS. There is an increasing body of evidence in both EAE (Tonra, 2002; Tonra et al., 2001) and MS (Mathews et al., 1993; Minagar et al., 2006) that subtle, progressive alterations in BBB integrity precede the formation of inflammatory lesions. These changes are detected in all MS disease subtypes, suggesting that a common abnormality in BBB function exists in the normal-appearing white matter of MS patients and may be a predisposing factor in initiating and propagating new inflammatory foci. Importantly, in our studies the WPB-related changes in BBB permeability also do not derive from T cell activity, indicating that WPBs play an important role in regulating BBB permeability in response to peripheral inflammatory stimuli. In this setting, understanding the mechanism of Bphs as a genetic model of BBB dysregulation is important.

The effector phase of Bphs is characterized by death due to hypotensive and hypovolemic shock within minutes of HA challenge (Bergman and Munoz, 1968). This time frame suggests that the effector phase may be associated with a sudden and rapid release of preformed factors generated during the sensitization phase rather than the induction of new gene expression by HA receptor signaling. Since inflammatory signals such as PTX induce the synthesis and storage of the vasoactive factors in the WPBs (Wolff et al., 1998) (Utgaard et al., 1998); (Utgaard et al., 1998) and because HA is a secretagogue for the release of these agents (Hattori et al., 1989), the shock following PTX sensitization and HA challenge could be due to the combined direct vasodilatory effects of HA and autocrine activity of the released stored products from WPBs.

However, our results in VWFKO mice demonstrate that the stored vasoactive factors in WPBs are not responsible for the sensitization and that VWF and/or other WPB components are instead protective in this model.

This observation was surprising given the fact that WPBs store several factors that are good candidates for the observed trait, the sudden release of which could change endothelial function in an autocrine fashion. WPBs are dynamic granules with very random movements in resting cells (Romani de Wit et al., 2003). WPBs are released from ECs in response to a large number of secretagogues, which can be divided into 2 distinct groups: those that act by elevating intracellular calcium levels such as thrombin and HA and those that act by raising cAMP levels such as epinephrine and vasopressin (Rondaij et al., 2006). Calcium raising agonists induce a periphery-directed movement of WPBs while cAMP-mediated agonists induce a transport-directed redistribution towards the center of the cell leading to a star-like cluster at the perinuclear region (Vischer et al., 2000). WPB clustering is believed to prevent excessive release of WPB constituents, and may also lead to a selective exclusion of subsets of WPBs from exocytosis. Clustering is induced by thrombin stimulation in human aortic EC (Vinogradova et al., 2000) but not in HUVECs (Rondaij et al., 2006). In HUVECs, PTX can inhibit both VWF and tissue plasminogen activator (tPA) release from WPBs in response to thrombin, most likely due to inhibition of calcium influx as well as inhibit HA-induced calcium release (van den Eijnden-Schrauwen et al., 1997). PTX causes ADP ribosylation of Gi/o family of G proteins that are negative regulators of G α s protein and its subsequent activation of adenylate cyclase. Through this mechanism, PTX treatment leads to increased intracellular cAMP concentration (Wettschureck and Offermanns,

2005),(Mittra and Bourreau, 2006), (Sugden et al., 2004; Zawilska et al., 2004). Hence, it is possible that the suppression of Bphs observed in mice that have VWF and WPBs could be due to PTX-induced, cAMP-mediated clustering of WPBs and sequestration of their contents in B6 mice and not in VWFKO mice.

