Identification of *Orch3*, a Locus Controlling Dominant Resistance to Autoimmune Orchitis, as Kinesin Family Member 1C

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Abstract

Experimental autoimmune orchitis (EAO), the principal model of non-infectious testicular inflammatory disease, can be induced in susceptible mouse strains by immunization with autologous testicular homogenate and appropriate adjuvants. As previously established, the genome of DBA/2J mice encodes genes that are capable of conferring dominant resistance to EAO, while the genome of BALB/cByJ mice does not and they are therefore susceptible to EAO. In a genome scan, we previously identified Orch3 as the major quantitative trait locus controlling dominant resistance to EAO and mapped it to chromosome 11. Here, by utilizing a forward genetic approach, we identified kinesin family member 1C (Kif1c) as a positional candidate for Orch3. Mechanistically, we showed that the resistant Kif1c*D2 allele leads to a reduced antigen-specific T cell proliferative response as a consequence of decreased MHC class II expression by antigen presenting cells, and that the P578 → P578 and S1027 → P1027 polymorphisms distinguishing the BALB/cByJ and DBA/2J alleles, respectively, can play a role in transcriptional regulation. These findings may provide mechanistic insight into how polymorphism in other kinesins such as KIF21B and KIF5A influence susceptibility and resistance to human autoimmune diseases.

Introduction

Experimental autoimmune orchitis (EAO) is a model of idiopathic male infertility mediated by autoreactive T cells [1,2]. It can be induced in mice by active immunization with mouse testicular homogenate (TH) emulsified in complete Freund’s adjuvant (CFA) and *Bordetella pertussis* toxin (PTX) [3]. In genetically susceptible mice, the inflammatory lesions comprised of monocytes, macrophages, lymphocytes, neutrophils, and eosinophils are mainly found in the seminiferous tubules of the testes in association with aspermatogenesis [3]. We previously have shown that MHC class II restricted CD4⁴ T cells are the primary effectors in autoimmune orchitis [4,5]. However, recent evidence suggests the involvement of CD8⁵ T cells during the onset and maintenance of chronic inflammation [6,7].

Various strains of inbred mice respond differently to EAO induction, indicating that susceptibility is genetically controlled. Previously, it was shown that BALB/cByJ (CB6J) mice are highly susceptible to EAO [8] whereas DBA/2J (D2) and (CB6J×D2F1) hybrids (CD2F1) are resistant [3,9]. This demonstrates that resistance to EAO is inherited as a dominant phenotype in this strain combination. Additionally, resistance can be adoptively transferred to CB6J mice with CD2F1 primed splenocytes [10]. Therefore, the factors that regulate EAO resistance appear to be governed by an immune-mediated dominant negative mechanism.

Genome exclusion mapping was utilized to map the immunosuppressive genes regulating dominant resistance to EAO [10] with significant linkages to multiple loci residing on chromosomes (Chr) 1 and 11 [10]. Of these, *Orch3* on Chr11 displayed the most significant linkage and accounted for the majority of disease resistance seen in D2 mice.

In this study, congenic mapping was employed to restrict *Orch3* to a ~1.3 Mb interval that identified *Kif1c* (kinesin family member 1c) as a positional candidate. By generating CB6J.CD11B-Kif1c*¹²* transgenic (Tg) mice, we demonstrated that *Kif1c* underlies *Orch3*. Mechanistically, we showed that the resistant *Kif1c*¹² allele leads to reduced antigen (Ag)-specific T cell responsiveness as a consequence of decreased MHC class II expression by myeloid cells, and that the L¹⁷⁶ → P¹⁷⁶ and S¹⁰²⁷ → P¹⁰²⁷ polymorphisms distinguishing the CB6J and D2 alleles, respectively, can play a role in regulating gene transcription.
Results

