CD5-Dependent CK2 Activation Pathway Regulates Threshold for T Cell Anergy

Christine M. Sester, Donald J. McGuire, Patrizia De Sarno, Emily C. Brantley, Gloria Soldevila, Robert C. Axtell and Chander Raman

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CD5-Dependent CK2 Activation Pathway Regulates Threshold for T Cell Anergy

Christine M. Sestero,* Donald J. McGuire,† Patrizia De Sarro,‡ Emily C. Brantley,§ Gloria Soldevila,¶ Robert C. Axtell,‖ and Chander Raman*†‡

CD5 activates casein kinase 2 (CK2), a serine/threonine kinase that constitutively associates with the CK2-binding domain at the end of its cytoplasmic tail. To determine the physiological significance of CD5-dependent CK2 activation in T cells, we generated a knock-in mouse that expresses a CD5 protein containing a microdeletion with selective inability to interact with CK2 (CD5ΔCK2BD). The levels of CD5 on developing and mature T cell populations from CD5ΔCK2BD mice and CD5 wild-type (WT) mice were similar. The thymus of CD5ΔCK2BD mice contained fewer double-positive thymocytes than that of both CD5WT and CD5 knockout (KO) mice, although the numbers of all other immature and mature T cell populations were unaltered. CD5ΔCK2BD T cells hypoproliferated and exhibited enhanced activation-induced cell death when stimulated with anti-CD3 or cognate peptide in comparison with CD5WT T cells. We also found that functional CD5-dependent CK2 signaling was necessary for efficient differentiation of naive CD4+ T cells into Th2 and Th17 cells, but not Th1 cells. We previously showed that experimental autoimmune encephalomyelitis (EAE) in CD5KO mice was less severe and delayed in onset than in CD5WT mice. Remarkably, CD5ΔCK2BD mice recapitulated both EAE severity and disease onset of CD5KO mice. Increasing the immunization dose of myelin oligodendrocyte glycoprotein 35–55 peptide, a model that mimics high-dose tolerance, led to decreased severity of EAE in CD5WT mice but not in CD5KO or CD5ΔCK2BD mice. This property was recapitulated in in vitro restimulation assays. These results demonstrate that CD5–CK2 signaling sets the threshold for T cell responsiveness and is necessary for efficient generation of Th2 and Th17 cells. The Journal of Immunology, 2012, 189: 000–000.

The cell surface glycoprotein CD5 has a well-recognized function as a negative regulator of Ag receptor activation in lymphocytes (1, 2). In mice, the receptor is constitutively expressed on developing and mature T cells, B-1a B cells, and the recently described CD1dαβ regulatory B cells (B10 cells) (3–5). Structurally, CD5 is closely related and linked in the genome to CD6 with an extracellular domain comprised of three group B scavenger receptor cysteine-rich extracellular domains (6–10). Although several ligands have been proposed for CD5, none has been independently verified (9). In developing and mature T cells, expression levels of CD5 correlate with avidity and/or affinity of T cell Ag receptor and are dynamically altered by changes in threshold of Ag receptor activation (11, 12). Reciprocally, changes in CD5 expression levels alter T cell activation thresholds. Other mechanisms that control CD5 expression are GATA3 levels during thymocyte selection, TCR signaling and p56lck expression levels in peripheral T cells, and a NFAT-dependent Cd5 enhancer linked with BCR engagement in B-1a B cells (1, 11, 13–16).

The cytoplasmic tail of CD5 contains three phosphorylatable tyrosines, two of which are in a configuration resembling an ITAM/ITIM domain (9). The CD5-mediated negative regulation of Ag receptor activation is primarily ascribed to its ITIM domain (3, 17). The regulatory activity of CD5 raises the threshold for T cell activation to control response to Ag and discourage autoreactivity (18). Although CD5 is generally regarded as an attenuator of lymphocyte activation, it also serves to enhance T cell function with its unique role in supporting prosurvival signaling. Increased surface expression of CD5 protects autoreactive CD4+ T cells from Fas-mediated activation-induced cell death (AICD) and represents a mechanism through which T cells, otherwise destined for death following activation by a strong antigenic stimulus, can survive (19, 20). Although there is not yet a comprehensive understanding of the CD5-mediated pathways resulting in prosurvival signaling in T cells, an important emerging player in this process is casein kinase 2 (CK2), which constitutively associates with a CK2 binding domain located in the distal portion of the CD5 cytoplasmic tail...
(21, 22), CK2 is a serine/threonine kinase that is commonly expressed in all cell types and phosphorylates a large number of substrates to participate in a variety of cell regulatory and survival pathways (21–26).

The first evidence that a major biological activity exerted by CD5 is prosurvival in activated T cells came from the study of experimental autoimmune encephalomyelitis (EAE) in the CD5 knockout (KO) mouse (27, 28). Although CD4⁺ T cells in CD5KO mice responded more vigorously to immunization with myelin oligodendrocyte glycoprotein (MOG) 35–55 peptide, the onset and severity of EAE in these mice was less severe than in CD5 wild-type (WT) mice. The decreased severity in CD5KO mice was at least in part associated with enhanced AICD. This finding provided an insight into the mechanisms underlying the absence of spontaneous autoreactivity in the CD5KO mouse despite T cell hyperactivity. To determine whether the prosurvival activity was associated with the ability of CD5 to activate a CK2-regulated pathway, we reconstituted the CD5KO mouse with a T cell expression-restricted CK2 binding/activation-deficient CD5 transgene (CD5ΔCK2BD-Tg) (27). Remarkably CD5ΔCK2BD-Tg mice developed EAE with lower incidence and severity than did CD5WT mice and CD5KO mice reconstituted with a CD5WT transgene. T cells from CD5ΔCK2BD-Tg mice also exhibited elevated AICD.

The previous study clearly established that the CD5-dependent CK2 signaling pathway is important for survival of activated CD4⁺ cells and can impact the outcome of EAE in mice. However, a major limitation of the CD5ΔCK2BD-Tg mouse was that the transgene was under the control of the CD2 promoter and enhancer; therefore, the expression of CD5 could not be physiologically regulated by the threshold of Ag receptor activation. To resolve this problem and to study the biological activities of the CD5–CK2 signaling pathway, in this study we generated a CD5 knock-in mouse in which the nucleotides encoding the four amino acids (S458-D-S-S461) necessary for CK2 interacting with CD5 were deleted in the genome. Using this novel mouse model, we show that the CD5–CK2 signaling pathway plays a critical role in regulating the threshold for the development of TCR nonresponsiveness in vivo and in vitro. We further determined that the CD5–CK2 signaling pathway is essential for efficient CD4⁺ and CD8⁺ T cell activation and differentiation of naive CD4⁺ T cells to Th2 and Th17, but not Th1, cells. In summary, our results reveal the CD5–CK2 signaling pathway represents a major signaling cascade initiated by CD5 that regulates the threshold of T cell activation and Th differentiation.

**Materials and Methods**

**Mice**

C57BL/6 mice (CD5WT) were purchased from National Cancer Institute–Frederick Cancer Research. CD5⁻/⁻ were backcrossed >12 generations into C57BL/6 (CD5KO) mice from our colony (28). The 2D2 TCR MOG recombineering protocol described by Lee et al. (30). Briefly, homology arms A and B were used to retrieve the region of the Cd5 gene that contains exons 6–10 and several kilobases of the 3′ noncoding region into the pS-K-M-TKI targeting plasmid from the C57BL/6 bacterial artificial chromosome (BAC) clone RP24-424H1 (accession no. AC132247) (Fig. 1A). This BAC clone contains the entire Cd5 gene. Using a combination of bacterial recombineering and QuiChange mutagenesis (Stratagene), we targeted a loxp-flanked Neo selection cassette between exons 9 and 10 and deleted the codons encoding the four amino acids necessary for CK2 binding (CD5Δ2BD). S458–S461 (21, 22). The targeting construct was transfected into B-4 (C57BL/6) embryonic stem cells and screened by Southern blot analysis of BamHI-restricted DNA using a screening probe 5′ of the targeting construct (Fig. 1A). Insertion of the loxp-flanked Neo cassette created a novel BamH1 site between exons 9 and 10 that allowed for the identification of correctly targeted clones. The embryonic stem cells were microinjected into C57BL/6 albino blastocysts and implanted into pseudopregnant females. A male chimeras that successfully transmitted the targeted allele was bred with a C57BL/6.Eae-Cre mouse (The Mouse Laboratory) to delete the Neo cassette (Fig. 1A). The targeted allele could be readily distinguished from the Cd5⁺ allele by PCR using a forward primer 5′ of exon 9 (5′-ATGACTCCGCAAGTGCTG-3′) and a reverse primer 3′ of the loxP site, but 5′ of exon 10 (5′-CTTGTGAGGATGTTGCCA-3′) (Fig. 1B).