Several studies have provided evidence in support of the existence of different subsets of WPBs that apart from VWF do not contain the same set of additional constituents (Fiedler et al., 2004; Oynebraten et al., 2004; Utgaard et al., 1998; Wolff et al., 1998). It has also been reported that different stimuli induce different WPB responses, depending on the physiological need. In the case of vascular damage, thrombin induces a rapid, local response leading to exocytosis of the WPBs while epinephrine induces a gradual release of WPBs (Vischer et al., 2000). Moreover, epinephrine induces the exocytosis of only the peripheral WPBs whereas thrombin stimulates the exocytosis of peripheral, as well as central WPBs (Vischer et al., 2000). This difference in release pattern and the fact that different stimuli, such as thrombin and epinephrine, induce WPB exocytosis via distinct mechanisms enables the cell to regulate the exocytosis of WPBs, and possibly the release of specific WPB constituents, in such a way that it meets the patho-physiological requirements induced by distinct triggers (Burgoyne and Morgan, 2003). Therefore in an inflammatory disease as complex as EAE, stored factors in WPBs may regulate a fine balance between pro-inflammatory and anti-inflammatory responses while in animals that lack WPBs this regulation is lost, which may explain increased susceptibility of VWFKO mice to EAE. In addition, VWF is an adhesion molecule for leukocytes (Pendur et al., 2006) that may be involved in their recruitment (Wagner DD, unpublished data). VWF has also been reported to mediate clearance of metastatic tumor

cells in lungs through a mechanism still not known (Pendur et al., 2006). Therefore, it is possible that VWF may be promoting the clearance of pathogenic autoimmune cells or proinflammatory debris in the CNS of B6 mice leading to lesser CNS inflammation than in VWF deficient mice.

The mechanism of BBB disruption in MS and EAE is unknown. Currently it is believed that neuroantigen-specific T cells within the systemic circulation interacting with ECs bring about the changes that lead to the formation of inflammatory foci and promote BBB permeability (Wingerchuk et al., 2001). Our results, however, indicate that disruption of the BBB in active EAE is independent of the encephalitogenic T cell responses and that this is caused by the interaction of EC with peripheral inflammatory stimuli such as CFA and PTX, and may also include neuropathic and inflammatory pain (Brooks et al., 2005; Inoue, 2006), which can be a major component of most forms of MS including benign disease (Glad et al., 2006). Overall, our study demonstrates that the interaction of EC with environmental agents other than those that lead to pathogenic T cell responses also influence the development of autoimmune disease by modifying BBB permeability. Taken together our findings underscore the potential importance of co-infection and/or non-autoimmune related gene-by-environment interactions in the etiology of MS.

Materials and Methods

Animals. B6.129S2-*Vwf^{tm1Wgr}* (VWFKO) mice (Denis et al., 1998) were maintained in the vivarium of the Given Medical Building at the University of Vermont (Burlington, VT). C57BL/6J (B6) mice were purchased from the Jackson Laboratory (Bar Harbor, ME). Animals were fed RMH 3000 Lab Diet Rodent Chow (Ralston-Purina, St. Louis, MO) and tap water ad libitum and maintained in accordance with the Animal Welfare Act and the Public Health Service Policy on the Humane Care and Use of Laboratory Animals. The experimental procedures used in this study were approved by the Animal Care and Use Committee of the University of Vermont.

Pertussis toxin *in vivo* intoxication. Mice were injected intravenously (i.v.) with purified PTX (List Biological Laboratories, Inc.) in 0.025 M Tris buffer containing 0.5 M NaCl and 0.017% Triton X-100, pH 7.6. Control animals received carrier.

Histamine sensitivity testing. HA sensitivity was determined by the i.v. injection of amounts of HA (mg/kg dry weight free base) suspended in PBS. Deaths were recorded at 30 min post challenge. The results are expressed as the number of deaths over the number of animals studied.

Induction and evaluation of EAE. EAE was induced as previously described (Teuscher et al., 2006a). Briefly, mice were injected subcutaneously in the flanks and neck with 0.1 ml of an emulsion containing 200 µg of myelin oligodendrocyte glycoprotein 35-55 (MOG₃₅₋₅₅) (Beckman Institute, Palo Alto, CA) in saline and an equal volume of complete Freund's adjuvant (CFA) containing 200 µg of *Mycobacterium tuberculosis* H37RA (Difco Laboratories, Detroit, MI). On the day of immunization, each mouse received 200 ng of PTX (List Biological Laboratories Inc., Campbell,