Congenic mapping of Orch3

In the genome scan in which Orch3 was identified, D11Mit219, D11Mit10, and D11Mit118 exhibited the most significant linkage [10]. As the first step in the positional-candidate gene cloning of Orch3, we used marker-assisted selection to introgress the Orch3 allele onto the susceptible CB1J background. Next, we generated overlapping interval specific recombinant congenic (ISRC) lines (Figure S1 and Figure S2) and studied them in a stepwise fashion for susceptibility and resistance to EAO (Figure 1). Importantly, since resistance to EAO is inherited as a dominant trait in CD2F1 mice [10], the pathology indices (PI) between homozygous and heterozygous congenic lines were not significantly different (data not shown), the data were pooled for each line. Control parental CB1J mice were clearly susceptible to EAO, whereas D2 and CD2F1 hybrid mice [10], and the pathology indices (PI) between orch3 heterozygous and homozygous congenic lines were not significantly different (data not shown), the data were pooled for each line. Control parental CB1J mice were clearly susceptible to EAO, with an average PI of 4.0, whereas D2 and CD2F1 hybrid mice were resistant, with an average PI of 0.1 and 0.8, respectively (Figure 2). C.D2-8 exhibited the most significant linkage with an average PI of 0.1 and 0.8, respectively with an average PI of 4.0, whereas D2 and CD2F1 hybrid mice were resistant, with an average PI of 0.1 and 0.8, respectively (Figure 2). C.D2-8 were resistant, with an average PI of 0.1 and 0.8, respectively whereas D2 and CD2F1 hybrid mice

EAO (Figure 3). Statistically significant differences in EAO susceptibility between D2 mice and Orch3 mice rendered animals autoimmune orchitis resistant, demonstrating that Orch3 is Orch3. We propose that Klf1c plays an immunoregulatory role by controlling the levels of MHC class II in antigen presenting cells and consequently impacting autoreactive orchogenic T cell responses. These finding are particularly relevant since polymorphism in other kinesins such as Klf18 and Klf5A have been associated with susceptibility and resistance to human autoimmune disease.

Figure 1. Histopathology of autoimmune orchitis. (A, C) Cross section of normal testis histology in an immunized C.D2-3 mouse: (A) Seminiferous tubules appear normal; (C) A seminiferous tubule (ST) containing normal meiotic spermatocytes and spermatids, with intact tubular boundary (arrows). (B, D) CB1J mouse with sever and diffuse orchitis: (B) All seminiferous tubules are necrotic and have lost cell nuclear staining; (D) Sever orchitis in one seminiferous tubule (arrows) that contains numerous neutrophils and occasional multinuclear giant macrophages (double arrow); the tubular boundary (arrows) is poorly defined. (H&E; A and B, ×4; C and D, ×40).

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CByJ.CD11B-Klf1c/D2 Tg (Tg-Klf1c/D2) mice are resistant to EAO

To confirm that Klf1c was the most likely candidate gene for Orch3 and to definitively exclude Nlp1a/b as a positional candidate, we generated overlapping sub-ISRC congenic lines across the C.D2-3.2 interval and studied them for susceptibility to EAO (Figure 3). Statistically significant differences in EAO susceptibility between C.D2-3.2, C.D2-3.2c and CB1J mice were observed (Figure 3, right panel). In contrast, the severity of EAO in C.D2-3.2a and C.D2-3.2b was not significantly different from that of CB1J mice. Moreover, dominant resistance co-segregated with Orch3 as evidenced by the fact that no significant difference in the PI between homozygous and heterozygous mice was detected across all congenic lines studied (Figure 2 and Figure 3). Taken together, these data support the hypothesis that Klf1c is the positional candidate locus of immunological relevance within the interval, the second gene being kinesin family member 1C (Klf1c).

Author Summary

Although the etiology of autoimmunity is not well known, a variety of studies have demonstrated that genetic predisposition is a major contributor to disease susceptibility and resistance. The major histocompatibility complex (MHC) is the primary genetic determinant of autoimmune disease susceptibility with multiple additional interacting loci required. However, the identification and characterization of non–MHC genes has been problematic, since most autoimmune diseases are polygenic with the individual genes exhibiting only partial or minimal penetrance. We previously identified Orch3 (mouse chromosome 11) as the most important immune-suppressive locus controlling dominant resistance to autoimmune orchitis, the principal animal model of non-infectious testicular inflammatory/autoimmune disease. Here, using congenic mapping, we identified kinesin family member 1C (Klf1c) as a positional candidate for Orch3. Furthermore, expression of the Klf1c resistant allele in susceptible mice rendered animals autoimmune orchitis resistant, demonstrating that Orch3 is Orch3. We propose that Klf1c plays an immunoregulatory role by controlling the levels of MHC class II in antigen presenting cells and consequently impacting autoreactive orchogenic T cell responses. These findings are particularly relevant since polymorphism in other kinesins such as Klf18 and Klf5A have been associated with susceptibility and resistance to human autoimmune disease.
Figure 2. Congenic mapping places Orch3 within the Kif1c/Nlrp1a/b/c interval. For convenience, D2 alleles have been shaded. The significance of differences in severity of EAO among CByJ, CD2F1 hybrids and CD2-ISRC lines was determined using the Kruskal-Wallis test (overall p-value<0.0001) followed by Dunn’s multiple comparison test. Region outlined in blue depicts the location of Orch3.

