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Tight regulation of diacylglycerol-mediated signaling is critical for proper invariant NKT cell development

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Abstract

Type I natural killer T (NKT) cells, or *i*NKT cells, express a semi-invariant T cell receptor characterized by its unique V a 14-Ja 18 usage (iV a 14TCR). Upon interaction with glycolipid/ CD1d complexes, the iV α 14TCRs transduce signals that are essential for iNKT selection and maturation. However, it remains unclear how these signals are regulated and how important such regulations are during iNKT development. Diacylglycerol (DAG) is an essential second messenger downstream of the TCR that activates the PKC θ -IKK α/β -NF κ B pathway, known to be crucial for *i*NKT development, as well as the RasGRP1-Ras-Erk1/2 pathway in T cells. DAG kinases (DGKs) play an important role in controlling intracellular DAG concentration and thereby negatively regulate DAG signaling. Here we report that simultaneous absence of DAG kinase a and ζ causes severe defects in *i*NKT development, coincident with enhanced IKK-NF κ B and Ras-Erk1/2 activation. Moreover, constitutive IKKβ and Ras activities also result in *i*NKT developmental defects. Thus, DAG-mediated signaling is not only essential but also needs to be tightly regulated for proper iNKT cell development.

INTRODUCTION

Natural killer T (NKT) cells are a subset of rare T cells that bridge innate and adaptive immunity. Despite their rarity, NKT cells play a significant role in the modulation and/or pathogenesis of infectious diseases, allergy, autoimmunity and cancer, in part due to their ability to secrete a vast array of cytokines within minutes to hours of stimulation (1, 2). Accumulating data supports the notion that the NKT population is actually comprised of a number of developmentally and functionally distinct subsets (3). The majority of NKT cells express a semi-invariant T cell receptor (TCR) with a unique V α 14-J α 18 chain and a limited V_β repertoire. These cells, called Type I NKT cells or *i*NKT cells, recognize glycolipids presented by CD1d, and can be readily detected by α-galactosylceramide (α-Galcer)-loaded CD1d-tetramers. While *i*NKT cells also arise from double positive (DP) thymocytes, they differ from conventional $\alpha\beta$ T ($\alpha\beta$ T) cells in that they are selected on fellow CD1d-expressing cortical thymocytes (as opposed to MHC-bearing thymic epithelial cells) (4, 5). Positively selected iNKT thymocytes down-regulate CD24 expression and

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undergo further maturation marked by sequential upregulation of CD44 and NK1.1 on the cell surface (3). While terminally mature CD44⁺NK1.1⁺ *i*NKT thymocytes become long-term residents of the thymus, for reasons yet to be completely understood, CD44⁺NK1.1⁻ *i*NKT thymocytes exit to the periphery, where they mature independently and acquire NK1.1 expression (6, 7).

Given the semi-fixed nature of the $iV\alpha 14TCRs$ and the fact that iNKT cells are selected on cortical thymocytes instead of thymic epithelial cells, it is not surprising that iNKT and $c\alpha\beta T$ cells have differential signaling requirements for their proper development. For instance, homotypic interactions of cortical thymocyte surface receptors Slamf1 and Slamf6 (8), as well as their associated signaling components Fyn (9, 10) and SAP (11, 12), are critically required for iNKT selection, but largely dispensable for $c\alpha\beta T$ cell development. Moreover, while the PKC θ -Carma1/Bc110-IKK-NF κ B pathway plays a minimal role in $c\alpha\beta T$ cell development, deficiency of various components of this pathway has been shown to affect iNKT selection and maturation at multiple stages (13–18).