**Induction of active EAE**

EAE in male (8- to 10-wk-old) mice was induced and evaluated as described previously (28). MOG35–55 peptide was obtained from CPC Scientific (San Jose, CA) and pertussis toxin came from List Biological Laboratories (Campbell, CA).

**Flow cytometry**

Staining was performed on peripheral lymphoid populations and spinal cord cells prepared as described previously (27). For characterization of cellular populations the following Abs were used: anti–CD4-PerCP (GK1.5), anti–CD8-PE-Cy7 (53-7.3), anti–CD25-PE (PC61.5), anti–CD25-PE-Cy7 (53-7.3), anti–CD4-allophycocyanin–Alexa Fluor 750 (RMO4-5), anti–B220-PE-Cy5 (RA3-6B2), anti-Foxp3-aloophycocyanin (FJK-16s), anti–retinoic acid-induced orphan receptor (ROR)γt-PE (AFKGS-9) (eBioscience, San Diego, CA), anti–IL-23 (R&D Systems, Minneapolis, MN), anti–goat IgG (H+L)-Alexa Fluor 488 (Invitrogen, Carlsbad, CA), anti–pSTAT1 (Ser727), anti–pSTAT3 (Tyr705) (Cell Signaling Technology, Danvers, MA), anti–rabbit IgG (H+L)-Alexa Fluor 488 (Jackson ImmunoResearch, West Grove, PA), anti–CD69-biotin (H.1.2F3) (BD Biosciences Pharmingen), anti–B220-PerCP (RA3-6B2), anti–CD8α-Alexa Fluor 700 (53-6.7), anti–mouse–IFN-γ–PE (XM1.2), anti–mouse–IL-17a–Alexa Fluor 488 (TC11-18H10.1), and anti–mouse–IL-4–Alexa Fluor 647 (11B1) (BioLegend, San Diego, CA). In some cases we used the Alexa Fluor 647 or Alexa Fluor 488 protein labeling kits (Invitrogen) to label anti–CD4 (GK1.5), anti–CD8α (53-6.7), or anti–CD5 (53-7.3) Abs produced from hybridomas obtained from the American Type Culture Collection (Rockville, MD). For all immunofluorescent analyses, Fc receptors were blocked with anti–CD16/32 (2.4G2, FcR block; American Type Culture Collection) before any staining procedure, and live cells were gated using staining with CD45FITC, CD48v stain or LIVE/DEAD aqua dead cell staining kit (Invitrogen). All stained samples were analyzed using the FACSCalibur and LSRII flow cytometers (BD Biosciences). Intracellular cytokine staining in PMA and ionomycin-stimulated cultures was performed as reported previously (27). Intracellular staining for phosphorylated STAT1 and STAT3 was conducted using the protocol described by Cell Signaling Technology (http://www.cellsignal.com/support/protocols/Flow.html).

**In vitro T cell differentiation**

CD4⁺CD25⁺ T cells were purified from lymph nodes and spleens of naive mice by two-step magnetic chromatography using cell purification reagents from Invitrogen (Dynabeads) and StemCell Technologies (EasySep; Vancouver, BC, Canada). The CD4⁺ T cells were stimulated with anti–CD3 (1.0 µg/ml) or MOG35–55 peptide (10 µg/ml) in culture medium (IMDM, 10% FBS, 1% sodium pyruvate, 1% nonessential amino acids, and 0.5 mM 2-ME) with or without added cytokines. For Abs for expression analysis, 10 ng/ml IL-2 plus 5 µg/ml anti–IL-4 (11B1) for Th1-polarized, 10 ng/ml IL-4 plus 10 µg/ml anti–IFN-γ (XM1.2) for Th2-polarized, or 5 ng/ml TGF-β plus 20 ng/ml IL-6 plus 10 ng/ml IL-23 plus 10 µg/ml anti–IFN-γ plus 5 µg/ml anti–IL-4 for Th17-polarized cultures in the presence of irradiated APCs. All cytokines were purchased from eBioscience or BioLegend. Irradiated Thy1.2 cell-depleted splenocytes or 6 d bone marrow-derived dendritic cells were used as APCs.

**Cell proliferation, apoptosis measurement, lymphocyte activation, and calcium mobilization**

For these experiments “untouched” CD4⁺CD25⁺ T cells and CD8⁺ T cells were purified from spleens of naive mice or from mice immunized with 150 MOG35–55 peptide 7 d previously as described above. Proliferation was measured by two independent approaches, [³H]thymidine incorporation.
ELISA. ELISA kits were purchased from eBioscience or BioLegend. For the measurement of dividing cells, EdU (10 μM) was added for the last 1 h of the proliferation assay and its incorporation was measured using the Click-iT EdU flow cytometry assay (Life Technologies) following the manufacturer’s recommended protocol. In some experiments, EdU incorporation or CFSE dilution was determined after coculturing WT-CD5− or ΔCK2BD-CD5+ expressing CD4+ T cells and stimulating with anti-CD3 mAb or CD5SS+SS peptide as appropriate. To distinguish between the two different CD5-expressing T cells, T cells from one of the groups was labeled with CFSE (CFDA-SE; Molecular Probes, Eugene, OR) just prior to coculturing. Dilution of CFSE in labeled, dividing CD4+ T cells was also used to track cell division.

For the measurement of apoptosis, CD4+CD25+ or CD8+ T cells were stimulated with varying concentrations of CD5SS+SS peptide or anti-CD3 for different time periods, and in some instances under Th17 polarizing conditions. The cells were then stained with annexin V–FITC (BD Biosciences) and 7-aminoactinomycin D (7-AAD; BioLegend) to quantify apoptotic cells (annexin V+7-AAD− 1 or 7-AAD alone to quantify dying cells by flow cytometry. To evaluate upregulation of CD25 and CD69, splenic cells were stimulated with varying concentrations of anti-CD3 for different time periods and then immunofluorescently stained with Abs to CD4, CD25, and CD69. The upregulation of CD25 and CD69 in CD4+ gated T cells was determined by flow cytometry.

In vitro cultured CD4+ and CD8+ T cells in CD4+ T cells were measured in flow-4 AM (Invitrogen)-loaded spleen cells stimulated with anti-CD3. Single-cell suspensions of splenocytes were surface stained with anti-CD4 and resuspended to a concentration of 5 × 10⁶ cells/ml in HBSA++ plus 3% FBS. Cells were incubated with flow-4 AM for 30 min at 25°C, washed, and placed on ice. Samples were loaded onto the FACSCalibur and events were collected at a rate of 200–400 events/s. After establishing a 1 min baseline, 0.1–10 μg/ml anti-CD3 (145-2C11) was added to the samples and analysis continued for 7 min. At the end of this time period, 10 μM ionomycin was added to the samples and data collection was continued for an additional 2 min.