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Figure 3. Identification of Orch3 as Kif1c. (CD2-3.2 ×CByJ) × CByJ backcross mice were screened from recombinants using microsatellite markers spanning the Orch3 interval. Three sub-ISRC lines were identified, fixed and homozygous progeny studied for susceptibility to EAO (D = D2 allele; C = CByJ allele). The significance of differences in EAO among CByJ, CD2-3.2a, CD2-3.2b, CD2-3.2c and Tg-Kif1cD2 transgenic mice was determined using the Kruskal-Wallis test (overall p-value<0.0001) followed by Dunn’s multiple comparison test (**p<0.01). Region outlined in red reflects location of Orch3 based on high resolution congenic mapping relative to the lower resolution mapping outlined in blue.

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together, these data restrict Oenk to a ~1.3 Mb interval distal of D11Mit298 (69339966–69340164) and proximal of D11Ds30 (70552627–70552762) which includes Kif1c but not Niph1b and Niph1b [Figure 3, left panel], thereby excluding them as positional candidates for Oenk.

Given the role of Kif1c in macrophage function [15], and that kinesins have been implicated in antigen processing and presentation [16], we decided to directly test the hypothesis that Oenk is Kif1c. We generated a transgenic mouse line that selectively expressed the resistant Kif1cD2 allele on the susceptible CB07 background using the human CD11b/ITGAM regulatory elements for macrophage/myeloid-specific expression of Kif1cD2 (Figure 4A).

The expression of the transgene did not affect macrophage/myeloid cell generation or homeostasis as similar percentages of splenic F4/80+ (Figure 4B) and CD11b+ cells (Figure 4C) were detected on Tg-Kif1cD2 mice compared to negative littermate control (NLC) mice. In addition, no differences in the expression of CD40 or CD86 were observed between strains at baseline (data not shown). Compared to NLC, greater Kif1c protein expression was seen in thioglycolate-induced Tg-Kif1cD2 cells (Figure 4D).

Despite the existence of polymorphisms upstream of Kif1c in potential regulatory regions (http://phenome.jax.org/), we did not observe differences in Kif1c expression at the mRNA level between the Kif1cCB07 and Kif1cD2 alleles (Figure 4E). NLC and Tg-Kif1cD2 mice were studied for susceptibility to EAO. The expression of Kif1cD2 in CD11b+ cells protected susceptible CB07 mice from developing EAO (Figure 3, right panel). This finding establishes Kif1c as being Oenk.

Tg expression of Kif1cD2 downregulates MHC class II expression and antigen presenting function of CD11b+ cells

To better understand the mechanism of resistance to EAO conferred by Kif1cD2, microarray analyses were performed on CD11b+ cells from NLC and Tg-Kif1cD2 mice. Using a false discovery rate (FDR) cutoff of 0.05, we determined that 164 genes were differentially expressed between NLC and Tg-Kif1cD2 CD11b+ cells (Table S1). An analysis for functional inference using Ingenuity Pathway Analysis (Ingenuity Systems, www.ingenuity.com) revealed that helper cell differentiation was the most significant pathway influenced by Kif1c (p<2.80 E-10; Figure S3 and Table S2). In addition, 18 of the top 20 pathways implicated a role for MHC class II, including antigen presentation. Indeed, compared to NLC CD11b+ cells, we observed a marked down regulation in MHC class II gene expression by Tg-Kif1cD2 CD11b+ cells (Table S1 and Figure 5A, dark blue dots). This is consistent with the role of kinesin as the motor that drives MHC class II to the plus end of microtubules toward the cell surface [16].