While much effort has been devoted to identifying signals required for *i*NKT development, mechanisms that regulate these signals and the importance of such regulation remain largely unexplored. DAG kinases (DGKs) are a family of ten enzymes that catalyze the phosphorylation of DAG to produce phosphatidic acid (PA); they thereby control intracellular concentrations of both these critical second messengers (19-21). Recent studies have revealed that DGK α and DGK ζ , isoforms expressed in T cells, play a critical role in preventing T cells from hyper-activation following TCR stimulation by inhibiting the DAG-RasGRP1-Ras-Erk1/2-AP1 signal cascade (22–24). Deficiency of either DGK α or ζ in mice results in hyper-responsiveness to TCR stimulation and correlates with decreased conversion of DAG to PA and enhanced activation of the Ras-Erk1/2-AP1 pathway (25, 26). While deficiency of either DGK α or ζ does not obviously alter c $\alpha\beta$ T cell maturation, simultaneous loss of both DGK α and ζ results in a significant decrease of CD4 or CD8 single positive (SP) thymocytes (27). In this report, we investigated the role of DGK α and ζ and the importance of tight regulation of DAG-mediated signaling for *i*NKT cell development. We demonstrate that DGK α and ζ play a redundant and essential role in *i*NKT cell ontogeny. Although *i*NKT cell numbers are not obviously altered in DGK α or ζ deficient mice, they are dramatically reduced in DGK α and ζ double knockout mice (DGK $\alpha\zeta$ DKO) mice at multiple stages during *i*NKT cell development. These developmental abnormalities are correlated with dysregulated signaling downstream of DAG, as manifested by enhanced activation of the IKK-NFkB and Ras-Erk1/2 pathways in DGKaζDKO thymocytes. Moreover, hyper-activating IKK β causes severe decreases of *i*NKT cell numbers in multiple stages during iNKT cell development correlated with increased death of these cells and decreased expression of ICOS. In contrast, hyper-activating Ras results in incomplete terminal differentiation of *i*NKT cells. Together, our data demonstrate that tight control of DAG-mediated signaling is critical for proper *i*NKT cell development and that DGK α and ζ redundantly inhibit IKK and Ras signaling pathways to ensure normal iNKT cell maturation.

MATERIALS AND METHODS

Mice

 $DGK\alpha^{-/-}$, $DGK\zeta^{-/-}$, and $DGK\alpha^{-/-}\zeta^{-/-}$ mice were previously described (25–27). The conditional constitutively active (CA)-KRas mice (28), CA-IKK β mice (29), and $TCR\beta^{-/-}\delta^{-/-}$ mice were purchased from the Jackson Laboratory. The CD4Cre transgenic mice were purchased from Taconic Farm. All mice were backcrossed onto B6 background for at least 9 generations. The experiments described in this study were reviewed and approved by the Duke University Institute Animal Care and Use Committee.

Isolation of liver mononuclear cells

Whole livers harvested from mice were thoroughly mashed in 20 ml of IMDM medium (10% fetal bovine serum). After the debris settled, the upper cell suspension was passed through nylon mesh and pelleted by centrifuging. The cell pellet was then resuspended in 12 ml of 35% percoll (GE Healthcare), carefully underlayed with 12 ml of 75% percoll, and centrifuged at 1000×g for 20 minutes at room temperature with no brake. Cells accumulated at the interface were collected, washed, pelleted, and again resuspended in 10 ml of IMDM medium (10% FBS). The cell suspension was then underlayed with 2ml of Lympholyte-M (Cedarlane Laboratories), and centrifuged at 1000×g for 15 minutes at room temperature with no brake. Cells accumulated at the interface (mononuclear cells) were collected, counted, and subjected to further analysis.

Antibodies and flow cytometry

PE-conjugated mouse CD1d tetramer loaded with α -GalCer was kindly provided by the NIH tetramer core facility. Live/Dead[®] Fixable Violet Dead Cell Stain was purchased from Invitrogen. Fluorescence-conjugated anti-mouse CD24, CD44, NK1.1, CD4, CD8, TCR β , CD45.1, CD45.2, CD122, T-bet, CD1d, ICOS, CD127, CD150 (SLAM), and Ly108 (SLAM6) antibodies were all purchased from BioLegend. Anit-Nur77 was from ebioscience. After surface staining of related *i*NKT lineage markers, the intracellular staining of T-bet was performed with the eBioscience Foxp3 staining buffer set following the manufacturer's manual. All flow cytometry data were collected on FACSCantoTM II (BD Biosciences), and analyzed using the Flowjo software.