Quantitative real-time RTPCR
RNA was collected from cultured cells using TRIzol reagent and cDNA was generated with the SuperScript VILO cDNA synthesis kit (Invitrogen) following the manufacturer’s instructions. EXPRESS SYBR GreenER qPCR Supermix Universal (Invitrogen) was used to detect Rorc and Il23a mRNA expression. Expression of both mRNAs was calculated by normalizing data to Gapdh mRNA expression. Primers for Rorc (forward, 5′-CGCGTGAAGGGCTTACAC-3′, reverse, 5′-TGACGAGTGAGCCA-CATTACA-3′), Il23a (forward, 5′-GCCAAGAACATCCCCGGA-3′, reverse, 5′-TCAGTCGATCACTATGGAGGACA-3′), and GAPDH (forward, 5′-TGGTGAAGGTCCTGTCGAAC-3′, reverse, 5′-CATGTT-AGTTGAAGTCACTATGGG-3′) were obtained from Eurofins MWG Operon (Huntsville, AL). Relative gene expression was calculated using the comparative Ct method and examining fold differences in target gene expression for CD5SS or CD8 expression in naive mice that were sublethally irradiated 18 h earlier with 350 rad x-irradiation and then adoptively transferred with 5 × 10⁶ cells. CD4+CD25+CD69+ T cells were stained with PE-Cy5 anti-CD4, CD25, and CD69. The upregulation of CD25 and CD69 in CD4+ gated T cells was determined by flow cytometry.

To determine the biological role of CD5-dependent CK2 activation in T cell function, we generated a knock-in mouse in which the nucleotides encoding the four amino acids necessary for binding of CK2 with CD5 (S458–S461; CK2 binding domain or CK2BD) were deleted in exon 10 of the mouse Cd5 gene (Fig. 1A) (22). The gene-targeted mouse was bred with the C57BL/6.E2a-Cre mouse to delete theloxP-flanked Neo selection cassette to generate theCd5ΔDK2BDmice, hereafter referred to as the CD5ΔCK2BD mouse (Fig. 1B). The strength of this novel model is that the expression of CD5 remains under the control of the endogenous promoter and regulatory elements. This is a very important consideration because the CD5 level on T cells is dynamically regulated by changes in strength of TCR signals both during early development in the thymus and later in the periphery (9, 11). In our previous study the CD5-dependent CK2 signaling-deficient mouse was generated by reconstituting the CD5KO mouse with a mutant CD5-expressing transgene under the control of the CD2 promoter (27).

The mean expression levels of CD5 on all T cell populations in the thymus, lymph nodes, and spleens of CD5WT and CD5ΔCK2BD mice were similar (Fig. 1C and data not shown). We next examined the effect of loss of CD5-dependent CK2 signaling on developing T cell populations in the thymus and in mature CD4+ and CD8+ T cells in the spleen and lymph nodes. As previously reported, the proportion and absolute numbers of CD4+ and CD8+ expressing double-positive (DP) and single-positive T cells in CD5WT and CD5KO mice were similar (Fig. 1D, Table I) (32). In contrast, the thymus of CD5ΔCK2BD mice contained significantly fewer DP cells compared with both CD5WT and CD5KO mice (Table I). The DP population in CD5ΔCK2BD mice contained an expanded population of cells that were CD4+CD8−, possibly representing preapoptotic cells. During negative selection, DP thymocytes go through a transitional CD4+CD8− step just before undergoing apoptosis (33). Double-negative thymocytes were higher in the thymus of CD5ΔCK2BD mice compared with that in CD5WT or CD5KO mice (Fig. 1D). The proportion and numbers of CD4+ or CD8+ single-positive cells in the thymus of CD5ΔCK2BD mice were not significantly different from those in the thymus of CD5WT or CD5KO mice (Fig. 1D). The lower numbers of peripheral CD4+ T cells might be related to loss of survival as a result of inability to activate the CD5-dependent CK2 activation pathway. However, the presence of fewer follicular B cells in the spleen was unexpected, as they do not express detectable levels of CD5. We observed that the frequency of natural regulatory T cells (nTregs; CD4+CD25+Foxp33) in lymph nodes and spleens of CD5ΔCK2BD mice were similar (Supplemental Fig. 1A). However, these tissues in CD5KO mice consistently contained a greater number of Tregs than those in either CD5WT or CD5ΔCK2BD mice. This observation is consistent with that previously reported in BALB/c mice (34). In contrast, Dasu et al. (35) reported equal numbers of nTregs in CD5WT and CD5KO mice in the C57BL/6 strain. The reason for the difference in the findings between the present study and that of Dasu et al. is currently unknown.
CD5-dependent CK2 signaling pathway regulates threshold for severity of EAE

We previously showed that both severity and incidence of MOG35–55 peptide-induced EAE in CD5KO mice reconstituted with aCD5CK2BD transgene was significantly reduced compared with CD5WT mice, CD5KO mice, and CD5KO mice reconstituted with CD5WT transgene (27). The finding demonstrated that the CD5–CK2 binding-dependent signaling pathway altered path-

![FIGURE 1. Generation and phenotypic characterization of CD5ΔCK2BD mice. (A) Targeting strategy to generate the Cds5Δ426Δ426Δ626Δ626 knock-in mouse. The targeting construct was generated with a region of Cd5 gene containing exons 6–10 retrieved from the BAC clone RP24-424J1 (C57BL/6). Nucleotides encoding the four amino acids necessary for binding of CK2 with CD5 (S458-S461) in exon 10 (*) of the mouse Cd5 gene were deleted in the targeting construct and founder chimeras were developed using Bruce-4–targeted embryonic stem cells. The Neo selection cassette was deleted by breeding with C57BL/6.E2a-Cre mice to generate the Cd5Δck2bd/Δck2bd Cre-deleted mouse. The 5′ probe used for screening embryonic stem cells based on the insertion of a novel BamH1 site (boxed) is represented in the 5′ arm A that was used to retrieve the Cd5 gene from the BAC clone. (B) PCR-based screening strategy for knock-in mice. Photomicrograph is shown of an agarose gel showing PCR product from tail DNA of Cd5Δck2bd/Δck2bd, Cd5wt/wt, and Cd5Δck2bd/wt mice amplified with specific forward (5′-ATGGACTCCCAAGAAGTGCTG-3′) and reverse (5′-CTTGATAGGATGATGTCGA-3′) primers targeting the 5′ region of exon 9 and the 3′ region of the loxp site. (C) Cd5 expression levels on T cell subsets in the thymus and lymph node of 6- to 8-wk-old CD5WT (red), CD5KO (green), and CD5ΔCK2BD (blue) male mice. (D) Frequencies of CD4+ and CD8+ lymphocytes in the thymus, lymph node, and spleen of 7- to 8-wk-old CD5WT, CD5KO, and CD5ΔCK2BD male mice. Numbers represent the average percentage of cells in each gate ± SEM. Arrows point to the CD4loCD8lo thymocytes. Data are representative from one mouse of six to nine mice per group. DN, double-negative. SP, single-positive.

CD5-dependent CK2 signaling pathway promotes differentiation of Th2 and Th17 cells

We previously showed that both severity and incidence of MOG35–55 peptide-induced EAE in CD5KO mice reconstituted with a CD5ΔCK2BD transgene was significantly reduced compared with CD5WT mice, CD5KO mice, and CD5KO mice reconstituted with CD5WT transgene (27). The finding demonstrated that the CD5–CK2 binding-dependent signaling pathway altered path-

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<th>Mouse Strain</th>
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<td>31.2 ± 2.2</td>
<td>24.0 ± 3.2</td>
<td>43.1 ± 3.0</td>
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<td>CD5ΔCK2BD</td>
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<td>1.7 ± 0.6</td>
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Data are presented as means ± SEM (n = 4–5 mice).

*p < 0.05; CD5ΔCK2BD versus CD5WT or CD5KO mice.