To corroborate diminished class II expression, flow cytometric analysis was performed using naïve TCRβCD19+CD11b+ splenocytes. The results presented in Figure 5B show lower MHC class II expression on Tg-Kif1cD2 cells compared to NLC, D2, and CD2-3.2 mice. Despite the differences in MHC II expression, no significant difference in the proportion of total splenic CD11b+ cells was observed (Figure 4C). Therefore, expression of the transgene in CD11b+ cells negatively regulates MHC II protein levels.
controls susceptibility to autoimmune orchitis. CD11b represents the log2 fold change (Tg- to NLC) minus NLC for each gene. Dark blue data points indicate H2 genes that were downregulated in splenic CD11b+ cells of Tg-Kif1cD2 mice. (B) Flow cytometric analysis of the frequency of TCRβ CD19 CD11b+ myeloid cells expressing MHC II in the spleen of Tg-Kif1cD2, D2, D2-C3.2, and NTC. Statistical significance was determined using the Kruskal-Wallis test (overall ***p-value<0.0001) followed by Dunn’s multiple comparison test (**p<0.01, *p<0.05). Data represent the mean ± SEM of at least 5 individual mice. doi:10.1371/journal.pgen.1003140.g005

Amino acid polymorphisms at residues 578 and 1027 on the C-terminal end of Kif1c regulate its function

Kif1c alleles possess amino acid substitutions at residues 578, 1027, and 1066 [17]. Four haplotypes have been identified: LSS (Kif1cLSS), PSS, PPS, and PPY (Kif1cPPY). In addition, it has been shown that the C-terminal region of KIF1c is involved in protein-protein interactions and cargo function [17–20]. Therefore, substitutions at 578, 1027, and/or 1066 may have a significant impact on Kif1c function. Given that KIF17b has been shown to control CREM-dependent transcription by regulating the intracellular location of the transcriptional coactivator ACT (activator of CREM in testis) [21,22], and CREM binding to the Il2 promoter suppresses its activity [23], we evaluated the effect of LSS Kif1cKif1cCByJ and PPY Kif1cKif1cD2 alleles on Il2 transcriptional activity as an in vitro assay of KIF1c allelic function. Jurkat cells were co-transfected with a plasmid containing the PPY Kif1cKif1cD2 allele, the LSS Kif1cKif1cCByJ allele, or an empty plasmid, and an Il2-promoter luciferase reporter. Cells were then activated with phorbol myristate acetate (PMA) and a control CREM-dependent transcription by regulating the intracellular location of the transcriptional coactivator ACT (activator of CREM in testis) [21,22], and CREM binding to the Il2 promoter suppresses its activity [23], we evaluated the effect of LSS Kif1cKif1cCByJ and PPY Kif1cKif1cD2 alleles on Il2 transcriptional activity as an in vitro assay of KIF1c allelic function. Jurkat cells were co-transfected with a plasmid containing the PPY Kif1cKif1cD2 allele, the LSS Kif1cKif1cCByJ allele, or an empty plasmid, and an Il2-promoter luciferase reporter. Cells were then activated with phorbol myristate acetate (PMA) and calcineurin, a calcium ionophore, and the luciferase activity quantified. Jurkat cells that were transfected with the plasmid containing the PPY Kif1cKif1cD2 allele displayed significantly decreased luciferase activity (mean decrease 31.46±0.59%, P=0.03) as compared to the plasmid containing the LSS Kif1cKif1cCByJ allele or the control plasmid (Figure 7A). These data demonstrate the functionality of the KIF1c structural polymorphism.

To further characterize the amino acid(s) responsible for the observed differences on Il2-promoter activity associated with the alleles, we replaced the D2-P578→L578 (LPY-KIF1c) or D2-I1027→S1027 (PSY-KIF1c) mutants resulted in increased Il2-promoter luciferase activity compared to the D2 PPY-KIF1c allele. Taken together, our data demonstrate that structural polymorphisms at position 578 and 1027 are critical for KIF1c allelic functions.