Bone marrow reconstitution

Recipient $TCR\beta^{-/-} \delta^{-/-}$ mice were sublethally irradiated (600 rad) one day before adoptive transfer. Bone marrow cells from age- and sex-matched CD45.1⁺ B6 and CD45.2⁺ DGKa ζ DKO or CA-IKK β mice were mixed at a 1:1 ratio. Ten million mixed cells were then intravenously injected into each recipient mouse. The resulting chimeric mice were analyzed 7 to 8 weeks later.

Western blot

5–10 million total thymocytes from WT or DGKαζDKO mice were rested in 0.5 ml PBS at 37°C for 20 min. Cells were then either left untreated or stimulated with an anti-CD3 antibody (500A2, 5 µg/ml, BD Biosciences) for 2 min. Cells were lysed in 1% NP-40 lysis buffer (1% NP-40, 150 mM NaCl, 50 mM Tris, pH 7.4) with protease and phosphatase inhibitors. Proteins in lysates were separated by SDS/PAGE and transferred onto nitrocellulose membrane. The blots were probed with anti-phospho-Erk1/2, anti-phospho-IkBα (Ser32), anti-total-IkBα, and anti-phospho-NFkB (Ser536), all of which were purchased from Cell Signaling. For loading control, the blots were stripped and reprobed with anti-β-actin (Sigma).

Real time PCR

Fifteen million viable CD4⁺CD8⁺ DP thymocytes from age- and sex-matched WT, DGK α ζDKO, and CA-IKK β mice were sorted on MoFlo Cell Sorter (Beckman Coulter), with post-sort purity>98%, and lysed in Trizol (Invitrogen). Total RNAs were extracted, and cDNAs were obtained using the Superscript III First-Strand Synthesis System (Invitrogen). Realtime PCR was prepared using the RealMasterMix (Eppendorf) and performed on the Mastercycler[®] ep realplex² system (Eppendorf). Primers used for different genes are listed in supplemental Table 1.

Assessment of V α -J α recombination

Five million viable CD4⁺CD8⁺ thymocytes from age- and sex-matched WT, DGKa ζ DKO, and CA-IKK β mice were sorted on MoFlo Cell Sorter (Beckman Coulter), with post-sort purity>98%, and genomic DNAs were extracted with phenol/chloroform, precipitated with 70% ethanol, and dissolved in TE buffer (10 mM Tris-0.5 mM EDTA, pH 8.0). For semi-quantitative PCR, decreasing amounts of DNA template (100 ng, 33 ng, 11 ng) from each sample were used. The forward primer for V α 14 segment was 5'-acactgccacctacatctgt-3'. The reverse primers for different J α segments were: J α 2 5'-ggttgcaaatggtgccactt-3'; J α 18 5'-gtagaaagaaacctactcacca-3'; J α 56 5'-tgtcatcaaaacgtacctggt-3'. Primers for CD14 PCR (loading control) were: forward 5'-gctcaaactttcagaatctaccgac-3', reverse agtcagttcgtggaggccggaaatc-3'.

Statistics

For statistic analysis, two-tail Student t-test was performed. *, p<0.05. **, p<0.01, ***, p<0.001.

RESULTS

Deficiency of DGK α or ζ has minimal impact on *i*NKT development

We first examined *i*NKT cell development in mice deficient of either DGK α or ζ . Total *i*NKT cells in the thymus, spleen, and liver were examined by dual surface staining of TCR β and α -Galcer-loaded CD1d-Tetramer (CD1d-Tet). No significant defects in percentages or absolute numbers of total *i*NKT cells were found in $DGK\alpha^{-/-}$ or $DGK\zeta^{-/-}$ mice except that liver *i*NKT cell number was slightly increased in $DGK\alpha^{-/-}$ mice (Fig 1A–B and D–E). Individual developmental stages within the CD1dTet⁺CD24⁻ thymic *i*NKT cells were further analyzed by their surface expression of CD44 and NK1.1, and no obvious differences were detected between $DGK\alpha^{-/-}$ or $DGK\zeta^{-/-}$ mice and WT controls (Fig 1C and F). Thus, absence of either DGK α or ζ does not drastically affect *i*NKT cell development.