*p < 0.05; CD5KO versus CD5WT or CD5ΔCK2BD mice.
ogeneration in a disease that is T cell dependent. We now wanted to test whether this observation was recapitulated in the CD5ΔCK2BD knock-in mouse where the expression of CD5 is physiologically regulated. We found that EAE in CD5ΔCK2BD mice and CD5KO mice was significantly delayed in onset and less severe than that in CD5WT mice (Fig. 2A, Table II). The incidence of disease in both of the CD5 mutant mice was also lower but the difference was not statistically significant. Because CD5 regulates the threshold of T cell activation, we asked whether the severity of EAE also correlated with increase in MOG35–55 peptide immunization dose. We observed that in CD5WT mice immunized with 150 μg MOG35–55 peptide, the onset of EAE was significantly earlier and more severe than for those immunized with 50 μg MOG35–55 peptide (Table II). Remarkably, EAE in CD5WT mice immunized with a higher immunization dose of 450 μg MOG35–55 peptide was significantly less severe (accumulative score) than that observed with 150 μg peptide, a characteristic that resembles the generation of high-dose tolerance. In contrast, the severity of EAE in both CD5KO and CD5ΔCK2BD mice correlated with immunization dose with no indication of high-dose anergy (Table II). Furthermore, with an increase in immunization dose the severity and time of onset of EAE in CD5KO mice and CD5ΔCK2BD mice approached and equaled that of CD5WT mice (Fig. 2B, 2C, Table II). A striking finding is that with respect to EAE disease severity, the mere deletion of the four amino acid CK2 binding domain within CD5 recapitulated the phenotype of the CD5KO mouse.

We analyzed the CNS cell infiltration in mice of all three CD5 strains to evaluate the correlation between disease severity and Th cell populations. The results showed that the proportion and absolute number of Th1 cells in the CNS of CD5WT, CD5KO, and CD5ΔCK2BD mice were similar. With respect to Th17 cells and Th1-IFNγ+IL17a+ cells (double producers), the spinal cords of CD5ΔCK2BD mice with EAE contained fewer cells of this population than did both CD5WT and CD5KO mice (Fig. 2D). Our results suggest that the CD5-dependent CK2 activation pathway has an impact preferentially on the generation of IL-17a–expressing Th cells, an observation also made in our previous study in the CD5ΔCK2BD-Tg mouse (27).

**CD5-dependent CK2 signaling pathway is necessary for efficient generation of Ag-specific Th2 and Th17 cells**

To test whether the CD5–CK2 signaling pathway has an impact on differentiation of naive CD4+ T cells to Th1 or Th17 cells under nonpolarizing and polarizing conditions, we bred the C57BL/6 MOG35–55-specific TCR Tg mouse, 2D2TCRMOG, with both the CD5KO mouse and CD5ΔCK2BD mouse. Under nonpolarizing conditions, the generation of Th1 cells following stimulation with MOG35–55 peptide was 2D2.CD5WT > 2D2.CD5ΔCK2BD > 2D2.CD5KO (Fig. 3A). Consistently, the proportion of Th1 cells in 2D2.CD5WT CD4+ T cell cultures was ~50% greater than in 2D2.CD5ΔCK2BD and 3-fold greater than in 2D2.CD5KO CD4+ T cell cultures. Under Th1 polarizing conditions, the proportion of Th1 cells generated was equivalent in CD4+ T cell cultures from 2D2.CD5KO mice and 2D2.CD5ΔCK2BD mice but marginally greater than that in 2D2.CD5WT mice (Fig. 3A). However, under Th17 polarizing conditions, the proportion of Th17 cells in 2D2.CD5ΔCK2BD CD4+ T cell cultures was less than half of that in CD4+ T cell cultures from 2D2.CD5WT and 2D2.CD5KO mice (Fig. 3A). This ex vivo result largely recapitulates the observation in spinal cords of mice with EAE (Fig. 2D).

The stimulation with anti-CD3 mAb (antigen nonspecific) had a different outcome than stimulation with MOG35–55 peptide (cognate peptide). The generation of Th1 cells was similar in T cell cultures under nonpolarizing conditions from all three strains of mice (Fig. 3B). Following anti-CD3 stimulation under Th1 polarization conditions, greater proportions of Th1 cells were obtained from CD5ΔCK2BD CD4+ T cell cultures than from CD5WT and CD5KO CD4+ T cell cultures. Unlike cognate peptide stimulation, the generation of Th17 cells from anti-CD3 mAb-stimulated Th17 polarization cultures was generally equivalent in CD4+ T cell cultures from the three strains of mice (Fig. 3A, 3B). We posited that this divergent outcome reflects direct engagement of TCR with anti-CD3 mAb versus cognate stimulation (peptide:MHC) rather than differences in CD5 signaling between T cells from C57BL/6 mice versus 2D2 mice. This was supported by our observation that the generation of Th1 and Th17 cells following stimulation of CD4+ T cells from the different CD5 genotypes of 2D2 mice with anti-CD3 mAb was similar to anti-CD3 mAb-stimulated C57BL/6 mice T cells (Supplemental Fig. 2A, 2B). CD5 is recruited to the immunological synapse (36). It is possible that direct stimulation of TCR versus cognate peptide:MHC induces a different type of receptor assembly that alters positioning of CK2. Such differences in receptor assembly may affect the manner in which CK2 activates Jak1 or Jak2 (37). We are now beginning to address these questions.

We also evaluated the contribution of the CD5–CK2 signaling pathway in the generation of Th2 T cells following stimulation with MOG35–55 peptide or anti-CD3 under Th2 polarization conditions. In MOG35–55 peptide-stimulated Th2-polarized cultures, the proportion of Th2 cells in CD4+ T cell cultures from 2D2.CD5ΔCK2BD was lower than that in T cell cultures from both 2D2.CD5WT and 2D2.CD5KO mice (Fig. 3A). As in Th17 polarization cultures, the generation of Th2 cells in anti-CD3–

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**FIGURE 2.** CD5-dependent CK2 signaling pathway regulates the threshold for EAE severity. (A–C) Clinical course of EAE in CD5WT, CD5KO, and CD5ΔCK2BD mice induced with 50 μg/ml MOG35–55 peptide (A), 150 μg/ml MOG35–55 peptide (B), and 450 μg/ml MOG35–55 peptide (C). Data are means ± SEM (n = 10–20 mice/group). Bars above plots denote regions of statistical significance. **p < 0.01 with Student t test. (D) Intracellular cytokine staining of infiltrating CD4+ T cell populations in spinal cords from CD5WT, CD5KO, and CD5ΔCK2BD mice analyzed 14 d postimmunization with 150 μg MOG35–55 peptide. Unbracketed numbers in each quadrant represent the average frequency of CD4+ T cells expressing IFN-γ and/or IL-17a ± SEM. Bracketed numbers represent average absolute cell counts for each subpopulation × 106 ± SEM. Data are representative of one of two to three experiments, with two to three mice per experiment per group.
stimulated cultures was similar between CD4+ T cell cultures from the three strains of mice (Fig. 3B, Supplemental Fig. 2A). Considering that stimulation of T cells with cognate peptide rather than anti-CD3 more closely represents normal physiology, the data indicate that loss of the CD5–CK2 signaling pathway results in preferential diminution in the generation of Th17 and Th2 cells but not Th1 cells.

FIGURE 3. Contribution of the CD5–CK2 signaling pathway to the generation of Th1, Th2, and Th17 cells from naive CD4+ T cells. Naive CD4+ T cells were cocultured with irradiated APCs and stimulated with MOG35–55 peptide (A) or anti-CD3 (B) under nonpolarizing (unpolarized) or polarizing conditions and generation of Th subpopulations was evaluated. Numbers in each quadrant represent the average frequency of CD4+ T cells expressing IFN-γ, IL-17a, and/or IL-4 ± SEM from four independent experiments performed with at least three mice per experiment. (C) Percentage 7-AAD−CD4+ T cells at 24 and 120 h and (D) RORγt+CD4+ T cells at 120 h following stimulation with MOG35–55 peptide under Th17 polarizing conditions. Data are means ± SEM of three independent experiments with at least two mice per group. (E) pSTAT1 (Ser727) and (F) pSTAT3 (Tyr705) in CD4+ T cells stimulated for 72 h with MOG35–55 peptide under Th17 polarizing conditions. The filled shaded histograms are unstimulated and the dashed histograms are isotype Ig-stained cell controls. For pSTAT1 (E), the mean fluorescence intensity for 2D2.CD5−CK2BD is 52 ± 4.8 and for 2D2.CD5WT is 30 ± 4.3. For pSTAT3 (F), the mean fluorescence intensity for 2D2.CD5−CK2BD is 32 ± 2.9 and for 2D2.CD5WT is 21 ± 3.5. Histograms represent data from one representative mouse per group from two mice per experiment (n = 3 experiments). *p < 0.05, **p < 0.01, ***p < 0.001.