Discussion

EAO is an organ-specific autoimmune disease that is a model of immunological male infertility [1,2]. We previously demonstrated...
that genetic control of EAO is complex and involves both H2-linked (Orch1) and non-H2-linked (Orch3, Orch4, and Orch5) genes [24,25]. The H2-linked immune response genes primarily control susceptibility to EAO, whereas the non-H2-linked genes suppress the phenotypic expression of disease associated with a susceptible Orch1/H2 allele [9]. Here we report the identification of Orch3 as Kif1c that suppresses EAO by decreasing MHC class II expression and impairing APC function. Importantly, Kif1c may be a shared-autoimmune gene controlling susceptibility to experimental allergic encephalomyelitis (EAE) [26]. Eae7, Eae22, and Eae23 are linked to Orch3 [27], and CByJ and D2 mice are susceptible and resistant to EAE, respectively [28].

With the exception of tyrosine kinase-2 (Tyrk2), in which a rare single nucleotide polymorphism in a well conserved APE motif within the pseudokinase domain is fully penetrant in controlling susceptibility to autoimmune diseases [29,30], the vast majority of non-MHC autoimmune loci identified to date are QTL that exhibit only partial to minimal penetrance. This has proven to be problematic as researchers have attempted to positionally clone such genes [31]. The fact that Orch3/Kif1c controls a dominant negative immunoregulatory mechanism that suppresses autoimmune orchitis with a high degree of penetrance [31,32], and characterizes such genes [31], the fact that Orch3/Kif1c (grey bar) alleles, or control plasmid (black bar), or (B) Kif1cD2 (PPY; open bar), mutant 578 (LPY; left striped bar), or mutant 1027 (PSY; right striped bar) plasmids, and I/2 promoter luciferase reporter. Cells were stimulated for 3 hours with PMA and calcineurin, and the luciferase activity was quantified. Data are representative of two independent experiments. doi:10.1371/journal.pgen.1003140.g007

Materials and Methods

Ethics statement

Mice were housed at 25°C with 12/12-h light-dark cycles and 40–60% humidity. The experimental procedures performed in this study were under the guidelines of the Animal Care and Use Committees of the University of Vermont (Burlington, VT) and University of Illinois at Urbana-Champaign (Urbana, IL).

Animals

BALB/cByJ (CBJ), DBA/2J (D2), and (BALB/cByJ×DBA/2J) F1 hybrid (CD2F1) mice were purchased from The Jackson Laboratory (Bar Harbor, ME). The congenic lines in this study were generated using (BALB/cAnPt×DBA/2Ncr)×BALB/cAnPt backcross mice [45]. Third generation backcross mice heterozygous at Evi2 or at Hba and Es3 were selected and backcrossed for six generations to BALB/cAnPt mice and fixed by brother-sister mating to generate the C.D2-Evi2 and C.D2-Hba/Es3 lines. Overlapping interval specific recombinant congenic (ISRC) lines were generated by crossing C.D2-Evi2 mice to CByJ mice. F2 hybrids were genotyped using tail snip DNA and PCR with Chr11 microsatellite markers discriminating CByJ and D2 mice across the Orch3 candidate interval. Founders were analyzed for background contamination at a density of 2–5 cM and mice

Figure 7. Structural polymorphisms at amino acid residues 578 and 1027 influence Kif1c function. Jurkat cells were co-transfected with a plasmid containing the (A) Kif1cD2 (open bar), Kif1cCByJ (grey bar) alleles, or control plasmid (black bar), or (B) Kif1cD2 (PPY; open bar), mutant 578 (LPY; left striped bar), or mutant 1027 (PSY; right striped bar) plasmids, and I/2 promoter luciferase reporter. Cells were stimulated for 3 hours with PMA and calcineurin, and the luciferase activity was quantified. Data are representative of two independent experiments. doi:10.1371/journal.pgen.1003140.g007