Severe developmental defects of *i*NKT cells in *DGKa*^{-/-} $\zeta^{-/-}$ mice

To determine whether DGK α and ζ play a redundant role in *i*NKT cell development, we analyzed mice deficient in both *DGK* α and ζ . Drastic reduction of CD1dTet⁺TCR β ⁺ *i*NKT cells was observed in the thymus, spleen, and liver of *DGK* α ^{-/- ζ -/-} (DGK $\alpha\zeta$ DKO) mice as compared to WT mice (Fig 2A–B). Further analysis of the few remaining *i*NKT cells revealed significant decreases in the percentage of stage 3 cells and corresponding increases in the percentage of stage 2 cells in DGK $\alpha\zeta$ DKO mice (Figure 2C–2D). However, due to the drastic decrease of total *i*NKT cells in DGK $\alpha\zeta$ DKO mice, the absolute numbers of CD44⁻NK1.1⁻ (stage 1), CD44⁺NK1.1⁻ (stage 2), and CD44⁺NK1.1⁺ (stage 3) DGK $\alpha\zeta$ DKO *i*NKT cells were all decreased as compared to WT controls (Fig 2D). Furthermore, high death rates could be detected in all three stages of DGK $\alpha\zeta$ DKO *i*NKT cells in DGK $\alpha\zeta$ DKO mice (Fig 2E). Together, these observations demonstrate that DGK α and ζ play redundant and crucial roles for normal *i*NKT development.

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Cell intrinsic defect of developing DGKaζDKO iNKT cells

*i*NKT cells are positively selected when their *i*V α 14TCRs interact with glycolipid-CD1d complexes presented by cortical thymocytes. Defects in CD1d expression itself (30, 31) or in the lipid antigen loading process (1, 32) will all lead to abolishment of the *i*NKT development. In addition, cortical thymocyte surface receptors Slamsf1 and Slamsf6 provide co-stimulatory signals that are also essential for *i*NKT selection and development (8, 33). First, we asked whether the combined deficiency of DGK α and ζ affects the expression of these cell surface molecules. No significant difference in the surface expression levels of CD1d were detected between WT and DGK α ζDKO CD4⁺CD8⁺ DP thymocytes (data not shown). Slamsf1 (SLAM), and Slamsf6 (SLAM6) were slightly increased in DP thymocytes but obviously increased in *i*NKT cells from DGK α ζDKO mice as compared to WT controls (Fig 3A), suggesting that the developmental defects of DGK α ζDKO *i*NKT cells are unlikely caused by decreased SLAM or SLAM6 expression. At present, it is unclear whether elevated SLAM and SLAM6 expression may contribute to the developmental abnormalities of DGK α ζDKO *i*NKT cells.

To further examine if the DGK $\alpha\zeta$ DKO *i*NKT developmental defects are cell intrinsic, CD45.2⁺ DGK $\alpha\zeta$ DKO bone marrow (BM) cells were mixed with an equal amount of CD45.1⁺ WT BM cells, and adoptively transferred into sublethally irradiated $TCR\beta^{-/-}\delta^{-/-}$ hosts. *i*NKT cell development in recipient chimeric mice was analyzed 7–8 weeks after reconstitution. As shown in Figure 3B, equal reconstitution of total thymocytes from WT and DGK $\alpha\zeta$ DKO BM cells was achieved in the recipient mice. However, CD1dTet⁺ *i*NKT cells could only be detected in the CD45.1⁺ WT thymocytes, but not in the CD45.2⁺ DGK $\alpha\zeta$ DKO compartment. Similar observations were made in the spleen and liver as well (Fig S1). Thus, the aforementioned *i*NKT developmental defects in the DGK $\alpha\zeta$ DKO mice are cell-intrinsic.