Table II. Analysis of disease parameters for active EAE in CD5WT, CD5KO, and CD5ΔCK2BD mice induced with different doses of MOG35–55 peptide

<table>
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<tr>
<th>MOG35–55 Peptide Dose (μg)</th>
<th>Mouse Strain</th>
<th>Day of Onset</th>
<th>Time to Peak</th>
<th>Accumulative Score</th>
<th>Incidence</th>
<th>Mortality</th>
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<tr>
<td>50</td>
<td>CD5WT</td>
<td>15.0 ± 1.9</td>
<td>18.6 ± 4.0</td>
<td>44.5 ± 10.4</td>
<td>20/20</td>
<td>1/20</td>
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<tr>
<td></td>
<td>CD5KO</td>
<td>19.0 ± 5.0</td>
<td>20.2 ± 4.4</td>
<td>29.8 ± 11.7</td>
<td>12/15</td>
<td>0/15</td>
</tr>
<tr>
<td></td>
<td>CD5ΔCK2BD</td>
<td>19.2 ± 5.2</td>
<td>20.0 ± 4.2</td>
<td>35.1 ± 14.4</td>
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<td>2/17</td>
</tr>
<tr>
<td>150</td>
<td>CD5WT</td>
<td>12.5 ± 1.5</td>
<td>15.8 ± 3.6</td>
<td>59.5 ± 8.7</td>
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<td>4/19</td>
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<tr>
<td></td>
<td>CD5KO</td>
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<td>18.6 ± 3.2</td>
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<td>15/15</td>
<td>1/15</td>
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<td>2/15</td>
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<td>CD5WT</td>
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<td>11/12</td>
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<tr>
<td></td>
<td>CD5ΔCK2BD</td>
<td>13.4 ± 1.7</td>
<td>17.7 ± 2.7</td>
<td>52.5 ± 11.7</td>
<td>9/10</td>
<td>0/10</td>
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</table>

Data are presented as means ± SEM (n = 10–20 mice). No scores were assigned following the day of death.

*p < 0.05; CD5WT 50 μg dose versus CD5WT 150 μg dose or CD5WT 450 μg dose.

*p < 0.05; versus CD5WT mice at same dose.

*p < 0.05; CD5KO 450 μg dose versus CD5KO 50 μg dose.

*p < 0.05; versus CD5ΔCK2 50 μg dose.

*p < 0.05; CD5WT 50 μg dose versus CD5WT 150 μg dose.

*p < 0.05; CD5WT 150 μg dose versus CD5WT 450 μg dose.

*p < 0.05; CD5WT 150 μg dose versus CD5WT 450 μg dose.

*p < 0.05; CD5WT 150 μg dose versus CD5WT 450 μg dose.

*p < 0.05; CD5WT 150 μg dose versus CD5WT 450 μg dose.
Cell death, RORγt expression, and activation of STAT1 and STAT3 in CD5ΔCK2BD T cells during Th17 polarization

The CD5–CK2 signaling pathway regulates survival of activated T cells and could represent a mechanism for the diminished Th17 cells in Th17-polarized cultures containing T cells from 2D2.ΔCD5ΔCK2BD mice (27). Consistent with this possibility we observed a greater proportion of dying T cells in Th17 polarization cultures of 2D2.ΔCD5ΔCK2BD mice than that in 2D2.CD5WT mice (Fig. 3C). The increased cell death was not compensated by greater cell division. The proportion of Th17 cells in cell cycle as measured by uptake of EdU during a 1-h pulse labeling was similar for both 2D2.CD5WT and 2D2.ΔCK2BD T cells (Supplemental Fig. 2D). The diminished Th17 generation with naive 2D2ΔCD5ΔCK2BD T cells was also associated with fewer T cells that have upregulated RORγt than that in 2D2.CD5WT cultures (Fig. 3D). However, the expression of Rorc (gene for RORγt) at a per-cell level was almost identical between 2D2.CD5WT and 2D2.ΔCK2BD T cells, indicating that loss of CD5–CK2 signaling pathway did not alter intrinsic RORγt expression (Supplemental Fig. 2C).

A recent report showed that CD5 costimulation enhanced differentiation of naive human T cells to Th17 cells that was associated with upregulation of IL-23R and elevated activation of STAT3 (38). We observed that the loss of the CD5–CK2 signaling pathway had no effect on IL-23R expression on Th17 cells (Supplemental Fig. 2B, 2C). However, 2D2.ΔCK2BD Th17 cells did contain greater levels of activated STAT1 and STAT3 compared with 2D2.CD5WT Th17 cells (Fig. 3E, 3F). Overall, the data indicate that the loss of CD5–CK2 signaling attenuates Th17 generation by enhancing cell death and enhanced activation of STAT1 and STAT3.

CD5ΔCK2BD T cells hyperproliferate in response to Ag receptor activation

CD5KO T cells hyperproliferate following stimulation of the Ag receptor, a property associated with the loss of CD5-dependent regulation (9). The inhibitory activity of CD5 is ascribed to the ITAM/ITIM domain of CD5, a domain that is intact in the CD5ΔCK2BD mouse. This mouse model now offers the opportunity to selectively determine the contribution of the CD5–CK2 signaling pathway to T cell activation. Ca2+ mobilization and upregulation of CD25/CD69 are parameters of early T cell activation. In response to TCR stimulation, CD4+ T cells from CD5WT mice and CD5ΔCK2BD mice behaved similarly for both of these parameters (Supplemental Fig. 1B, 1C, and data not shown). In contrast, CD5KO CD4+ T cells exhibited a lower threshold for Ca2+ flux and more accelerated kinetics for upregulation of CD25 and CD69 (Supplemental Fig. 1B, 1C). This observation is similar to that previously reported for thymic T cells (1). The results indicate that the CD5–CK2 signaling pathway does not have an impact on proximal events of TCR signaling.

CK2 is a major promoter of cell proliferation and cell survival, and inhibitors of this kinase attenuate cell cycle progression (26). We therefore tested the prediction that loss of CD5-dependent CK2 signals attenuates cell proliferation. Consistent with our prediction, we observed that at all concentrations of anti-CD3, CD4+ T cells from CD5ΔCK2BD mice significantly hyperproliferated in comparison with CD4+ T cells from CD5WT mice (Fig. 4A). As expected, CD4+ T cells from CD5KO mice hyperproliferated following stimulation with anti-CD3. A similar observation was noted when Ag-specific T cells were stimulated with MOG35–55 peptide (Fig. 4B). 2D2.CD5ΔCK2BD T cells significantly hyperproliferated and 2D2.CD5KO T cells hyperproliferated in comparison with 2D2.CD5WT T cells following stimulation with cognate peptide. Because CK2 also promotes cell survival, we wanted to test whether the apparent diminished proliferation of CD5–CK2 signaling-deficient T cells reflected enhanced AICD. When anti-CD3 was used for activation, we found that the proportion of CD4+ T cells undergoing apoptosis (annexin V7-AAD) was similar in cultures from CD5ΔCK2BD mice and CD5WT mice (Fig. 4C). However, in MOG35–55 peptide-stimulated cultures, apoptosis was significantly greater when CK2 binding to CD5 was selectively abrogated (Fig. 4D, Table III). CD5KO T cells consistently exhibited enhanced AICD following stimulation with anti-CD3 or cognate peptide (Fig. 4C, 4D). Taken together, the above results indicate that decreased survival in CD5–CK2 signaling-deficient T cells contributes only partially to the diminished proliferation that follows T cell activation.