Kinesin family members are involved in the activation of immune cells and inflammatory responses [38,39], and autoimmune disease GWAS identified KIF21B and KIF5A as candidates for autoimmune disease genes [40,41], suggesting an immunoregulatory role for kinesin family members. In addition, kinesin proteins have been identified as the major molecular motor of microtubule-based intracellular transport [42]. Kif1c is expressed in a variety of tissues [43] and overexpression of a dominant negative form disrupts molecular motor-dependent Golgi-to-Endoplasmic Reticulum (ER) retrograde vesicular transport [18]. It is known that Kif1c alleles possess amino acid substitutions at residues 578, 1027, and 1066 [17]. Here, we demonstrated that residues 578 and 1027 are functionally significant. Although the amino acid polymorphism at residue 1027 is not in an evolutionarily conserved domain [17], it is in the C-terminal region believed to participate in cargo binding. In fact, alterations of this domain have been shown to modify virulence kinesin protein function [19]. Moreover, it has been shown that the C-terminal tail domain of KIF1c (amino acids 811–1090) is involved in the interaction with bicaudal-D-related protein 1 (BDRP1) and this interaction regulates secretory transport required for neurite development [20]. Therefore, the ability of Kif1c to bind and transport cargo may be altered by polymorphism in this region. However, motor-dependent Golgi-to-ER transport functions normally in Kif1c knockout mice [44]. Immunohistochemical staining partially co-localized KIF1c with the Golgi marker CTR433, suggesting that KIF1c may also be involved in transport around the Golgi apparatus rather than only Golgi-to-ER transport. Accordingly, Wubbolts, et. al. [16] showed that kinesin plays a role in the vesicular transport of MHC II-containing lysosomes from the microtubule organizing center region towards the cell surface. Here, we provide evidence that the resistant Kif1cD2 allele negatively regulates the expression of MHC II proteins on APCs, since Tg-Kif1cD2 CD11b+ cells express lower mRNA and protein levels. The reduction in MHC II expression by CD11b+ Tg-Kif1cD2 cells was directly correlated with impaired antigen presentation as reflected by diminished Ag-specific T cell proliferative response. Whether amino acids at position 578 and 1027 on Kif1c are involved in MHC II expression is currently under investigation. Taken together, our results nevertheless provide mechanistic insight into how polymorphism in other kinesins including KIF21B and KIF5A influence human autoimmune disease susceptibility.
FACS sorting and flow cytometric analysis

NLC and Tg-Kif1c<sup>Δ2</sup> myeloid cells from erythrocyte-free spleens were first enriched by negative selection (using magnetic beads, Qiagen, Hilden, Germany) to deplete cells expressing CD8, CD4, and IgM. For FACS isolation, negatively selected enriched-myeloid cells were stained with anti-CD11b-Pacific Blue (BD Pharmingen, Franklin Lakes, NJ), anti-CD11c-PE-Cy5.5 (Invitrogen, Camarillo, CA), anti-TCRβ-FITC, and anti-IA/IE-PE (eBioscience, San Diego, CA), and sorted on a FACSAria (BD Biosciences, San Jose, CA) by gating in the TCRβ<sup>+</sup>/IE<sup>+</sup>CD11c<sup>+</sup>CD11b<sup>+</sup> myeloid cell population. Antibodies against B220 and CD19 (eBioscience) were also used for flow cytometry.

Microarray analysis

Total RNA was extracted and purified from TCRβ<sup>+</sup>/IE<sup>+</sup>CD11c<sup>+</sup>CD11b<sup>+</sup> myeloid cells from naive NLC and Tg-Kif1c<sup>Δ2</sup> mice (n = 6 to 10 mice/strain) using RNeasy isolation reagent (Qiagen Inc.). Purified RNA was quantified using a Nanodrop ND1000<sup>™</sup> spectrophotometer (Thermo Scientific, Wilmington, DE) and quality was assessed using an Agilent 2100 bioanalyzer (Agilent Technologies, Palo Alto, California). The RNA integrity number of all samples was greater than 8. For microarray analysis, two RNA pools were created so that each pool contained RNA from 3 to 5 mice, and two arrays per strain were analyzed.

RNA amplification and microarray analysis was performed at UVM Microarray Core Facility using previously described protocols [49]. Briefly, 2 μg of total RNA from each pooled sample were reverse transcribed to the single stranded cdDNA using T7-oligo(dT) primer. T4 DNA polymerase was used to synthesize double-stranded cdDNA, which served as a template for <i>in vitro</i> transcription using T7 RNA polymerase to produce biotinylated cdRNA. The biotinylated cdRNAs were fragmented into 50- to 200-base fragments and then hybridized to GeneChip Mouse Genome 430A 2.0 Arrays for 16 h at 45°C in a rotating Affymetrix GeneChip Hybridization Oven 320. After hybridization, arrays were washed and stained with streptavidin-phycocerythrin on an automated Affymetrix GeneChip Fluidic Station F450. The arrays were scanned with an Affymetrix GeneChip Scanner 2700 and the images quantified using Affymetrix GeneChip Operating Software.