Intrinsically, the most important driving force for *i*NKT cell development is the generation of functional, CD1d-restricted *i*V α 14TCRs by the cortical DP thymocytes. Insufficient V α 14-J α 18 recombination has been shown to cause severe early block in *i*NKT development (34, 35). We found that the DGK α ζDKO DP thymocytes are equally capable of rearranging the V α 14 segment to J α 18, J α 2 or J α 56 segments as compared to the WT controls (Fig 3C), suggesting a normal frequency of *i*V α 14TCR-expressing *i*NKT precursors at the DP stage. In addition, many other intrinsic factors have been identified as critical for early *i*NKT cells development, including signaling proteins SAP and Fyn as well as transcription factors ROR γ t (35, 36), Runx1 (36), cMyc (37), and HEB (34). However, no obvious decreases in mRNA expression levels of these molecules were detected between WT and DGK α ζDKO DP thymocytes (Fig 3D).

Altered signaling in DGKαζDKO thymocytes

Based on the data discussed above, we reasoned that the intrinsic developmental defects in DGK $\alpha\zeta$ DKO *i*NKT cells are most likely caused by dysregulated intracellular signaling activities. Next, we investigated how *DGK* α and ζ deficiency may affect TCR-induced DAG-mediated signaling pathways in thymocytes. As shown in Figure 3E, TCR induced phosphorylation of IkB α at serine 32 and NFkB at serine 536, both IKK dependent events, were elevated in DGK $\alpha\zeta$ DKO thymocytes as compared to WT thymocytes. IkB α phosphorylation leads to its ubiquitination and degradation, allowing for the nuclear translocation of NFkB. Indeed, total IkB α protein level was decreased in DGK $\alpha\zeta$ DKO thymocytes following TCR engagement as compared with WT thymocytes. Similar to previous observations derived from studies performed with mice in 129/B6 mixed background, TCR-induced Erk1/2 phosphorylation was also elevated in DGK $\alpha\zeta$ DKO thymocytes of C57B6/J background. Together, these data suggest that in DGK $\alpha\zeta$ DKO

thymocytes, DAG-mediated activation of both the Ras-Erk1/2 and PKC θ -IKK-NF κ B pathways is enhanced.

Defective iNKT cell terminal maturation due to enhanced Ras signaling

Since the Ras-Erk1/2 pathway is significantly enhanced in DGK $\alpha\zeta$ DKO thymocytes, we asked how elevated Ras signaling might affect *i*NKT cell development. We generated mice expressing a T-cell specific CA-KRas by breeding mice carrying a conditional CA-KRas allele with CD4-Cre transgenic mice. These mice carry a point mutation (G12D) in the KRas gene whose expression is normally blocked by the presence of a loxP-flanked transcription stop cassette (28). CD4-Cre mediated deletion of the stop cassette turns on the CA-KRas expression before the DP stage, which is when *i*NKT development begins. In contrast to DGKa(DKO mice, total iNKT cell numbers are only moderately decreased in these CA-KRas mice (Fig 4A–B). Strikingly, the mature CD44⁺NK1.1⁺ subset, which generally dominates the iNKT cell pool in WT thymus, was dramatically decreased in the CA-KRas mice and correlated with a significant accumulation of the CD44⁺NK1.1⁻ cells (Fig 4C–D). Such a maturation block, albeit less severe, was also observed in the periphery (Fig S2). Interestingly, an increase of death of stage 3 *i*NKT cells was observed in CA-KRas mice as compared with WT mice, which may contribute to the decrease of total stage 3 iNKT cells in CA-KRas mice. However, different from DGK α DKO mice, the death rates of stage 1 and 2 iNKT cells in CA-KRas mice were not increased (Fig 4E).