CA) by i.v. injection. The mice were assessed daily for clinical signs of EAE using the following scale: 0, normal; 1, limp tail or mild hind limb weakness; 2, moderate hind limb weakness or mild ataxia; 3, moderately severe hind limb weakness; 4, severe hind limb weakness or mild forelimb weakness or moderate ataxia; 5, paraplegia with no more than moderate forelimb weakness; 6, paraplegia with severe forelimb weakness or severe ataxia or moribund condition

Brains and spinal cords (SC) were dissected from calvaria and vertebral columns, respectively, and fixed by immersion in 10% phosphate-buffered formalin (pH 7.2). Following adequate fixation, brain and SC were trimmed and representative transverse section embedded in paraffin, sectioned at 5 μ m, and mounted on glass slides. Sections were stained with hematoxylin and eosin for routine evaluation and Luxol fast blue-periodic acid Schiff for demyelination. Sections from representative areas of the brain and SC were scored in a semi-quantitative fashion for the various histopathologic parameters, as previously described (Teuscher et al., 2006a).

Blood brain barrier permeability determinations. Blood brain barrier (BBB) permeability was assessed as previously described (Tang et al., 1996). Briefly, a 50 μ g/g dose of FITC-labeled BSA (Sigma, St. Louis, MO) was injected i.v. into B6 and VWFKO mice on day 8, 10 or 12 post immunization with CFA+PTX+MOG₃₅₋₅₅, CFA+PTX, CFA or PTX. Cerebrospinal fluid and blood were collected after 4 h. Both CSF and plasma samples, prepared by centrifugation at 3000 rpm for 15 min, were diluted in PBS, and the fluorescence intensity was measured with a microplate fluorescence reader (Flx-800-I, Bio-Tek Instruments Inc, Winooski, VT) using the software KC-4, with an excitation wavelength of 485 nm and an emission wavelength of

528 nm. The BBB permeability index is expressed as the ratio of the fluorescence intensity of the CSF divided by the fluorescence intensity of the plasma.

Statistical analysis. Statistical analyses, as indicated in the figure legends, were performed using GraphPad Prism 4 software (GraphPad software Inc, San Diego, CA).

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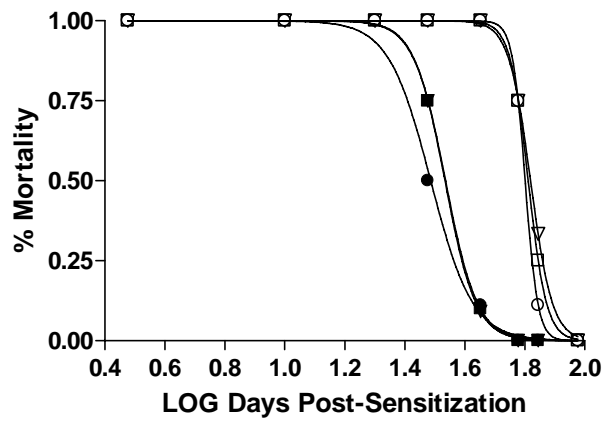


Figure 1. Assessment of Bphs in B6 and VWFKO.

Mice were sensitized with 200 ng purified PTX by i.v. injection on day 0. Mice were challenged with HA (mg dry weight free base) by i.v. injection on the indicated day and deaths were recorded at 30 min post challenge. The results are expressed as the number of animals dead over the number of animals studied (% mortality).

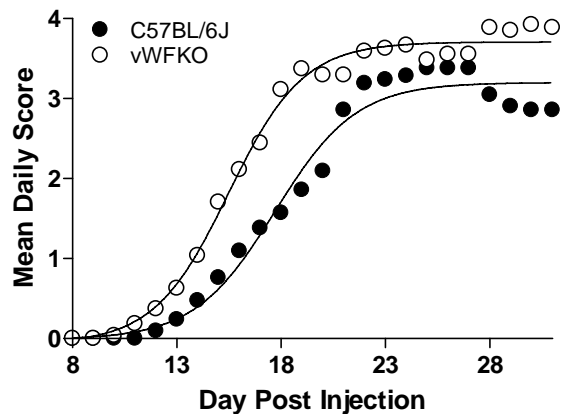


Figure 2. Early onset and severe clinical course of EAE in VWFKO mice.