The signal intensity for each probe on each chip was calculated from scanned images using GeneChip Operating Software (Affymetrix), and signal intensities were analyzed using BioConductor (http://www.bioconductor.org). Probe intensities were background corrected, normalized, and summarized using the Robust Multichip Average method described by Speed and coworkers [50,51]. An alternative normalization method based on reference genes did not significantly change the results. The FDR for differential expression between NLC and Tg-Kif1c<sup>Δ2</sup> for each individual gene was calculated using the method of Benjamini and Hochberg [52]. Gene expression data were analyzed using a threshold of FDR<sub>α</sub> of 0.05 to identify differentially expressed genes.

T cell stimulatory capacity of antigen presenting cells (APCs)

NLC and Tg-Kif1c<sup>Δ2</sup> mice were immunized at d0 and d7 s.c. in the posterior right and left flank and the scruff of the neck with a sonicated PBS/oil emulsion containing 20 μg of OVA, faction V (Sigma-Aldrich, St. Louis, MO), or 100 μg of PLP<sub>180-199</sub> in CFA supplemented with 200 μg of <i>Mycobacterium tuberculosis</i> H37Ra. Spleens and LN were harvested on d10. APCs from erythrocyte-free spleens were obtained by anti-CD4/anti-CD8 complement...
depletion and treated with mitomycin C (25 μg/ml; Sigma-Aldrich). Responder CD4 T cells from LN and spleens were isolated by negative selection as previously described [40]. Single cell suspensions of OVA- or PLP\textsubscript{180-199} APCs (2 × 10\textsuperscript{5} cells/well) and Ag-specific responder CD4 T cell (1 × 10\textsuperscript{5} cells/well) suspensions were prepared in RPMI 1640 (5% FBS), and plated on standard 96-well U-bottom tissue culture plates. Cells were stimulated with 1, 10, and 25 μg/ml of OVA or 2.5, 10, and 50 μg/ml of PLP\textsubscript{180-199} for 72 h at 37°C. During the last 18 h of culture, 1 μCi of [\textsuperscript{3}H] thymidine (PerkinElmer, Santa Clara, CA) was added. Cells were harvested onto glass fiber filters and thymidine uptake was determined with a liquid scintillation counter.

Preparation of Jurkat cells, transfection, stimulation, and luciferase assays

Jurkat cells were cultured in RPMI containing 10% FBS without stimulation for 24 hours at a concentration of 1 × 10\textsuperscript{6} cells/ml. Plasmids encoding Kif1c\textsuperscript{D2}, Kif1c\textsuperscript{CByJ} alleles, LPY-KIF1c and PSY-KIF1c mutants, corresponding empty vector (pcDNA, Invitrogen, Carlsbad, CA), II2 promoter (-575 to +57 base pairs) luciferase reporter, and control pGL2 luciferase reporter (Promega, Madison, WI) were used for transfection. Five micrograms of each plasmid were used for the transfection of approximately 5 × 10\textsuperscript{5} Jurkat cells by electroporation at 250 mV and 900 μF in 250 μl of RPMII with a BioRad electroporator (BioRad, Hercules, CA). Cells were subsequently cultured in RPMI and 10% FBS for 24 hours and then stimulated with PMA (10 ng/ml) and calcium ionophore calcimycin (0.5 μg/ml) for 3 hours. Cell lysates were prepared and supernatants collected to quantify luciferase activity was normalized using the β-galactosidase value.