IL-15 and T-bet are two factors identified so far that specifically affect the terminal maturation of *i*NKT cells. The expression of both IL-15R β (CD122) and T-bet is progressively upregulated as the *i*NKT cells mature (38, 39). Mice with either IL-15 or IL-15 receptor deficiency lack the mature NK1.1⁺ *i*NKT cells (40, 41), and T-bet^{-/-} mice exhibit a similar block in *i*NKT maturation as observed in the CA-KRas mice (38). We asked whether elevated Ras signaling affected T-bet and/or IL-15R expression during *i*NKT development. As shown in Figure 4F, we found both intracellular T-bet and surface IL-15R β expression to be moderately lower in the CA-KRas CD44⁺NK1.1⁻ cells as compared to WT, but relatively normal in the CD44⁻NK1.1⁻ cells and CD44⁺NK1.1⁺ cells. These data suggest that the impaired *i*NKT maturation from stage 2 to stage 3 in CA-KRas mice might have resulted from insufficient IL-15 signaling and/or defective T-bet-mediated transcription programming at stage 2.

Overall, CA-KRas causes a late maturation block of *i*NKT cells and increased death of stage 3 *i*NKT cells, suggesting that enhanced Ras activation in DGK α CDKO mice may have contributed to the inefficient stage 2 to stage 3 transition observed in these mice.

iNKT cell developmental defect in thymocytes expressing constitutively active IKKβ

As shown above, enhanced Ras-Erk activation cannot account for the dramatic decrease of *i*NKT cells observed in the DGKa ζ DKO mice. Since DGKa ζ DKO thymocytes also manifest elevated IKK-NF κ B signaling, we asked how enhanced signaling from this pathway might affect *i*NKT cell development. We generated mice expressing a CA-IKK β in T cells by breeding mice carrying a conditional CA-IKK β allele with CD4-Cre transgenic mice. In these CA-IKK β mice, a floxed transcription stop cassette is located 5' of the CA-IKK β gene to prevent its expression until Cre-mediated deletion of this cassette occurs (29). Similar to DGKa ζ DKO mice, a severe decrease of *i*NKT cells was observed in thymus, spleen, and liver of the CA-IKK β mice (Figure 5A–B). However, different from DGKa ζ DKO and CA-KRas mice, a majority of the rare *i*NKT cells found in the CA-IKK β mice expressed high levels of NK1.1 (Fig 5C–D). Due to the severe decrease of *i*NKT cell numbers in CA-IKK β mice, stages 1, 2, and 3 *i*NKT cell numbers were all decreased (Fig 5C). A potential cause of the developmental defect of CA-IKK β *i*NKT cells could be caused by enhanced negative

selection due to hyperactivation of IKK β . However, no obvious difference of Nur77 expression between WT and CA-IKK β DP thymoyctes or *i*NKT cells was observed following intracellular staining (Fig 5F), suggesting that CA-IKK β may not enhance negative selection of *i*NKT cells. In contrast, expression of ICOS, a costimulatory molecule known to be important for *i*NKT cell homeostasis (21, 24, 42), was decreased in *i*NKT cells as well as in c $\alpha\beta$ T cells but not in DP thymocytes from CA-IKK β mice. Although it has been proposed that ICOS promotes IL7 α (CD127) expression, there was no obvious decrease of CD127 expression in CA-IKK β *i*NKT cells. However, there were substantial increases of death of stage 1 to 3 CA-IKK β *i*NKT cells as compared to WT controls (Fig 5E). Together, the observations demonstrate that CA-IKK β causes severe decreases of *i*NKT cells correlated with decreased ICOS expression and increased *i*NKT cell death.