EAE was induced in B6 (n = 18) and VWFKO (n = 27) mice by immunization with MOG₃₅₋₅₅+CFA+PTX. Regression analysis (Teuscher et al., 2006a) indicates that the disease course in both strains fits a variable slope sigmoidal curve and is significantly different between the two strains (F = 32.5; p < 0.0001).

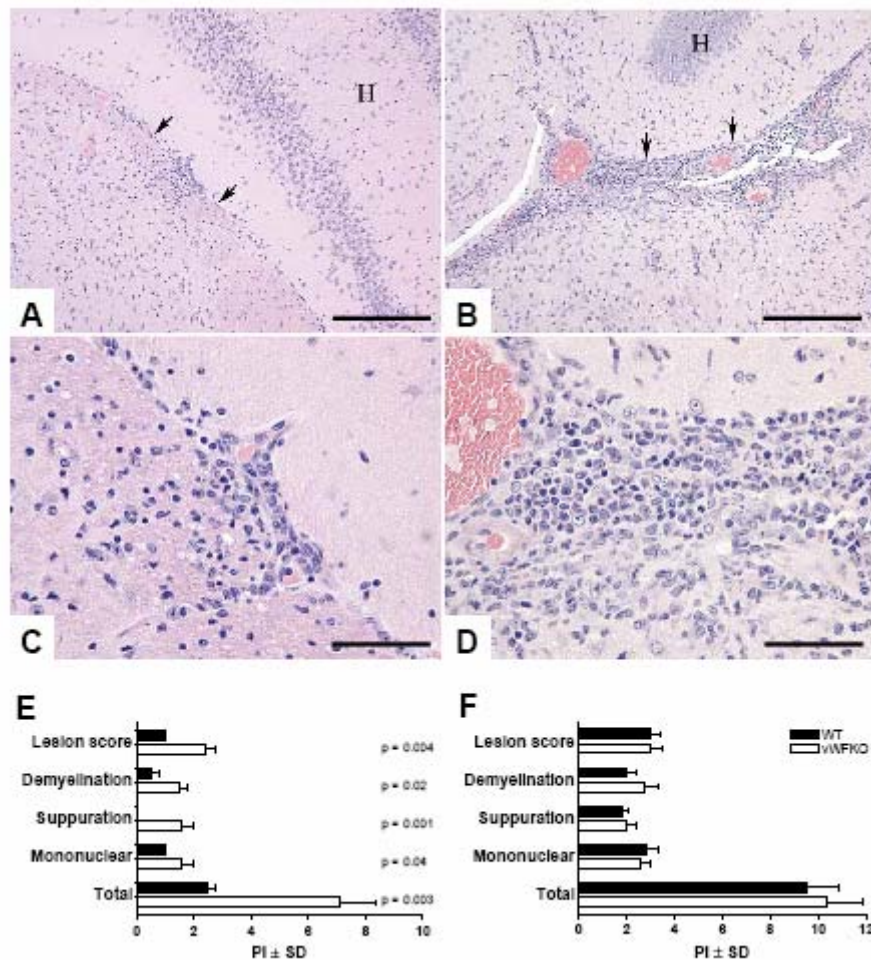


Figure 3. Severe histopathological EAE in VWFKO brain.

Comparison of the histopathologic lesions caused by EAE in the brains of B6 (**A, C**) and VWFKO (**B, D**) strains of mice. Note the minimal inflammatory response around capillaries and post capillary venules in the interface area between the brainstem and hippocampal formation (H) in the B6 brain than the marked inflammatory response in VWFKO brain. The inflammatory cells consisted of an admixture of lymphocytes and monocytes with occasional neutrophils and rare eosinophils. There was no primary demyelination in these areas of inflammation in B6 while minimal to mild primary demyelination was observed in VWFKO brain. H&E stain, scale bar = 200 μ m. (**B and D**) higher magnification of B6 and VWFKO mouse brain, respectively. H&E stain, scale bar = 200 μ m. Quantification of lesion severity in B6 and VWFKO mice revealed that the lesions in the brains (**E**) but not in SC (**F**) of MOG₃₅₋₅₅+CFA+PTX immunized VWFKO mice are more severe compared to WT controls. Significance of differences was determined using the Student's t-test.