We directly interrogated whether loss of CD5–CK2 signaling impairs entry into the cell cycle. To address this question we used EdU to pulse label cells for the last 1 h following 72 h stimulation with anti-CD3 or cognate peptide. We then quantitated the amount of EdU uptake by a flow cytometric assay. This approach enumerates the proportion of cells progressing through the cell cycle during the short pulse labeling and therefore overcomes confounders such as cell death. We found that the proportion of EdU+ CD4+ CD5–CK2 signaling-deficient T cells stimulated with either anti-CD3 or MOG35–55 peptide was lower than that for CD5WT T cells stimulated similarly (Fig. 4E, 4F). In contrast, the proportion of EdU+ CD4+ CD5-deficient T cells was always greater than that in stimulation cultures containing CD5WT T cells. The hypoproliferation of CD5ΔCK2BD or 2D2.ΔCK2BD T cells may not be intrinsic to the activation threshold but rather influenced by the differences in the cytokine environment. To address this possibility, we cocultured WT-CD5–expressing CD4+ T cells with ΔCK2BD–CD5–expressing CD4+ T cells and stimulated them with anti-CD3 or MOG35–55 peptide for 48 or 72 h. To distinguish between the two T cell populations, for analysis WT-CD5 T cells were labeled with CFSE. Proliferation was assessed by measuring EdU uptake. We observed that the proportion of dividing CD5–CK2 signaling-deficient CD4+ T cells was significantly less than total dividing WT-CD5–expressing CD4+ T cells even when cultured under the same environmental conditions (Fig. 4G, 4H). Similar results were obtained with cocultures containing labeled ΔCK2BD–CD5–expressing T cells with CFSE and unlabelled WT-CD5–expressing T cells, demonstrating that CFSE labeling did not introduce any artifact (data not shown). These results demonstrate that CD5–CK2 signaling-deficient CD4+ T cells are intrinsically hypoactive to Ag receptor-induced proliferation.

We next asked whether the CD5–CK2 signaling pathway also promotes TCR signaling-initiated proliferation and cell cycle entry in CD8+ T cells. We found that the extent of CD8+ T cell proliferation following anti-CD3 stimulation recapitulated the observations made with CD4+ T cells (Fig. 4I). The frequencies of CD8+ T cells in cell cycle from CD5WT, CD5KO, or CD5ΔCK2BD mice were not significantly different from each other (Fig. 4J). This result suggests that differences in proliferation probably reflect variances in susceptibility to AICD. Overall, our results indicate that the CD5–CK2 signaling pathway promotes cell cycle progression in CD4+ T cells following TCR activation.

The CD5–CK2 signaling pathway regulates T cell conversion to nonresponsiveness

CD5WT mice immunized with 450 μg MOG35–55 peptide developed less severe EAE than did mice immunized with a lower dose of 150 μg peptide, a characteristic similar to high-dose tolerance (Fig. 2A, Table II). However, in both CD5KO and CD5ΔCK2BD mice, the severity of EAE directly correlated with Ag dose. This suggested that the CD5–CK2 signaling pathway...
may be involved in regulating T cell response to Ag re-exposure. To directly test this, we performed an in vitro recall assay where CD4+ T cells were activated with anti-CD3 or cognate peptide, rested, and then restimulated with anti-CD3 or MOG35-55, respectively. We measured proliferation and cell cycle entry. We observed that CD4+ T cells from CD5WT, CD5KO, and CD5ΔCK2BD

Table III. CD5–CK2 signaling pathway regulates TCR-induced apoptosis in T cells

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<thead>
<tr>
<th>Anti-CD3 (µg/ml)</th>
<th>CD5WT</th>
<th>CD5KO</th>
<th>CD5ΔCK2BD</th>
<th>MOG35-55 (µg/ml)</th>
<th>2D2.CD5WT</th>
<th>2D2.CD5KO</th>
<th>2D2.CD5ΔCK2BD</th>
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<tr>
<td>0</td>
<td>9.7 ± 1.3</td>
<td>10.7 ± 1.8</td>
<td>9.8 ± 0.3</td>
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<td>15.0 ± 1.1</td>
<td>27.0 ± 3.6</td>
<td>26.2 ± 2.8</td>
</tr>
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<td>0.1</td>
<td>9.6 ± 0.7</td>
<td>10.9 ± 0.1</td>
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<td>19.6 ± 0.6</td>
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<td>35.9 ± 1.5</td>
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<td>14.0 ± 1.3</td>
<td>9.6 ± 0.7a</td>
<td>1</td>
<td>33.1 ± 0.3c</td>
<td>43.1 ± 2.6</td>
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<td>100</td>
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<td>71.4 ± 4.4</td>
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</table>

Cells were stimulated with varying concentrations of anti-CD3 or MOG35-55 peptide in the presence of irradiated APCs for 24 h. Apoptosis was evaluated by staining cells with annexin V and 7-AAD. Data are presented as percentages of events ± SEM.

*p < 0.01; versus CD5KO mice.

*p < 0.05; 2D2.CD5KO versus 2D2.CD5WT mice.

p < 0.001; versus 2D2.CD5WT mice.

*p < 0.05; 2D2.CD5CO mouse versus 2D2.CD5ΔCK2BD mice.

*p < 0.01; 2D2.CD5WT mouse versus 2D2.CD5ΔCK2BD mice.

*p < 0.01; 2D2.CD5KO mouse versus 2D2.CD5ΔCK2BD mice.

*p < 0.001; versus 2D2.CD5ΔCK2BD mice.

*p < 0.01; 2D2.CD5KO mouse versus 2D2.CD5WT mice.
mice proliferated equally when restimulated with 0.1 μg/ml anti-CD3 (Fig. 5A). In contrast, at 1 μg/ml anti-CD3, CD5KO and CD5ΔCK2BD T cells proliferated more vigorously than did CD5WT T cells. We next wanted to determine whether this property of CD5 was active when T cells were stimulated with cognate peptide. MOG35–55 peptide-activated and rested CD4+ T cells from 2D2.CD5WT, 2D2.CD5KO, or 2D2.CD5ΔCK2BD mice were restimulated with 1 and 10 μg/ml MOG35–55 peptide and proliferation was measured. The proliferation of CD4+ T cells from 2D2.CD5ΔCK2BD mice was several fold greater than CD4+ T cells from either 2D2.CD5WT and 2D2.CD5KO mice at both MOG35–55 concentrations (Fig. 5B). We then evaluated cell cycle entry using the EdU incorporation assay. We observed that fewer CD4+ T cells from CD5WT mice stimulated with anti-CD3 or MOG35–55 peptide entered cell cycle than did similarly stimulated CD4+ T cells from CD5KO or CD5ΔCK2BD mice (Fig. 5C, 5D). Consistently, CD5ΔCK2BD CD4+ T cells responded more vigorously to restimulation than did CD5KO CD4+ T cells. Similar to CD4+ T cells, CD8+ T cells from CD5KO mice or CD5ΔCK2BD mice responded more vigorously when restimulated than did CD5WT CD8+ T cells (Fig. 5E).

Considering that WT-CD5–expressing T cells and ΔCK2BD-CD5–expressing T cells produce different levels of cytokines, we evaluated their proliferation in cocultures following restimulation with anti-CD3 or MOG35–55 peptide. At all time points of measurement, we observed significantly greater proportions of ΔCK2BD-CD5–expressing T cells in cell cycles compared with WT-CD5–expressing T cells (Fig. 5F, 5G). The CFSE dilution assay showed that CD5–CK2 signaling-deficient T cells went through one or more generations of cell division than did WT T cells (Supplemental Fig. 3A). The decreased proliferation in WT-CD5–expressing T cells was not associated with enhanced cell death (Supplemental Fig. 3B).