Mutagenesis

Point mutations were introduced in the plasmid encoding the Kif1c allele from the D2 mouse using the QuickChange Site-Directed mutagenesis kit (Stratagene, USA). Briefly the plasmid was denatured and then annealed with the appropriate mutagenic primer that contained the desired mutation. Using Pfu DNA polymerase, new mutagenized strands were created. The parental DNA template was digested with DpnI and the new mutagenized plasmid was used to transform E. coli. The plasmid DNA was extracted using the Qiagen Maxi-Prep kit (Qiagen, Valencia, CA). The primers used for mutagenesis of the nucleotide at position 1033 (amino acid 578) of the D2 allele were: forward: 5'-GGCTGCGAAGGAGCTTGTTGCGTAGTGTCGTCGAC-3'; reverse: 5'-GACTTTCAAGCAGCAGTCCCAGGCTCACGAC-3'; and for the nucleotide at position 3079 (amino acid 1027): Forward: 5'GGAACACCCACGCTTCTCGGAGGATTTCCG-3', and Reverse: 5'GGGAATTCCCTTGGAGAACGGTGGGCTCTTCG-3'.

Supporting Information

Figure S1 Genealogy of the congenic and interval specific congenic lines used in this study. Third backcross generation (BALB/cAnPt\timesDBA/2NCr)\timesBALB/cAnPt mice heterozygous at Evi2 or at Hba and Evi3 were selected and backcrossed for six generations to BALB/cAnPt mice. Homozygous lines C.D2-Evi2 and C.D2-Hba/Evi3 were fixed by brother-sister mating. Overlapping interval specific recombinant congenic (ISRC) lines were generated by crossing C.D2-Evi2 mice to CByJ mice. F\textsubscript{2} hybrids were genotyped using tail sniff DNA and PCR with Chr11 microsatellite markers discriminating CByJ and D2 mice across the Orch\textsubscript{3} candidate interval [10]. Founders were analyzed for background contamination and mice carrying CByJ alleles at all background marker loci were backcrossed an additional two generations to CByJ mice. Homozygous C.D2-3, C.D2-5, C.D2-8, and C.D2-9 ISRC lines were fixed by brother-sister mating. Similarly, higher order resolution mapping panels of ISRC lines were generated by screening (C.D2-3×CByJ)×CByJ, (C.D2-8×CByJ)×CByJ, and (C.D2-3.2×CByJ)×CByJ backcross mice for recombinants.

Figure S2 Genotypes of congenic and interval specific congenic lines used in this study. Microsatellite and SNP based genotyping was done using tail sniff DNA and PCR [10]. Locations are as given on either Ensembl or MGI. Hba alleles were determined by isoelectric focusing as described in [53]. Dye marker and deletion mutation locations are as described in [54]. Evi2 and Evi3 alleles were determined as described in [55].

Figure S3 Illustration of the potential effect of altered MHC Class II expression on T helper (TH) cell differentiation. (Figure generated using Ingenuity Pathway Analysis, Ingenuity Systems. Green = expression decreased in Tg-Kif1c\textsuperscript{D2} relative to NLC).

Table S1 Genes differentially expressed between NLC and Tg-Kif1c\textsuperscript{D2} CD11b\textsuperscript{+} cells. TCR\textsuperscript{A} IA/IE\textsuperscript{C} CD11c\textsuperscript{+} CD11b\textsuperscript{+} myeloid cells were harvested from naïve NLC and Tg-Kif1c\textsuperscript{D2} mice and differential gene expression was detected using Affymetrix GeneChip Mouse Genome 430A 2.0 Arrays. \textsuperscript{1}Chr = chromosome. \textsuperscript{2}logFC = log\textsubscript{2} signed fold change.

Table S2 Transgenic expression of Kif1c\textsuperscript{D2} on CD11b\textsuperscript{+} cells influences pathways involving MHC Class II (genes in bold). TCR\textsuperscript{A} IA/IE\textsuperscript{C} CD11c\textsuperscript{+} CD11b\textsuperscript{+} myeloid cells were harvested from naïve NLC and Tg-Kif1c\textsuperscript{D2} mice and differential gene expression was detected using Affymetrix GeneChip Mouse Genome 430A 2.0 Arrays. Pathway analysis was conducted using Ingenuity Pathway Analysis software (Ingenuity Systems, www.ingenuity.com). To ensure biological relevance, cell type was restricted to B-cells, dendritic cells, and macrophages.

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Author Contributions

Conceived and designed the experiments: RdR RDM NDM GCT CT. Performed the experiments: RdR RDM NDM VCK. Analyzed the data: RdR EHW JPB KSKT VCK GCT CT. Wrote the paper: RdR EHW CT.
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