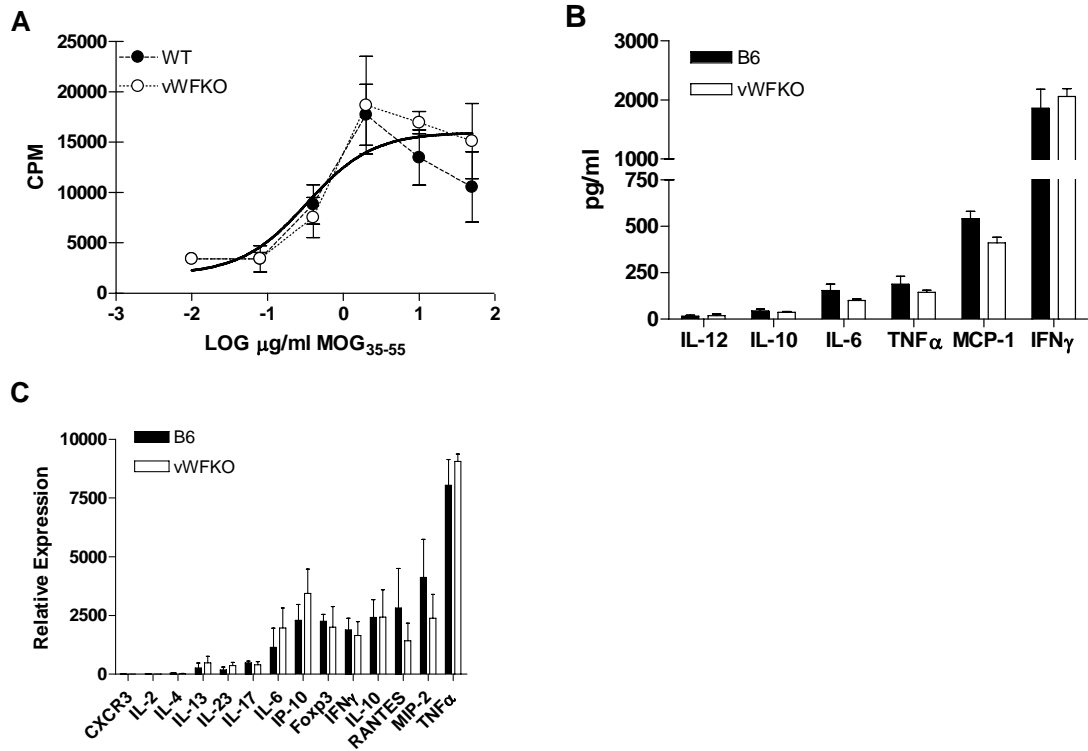


Figure 4. Normal T cell responses in EAE induced B6 and VWFKO mice.

(A) B6 and VWFKO CD4 T cells have equivalent *ex vivo* proliferative responses to MOG₃₅₋₅₅ ten days following immunization with MOG₃₅₋₅₅+CFA+PTX. Mean CPM \pm SD were calculated from triplicate wells. (B) Production and/or (C) expression of cytokines/chemokines by MOG₃₅₋₅₅ stimulated splenocytes does not differ between B6 and VWFKO mice immunized with MOG₃₅₋₅₅+CFA+PTX ten days earlier. Cytokine production was determined by ELISA or cytometric bead assay and the expression were determined by real time RT-PCR. Significance of differences between B6 and VWFKO CD4 T-cells responses was determined using the Student's t-test with a p-value of 0.05 as the significance threshold.