We next evaluated whether the CD5–CK2 signaling pathway also regulated re-exposure to Ag when the initial priming was performed in vivo. CD5WT or CD5ΔCK2BD mice were immunized with MOG35–55 peptide and 7 d later, CD4+ T cells from spleens and lymph nodes were isolated from each group of mice and cocultured with MOG35–55 peptide. We again observed that a significantly greater proportion of CD5ΔCK2BD T cells incorporated EdU than did CD5WT T cells (Fig. 5H). There was no difference in T cell death between the two groups of mice (Supplemental Fig. 3C). Overall, our results show that the CD5–CK2 signaling pathway regulates response to re-exposure to Ag.

**CD5 regulates cytokine production in CD4+ T cells**

2D2.CD5KO and 2D2.CD5ΔCK2BD CD4+ T cells cultured under nonpolarizing conditions contain fewer IFN-γ–expressing T cells than do their 2D2.CD5WT counterparts (Fig. 3A). Therefore, we examined whether the CD5–CK2 signaling pathway regulated Ag

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**FIGURE 5.** CD5–CK2 signaling pathway-deficient T cells are resistant to development of anergy. Purified CD4+ T cells were stimulated for 24 h with anti-CD3 or MOG35–55 peptide, rested for 72 h, and then restimulated for 48 h with anti-CD3 or MOG35–55 peptide. (A and B) Frequency of CD4+ T cells incorporating [3H]thymidine following 48 h restimulation with varying concentrations of anti-CD3 (A) or MOG35–55 peptide (B). Data ± SEM represent the average of two mice per group per experiment (n = 3 experiments). (C and D) EdU incorporation by CD4+ T cells restimulated with anti-CD3 (C) or MOG35–55 peptide (D). Cells were pulse labeled with EdU after 48 h restimulation. (E) EdU incorporation in CD8+ T cells 48 h after restimulation with 1 μg/ml anti-CD3. (F and G) EdU incorporation in cocultures of (F) CFSE-labeled CD5WT and unlabeled CD5ΔCK2BD CD4+ T cells restimulated with anti-CD3 mAb, or (G) CFSE-labeled 2D2.CD5WT and unlabeled 2D2ΔCK2CD CD4+ T cells restimulated with MOG35–55 for the indicated times. (H) Effect of in vitro restimulation on in vivo-primed T cells. CD5WT mice and CD5ΔCK2BD mice were immunized with 150 μg MOG35–55 peptide in CFA, s.c. Seven days later CD4+ T cells from spleens of both groups of mice were cocultured in the presence of MOG35–55 peptide and proliferation was assessed by EdU incorporation at the indicated time points. Data ± SEM represent the average of two to three mice per group per experiment, from at least three experiments. Bars above plots denote regions of statistical significance. *p < 0.05, **p < 0.01, ***p < 0.001 with Student t test.
receptor-induced cytokine production. To address this question, naïve CD4+ T cells from 2D2.CD5WT, 2D2.CD5KO, and 2D2.CD5ΔCK2BD mice were stimulated with MOG35–55 peptide (10 and 100 μg/ml) and supernatants collected on days 1, 2, 3, and 5 were analyzed for levels of IFN-γ, IL-17a, IL-6, and IL-2 and IL-10. At each time point, the levels of IFN-γ, IL-17a, and IL-6 in 2D2.CD5ΔCK2BD T cell cultures were dramatically greater than those in CD4+ T cell cultures from 2D2.CD5WT mice (Fig. 6A–C, Supplemental Fig. 3A–C). Although T cell cultures from 2D2.CD5KO mice contained higher levels of these three cytokines than did 2D2.CD5WT T cell cultures (day 2–day 5), they were consistently lower than 2D2.CD5ΔCK2BD T cell cultures. The levels of IL-2 and IL-10, cytokines associated with Treg function, followed different kinetics. Although IL-2 levels in T cell cultures from 2D2.CD5WT and 2D2.CD5KO increased rapidly, the cytokine persisted longer than when the T cells were obtained from 2D2.CD5WT mice (Fig. 6D, Supplemental Fig. 3D). In contrast, detectable levels of IL-2 in T cell cultures from 2D2.CD5ΔCK2BD mice did not increase beyond day 1 of stimulation. The level of this cytokine had contracted to basal levels by day 3 in 2D2.CD5KO and 2D2.CD5ΔCK2BD T cell cultures and by day 5 in 2D2.CD5WT T cell cultures. This contraction is probably associated with T cell exhaustion. IL-10 levels rose and contracted in 2D2.CD5ΔCK2BD T cell cultures (Fig. 6E, Supplemental Fig. 3E). In contrast, IL-10 levels continuously increased in T cell cultures from 2D2.CD5WT and 2D2.CD5KO mice (Fig. 6E). A striking finding is that although MOG35–55 peptide-stimulated unpolarized CD11b−CD4+ T cells contain fewer Th1 and Th17 cells, respectively (Fig 3A), the levels of IFN-γ and IL-17a produced were the greatest. This would suggest that the CD5–CK2 signaling pathway is needed for the expansion of these subsets rather than production of these cytokines.

We also determined the cytokine levels in cultures of anti-CD3-stimulated T cells. Cytokine levels in CD4+ T cell cultures stimulated with anti-CD3 in the presence of irradiated APCs reflected the general trend of MOG35–55-stimulated cultures. However, the main difference was that the CD5KO T cell cultures contained greater levels of all cytokines than those in the T cell cultures from CD5WT or CD5ΔCK2BD mice (Supplemental Fig. 4).

**CD5 signaling differentially regulates Th1 versus Th17 disease**

Th1 and Th17 T cells are the major effector T cell populations in multiple sclerosis and EAE that cross-regulate each other (39). Furthermore, we recently showed that multiple sclerosis broadly stratifies into a Th1- or Th17-predominant disease (31). We therefore wanted to determine whether loss of the CD5–CK2 signaling pathway differentially affects the outcome of EAE disease induced by encephalitogenic Th1 cells versus Th17 cells. To address this question, encephalitogenic Th1 or Th17 cells generated from MOG35–55 peptide-immunized CD5WT, CD5KO, or CD5ΔCK2BD mice were adoptively transferred into CD5WT mice and development of EAE was monitored. For Th1 disease, we found that encephalitogenic CD5ΔCK2BD Th1 cells induced the most severe EAE mean maximum disease score based on accumulative score and mortality (Fig. 7A, Table IV). Although EAE induced by encephalitogenic CD5KO Th1 cells was more severe than that induced by CD5WT Th1 cells, the difference was not statistically significant. Unlike Th1 disease, encephalitogenic Th17 cells from CD5ΔCK2BD mice induced slightly less severe EAE than did CD5WT Th17 cells; however, the difference was not significant (Fig. 7B, Table IV). Th17 cells from CD5KO mice induced the least severe disease.

**Discussion**

The development of the CD5KO mouse more than 15 y ago led to a major revision in our understanding of CD5 biology (1). That study reversed the existing dogma that CD5 was a costimulator to that of an attenuator in T cell activation. Using the CD5KO mouse we determined that CD5 had an important role in promoting survival of activated T cells (28). This discovery resolved the puzzle as to why loss of negative regulation in the CD5KO mice did not lead to the development of spontaneous autoimmunity. We subsequently demonstrated that the prosurvival activity required the CK2 binding domain located within the distal portion of CD5 cytoplasmic tail (27). In this study, we developed a knock-in mouse with a 12-nucleotide deletion in exon 10 of the CD5 gene encoding the codons for the four amino acids (S458–S461) necessary for CK2 to interact with CD5. This mouse gave us the opportunity to examine the consequence of loss of the CD5-dependent CK2 signaling pathway in a context that maintains physiological regulation of CD5 expression. We found that the expression of CD5 on all T and B lymphoid populations in this CD5-dependent CK2 signaling-deficient mouse was identical to that in the CD5WT mouse. This observation suggests that the CD5–CK2 signaling pathway does not alter TCR or BCR signaling events that directly affect CD5 expression (11, 14, 40, 41). In fact, we found that Ca2+ mobilization and upregulation of CD25 or CD69 following TCR stimulation was unaltered in both CD4+ and CD8+ T cells from the CD5ΔCK2BD mouse. Both of these proximal parameters of Ag receptor signaling are tyrosine kinase dependent and were elevated in T cells from the CD5KO mouse as previously reported (1). Although the loss of CD5–CK2 signaling did not dramatically alter mature T cell populations in the C57BL/6 mouse, the absolute numbers of CD4+CD8+ DP cells were significantly lower than