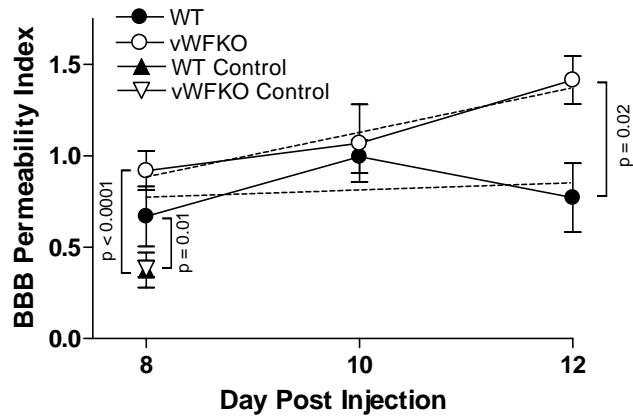


Figure 5. VWFKO mice exhibit increased BBB permeability compared to B6 mice following injection with MOG₃₅₋₅₅+CFA+PTX.

The permeability indices were calculated by determining the fluorescence in the CSF and the plasma collected 4h after i.v. injection of FITC-BSA and is the ratio of the fluorescence intensity of the CSF divided by the fluorescence intensity of the plasma. Changes in BBB permeability differ significantly over time ($F = 5.61$; $p = 0.02$).

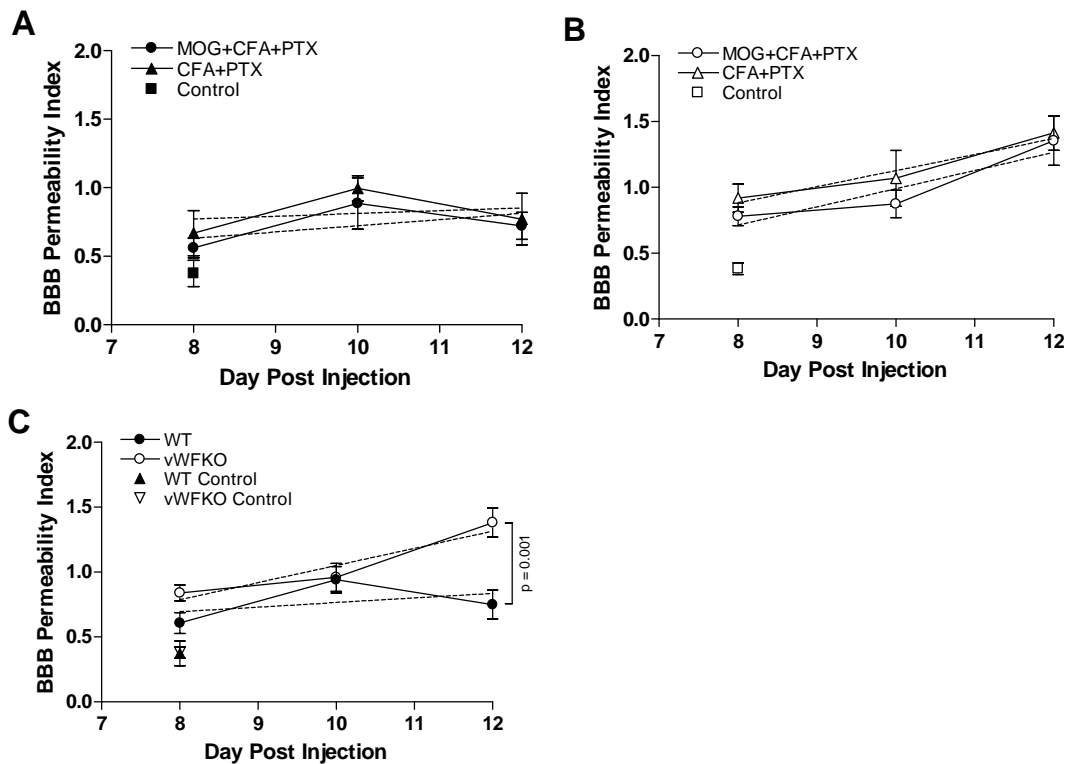


Figure 6. Increased BBB permeability in VWFKO mice is independent of encephalitogenic T cells.

BBB permeability in MOG₃₅₋₅₅+CFA+PTX and CFA+PTX immunized B6 (A), VWFKO mice (B). There was no difference in BBB permeability by treatment ($p = 0.45$) or over time ($p = 0.08$) in B6 animals while there was a significant difference in vWFKO animals over time ($p = 0.003$) but not by treatment ($p = 0.47$). Since there was no difference between MOG₃₅₋₅₅+CFA+PTX and CFA+PTX immunized animals, the data was pooled and re-analyzed (C). Changes in BBB permeability differ significantly over time between B6 and VWFKO mice ($p = 0.001$).

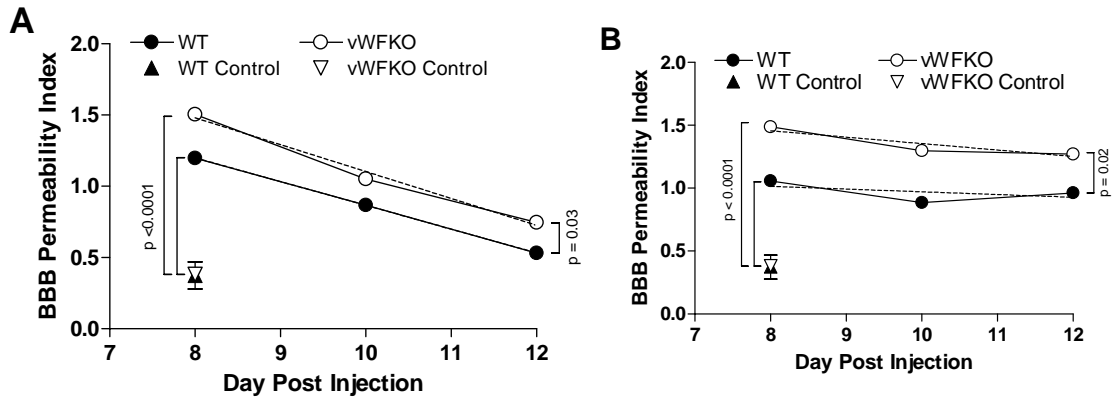


Figure 7. BBB compromise and repair by endothelial cells differs depending on the peripheral inflammatory stimulus.

BBB permeability in WT and VWFKO animals immunized with CFA alone (A), and PTX alone (B). Changes in BBB permeability differ significantly between WT and VWFKO mice ($p < 0.05$).

Figure 8

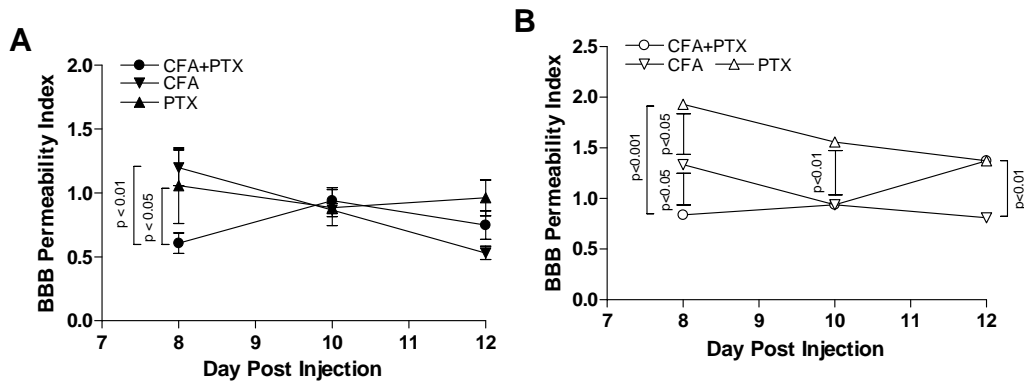


Figure 8. Comparison of BBB permeability in animals immunized with components of adjuvants either alone or in combination.

BBB indices in B6 (A) and VWFKO mice (B) immunized with CFA or PTX or both CFA+PTX. The p-values for the different interactions are shown.

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