**FIGURE 6.** CD5–CK2 signaling pathway regulates Ag receptor-induced cytokine production. Naïve 2D2.CD5WT, 2D2.CD5KO, and 2D2.CD5ΔCK2BD CD4+ T cells were cocultured with irradiated APCs and stimulated with 100 μg/ml MOG35–55 peptide for 1–5 d. Supernatants were collected on days 1, 2, 3, and 5 to quantify secreted levels of IFN-γ (A), IL-17a (B), IL-6 (C), IL-2 (D), and IL-10 (E) by ELISA. Data ± SEM represent readings from one mouse of two to three mice per group per experiment, from at least four experiments.
whereas CD5 immunization dose CD5WT mice developed less severe EAE, conditions with MOG 35–55 peptide for 72 h. Cells were transferred to sublethally irradiated CD5WT mice to induce disease. Data (28). Remarkably, we found that EAE in CD5 less severe and delayed in onset compared with that in CD5WT mice this question.

We previously reported that EAE in CD5KO mice was significantly less severe and delayed in onset compared with that in CD5WT mice (27). In our previous study, the CD5ΔCK2BD transgene was expressed at lower levels than the endogenous CD5 in CD5WT mice and was under the control of the CD2 promoter, with no dynamic regulation of expression by TCR signals. These significant distinctions could account for the differences between these studies. Nevertheless, the overall findings show that the CD5 signaling pathway is an important regulator for setting threshold for response to immunization and represents a critical signaling pathway in T cells.

We determined that the CD5–CK2 signaling pathway was necessary for the differentiation of naive CD4+ T cells to Th17 or Th2 cells stimulated with cognate peptide under polarizing conditions. Similarly, the CNS of CD5–CK2 signaling-deficient mice with EAE also contained fewer IL-17–expressing Th cells but not Th1 cells than that in CD5WT mice. A recent report showed that CD5 is an important costimulator for Th17 differentiation; however, the mechanism was not resolved (38). Another recent study made the elegant finding that CK2 is recruited to IAK1 and IAK2 and participates in the activation of STAT3 and STAT5 (37). STAT3 is required for Th17 differentiation, and STAT5 is required for Th2 differentiation (42, 43). Additional studies still need to be performed to elucidate the precise CD5–CK2 signaling pathway that promotes Th2 and Th17 differentiation. However, one mechanism for promoting Th17 generation might be by regulating STAT1 activation (44). In fact, we find that the loss of the CD5–CK2 signaling pathway leads to hyperactivation of STAT1. We also observed enhanced activation of STAT3 in CD5–CK2 signaling-deficient Th17 cells. This enhanced STAT3 activation may be a consequence of gain of STAT1 activity, which has been recently observed in humans (45). Although STAT3 phosphorylation in response to STAT3 activating cytokines such as IL-6 and IL-21 was augmented, the study showed that the enhanced STAT1 activity inhibited Th17 differentiation. This cross-regulation by STAT1 on STAT3-induced genes may be one explanation for our finding that in the absence of CD5–CK2 signaling pathway Th17 differentiation was inhibited, but greater levels of both IL-17A and IL-6 were produced by activated CD5ΔCK2BD T cells. We also found that the differentiation of naive CD4+ T cells to Th1 cells stimulated with cognate peptide under nonpolarizing conditions was diminished when the CD5–CK2 signaling pathway was ablated. This observation is consistent with decreased IFN-γ-stimulated STAT1 activation when CK2 activity is inhibited (37). However, under polarizing conditions, the absence of CD5–CK2 signaling led to increased Th1 differentiation. This finding perhaps explains the enhanced passive EAE observed when encephalitogenic Th1 cells

Table IV. Analysis of disease parameters for EAE induced by passive transfer of Th1- or Th17-polarized encephalitogenic T cells from CD5WT, CD5KO, and CD5ΔCK2BD into CD5WT mice

<table>
<thead>
<tr>
<th>Cell Source (CD8+CD25+)</th>
<th>Day of Onset</th>
<th>Max. Score</th>
<th>Time to Peak</th>
<th>Accumulative Score</th>
<th>Incidence</th>
<th>Mortality</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Th1</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>CD5WT</td>
<td>19.9 ± 3.3</td>
<td>3.4 ± 0.8</td>
<td>23.3 ± 3.0</td>
<td>30.7 ± 9.8</td>
<td>9/9</td>
<td>0/9</td>
</tr>
<tr>
<td>CD5KO</td>
<td>16.0 ± 4.5</td>
<td>3.6 ± 1.1</td>
<td>20.0 ± 2.2a</td>
<td>48.0 ± 23.1</td>
<td>6/6</td>
<td>0/6</td>
</tr>
<tr>
<td>CD5ΔCK2BD</td>
<td>15.2 ± 4.9a</td>
<td>4.4 ± 0.7a</td>
<td>23.8 ± 1.9</td>
<td>48.9 ± 10.5a</td>
<td>6/6</td>
<td>2/6</td>
</tr>
<tr>
<td><strong>Th17</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CD5WT</td>
<td>16.8 ± 1.5</td>
<td>3.8 ± 0.9</td>
<td>20.6 ± 1.9</td>
<td>37.5 ± 8.3</td>
<td>10/10</td>
<td>1/10</td>
</tr>
<tr>
<td>CD5KO</td>
<td>21.5 ± 3.7b</td>
<td>2.6 ± 1.2b</td>
<td>22.3 ± 3.6</td>
<td>19.9 ± 7.7b</td>
<td>11/11</td>
<td>1/11</td>
</tr>
<tr>
<td>CD5ΔCK2BD</td>
<td>18.5 ± 4.2</td>
<td>3.3 ± 1.4</td>
<td>20.1 ± 3.3</td>
<td>30.4 ± 13.3</td>
<td>8/8</td>
<td>1/8</td>
</tr>
</tbody>
</table>

Data are presented as means ± SEM (n = 6–11 mice).

* p < 0.05; disease induced with CD5ΔCK2BD Th1 cells versus disease induced with CD5WT Th1 cells.

** p < 0.05; disease induced with CD5KO Th17 cells versus disease induced with CD5WT Th17 cells.
are generated from CD5-ΔCK2BD donor mice. Overall, our results now support a growing paradigm for a Th differentiation that involves cross-talk of cytokine-dependent Jak/Stat signaling and the CD5–CK2 activation pathway.

CK2 is an important participant in various stages of cell division, including cell cycle entry (26). Therefore, our finding that CD4+ and CD8+ T cells hypoproliferate in response to TCR stimulation with anti-CD3 or cognate peptide was predictable. Because CK2 is also an important regulator of cell survival, and we showed in this and a previous study that ablation of CD5-conditioned CK2 activation leads to enhanced AICD, it was important to determine whether the decreased proliferation merely reflects enhanced cell death (27). Using the thymidine analog EdU we found that T cells from the CD5-ΔCK2BD mouse exhibited diminished cell cycle entry, demonstrating that the hypoproliferation was independent of cell death.

The in vitro recall response following a short rest after primary stimulation is an effective assay for determining threshold for development of anergy in T cells. We found that CD5–ΔCK2 signaling-deficient T cells proliferated more efficiently, with a greater proportion entering into cell cycle than in CD5WT T cells. This of course is not surprising. Because CK2 is involved in cross-talk of cytokine-dependent Jak/Stat signaling with anti-CD3 or cognate peptide was predictable. Because CK2 from the CD5-dependent CK2 activation leads to enhanced AICD, it was important to determine whether the decreased proliferation merely reflects enhanced cell death (27). Using the thymidine analog EdU we found that T cells from the CD5-ΔCK2BD mouse exhibited diminished cell cycle entry, demonstrating that the hypoproliferation was independent of cell death.

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Disclosures
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References