To determine the cell-intrinsic role of IKK β signaling in the development and homeostasis of *i*NKT cells, we reconstituted sub-lethally irradiated $TCR\beta^{-/-}\delta^{-/-}$ mice with a 1:1 mixture of WT and CA-IKK β BM cells (Fig S3A–D). About 98% of total thymocytes in the recipient mice were derived from CD45.1⁺ WT BM, indicating that CA-IKK β progenitors have a severe competitive disadvantage. Nevertheless, CD1dTet⁺ *i*NKT cells were notably absent from the CA-IKK β mice was also cell-intrinsic. A similar trend was observed in spleen and liver of the recipient mice. Akin to DGK α CDKO mice, normal level of V α 14 to J α 18 recombination was also observed in CA-IKK β DP thymocytes (Fig S3E). CD1d, SLAM and SLAM6 expression on CA-IKK β DP thymocytes was similar to WT controls. SLAM and SLAM6 expression in CA-IKK β *i*NKT cells was slightly increased as compared to WT *i*NKT cells (Fig S3F). Moreover, we did not observe a significant reduction of various factors known to affect early *i*NKT development, such as SAP, Fyn, ROR γ t, RUNX1, cMyc, and HEB, between CA-IKK β and WT DP thymocytes (Fig S3G).

While it is known that some activity of the PKC θ -Carma1/Bcl10-IKK-NF κ B pathway is necessary for normal *i*NKT cell development, our data shows that elevated IKK signaling also proves detrimental to this process, thereby suggesting the need to maintain an optimal amount of signaling.

DISCUSSION

It has been well established that the *i*V α 14TCR signal plays a crucial role in *i*NKT cell development. Among TCR signaling pathways downstream of DAG and IP₃, the PKC θ -Carma1/Bc110/Malt-IKK-NF κ B pathway (13–18) and the Ca⁺⁺-calcineurin-NFAT pathway (43) have been demonstrated to be essential for *i*NKT cell development. However, the mechanisms regulating these TCR signaling cascades and the importance of such regulation during *i*NKT development have been poorly understood. In this report, we demonstrate that dysregulation of DAG-mediated signaling pathways hinders *i*NKT cell maturation and that DGK α and ζ redundantly promote *i*NKT cell development by fine-tuning these DAG-mediated signaling pathways.

Although the PKC θ -Carma1/Bcl10/Malt-IKK-NF κ B pathway is not essential for c $\alpha\beta$ T cell development, it is critical for the development of *i*NKT cells as well as regulatory T cells (Treg) (15, 44–46). It has been proposed that activation of NF κ B induces transcription of molecules promoting cell survival. In this regard, it is surprising that enhanced IKK-NF κ B signaling in the CA-IKK β mice leads to severe decrease of *i*NKT cells. *i*NKT cells appear to be more sensitive to an increase of IKK β activity than conventional $\alpha\beta$ T cells. It has been reported that deficiency of CYLD, a tumor suppressor with deubiquitinase function, also causes decrease of *i*NKT cell numbers due to increased NF κ B activation and cell death (24, 42). Our data are consistent with these observations and further support the importance of

tight regulation of the IKK-NF κ B pathway through multiple mechanisms as dysregulation of this pathway is detrimental to *i*NKT cells by inducing increased cell death.

Different from CA-IKK β , enhanced Ras activity in the CA-KRas mice does not appear to inhibit early iNKT cell development, suggesting that the RasGRP1-Ras pathway may not be involved in negative selection of *i*NKT cells. Yet the *i*NKT terminal maturation from stage 2 to stage 3, often referred to as the checkpoint 2, was dramatically blocked in the CA-KRas mice, resulting in a severe loss of mature CD44⁺NK1.1⁺ cells and a simultaneous accumulation of the CD44⁺NK1.1⁻ cells in the thymus, accompanied by selectively reduced T-bet and IL15R β expression at the CD44⁺NK1.1⁻ stage. Previous studies have shown that CD1d expression is required for *i*NKT terminal maturation (47), suggesting that continued signaling from $iV\alpha$ 14TCR remains critical at this checkpoint. In addition, IL-15 signaling and T-bet have been demonstrated to play essential and selective roles in promoting the iNKT maturation from stage 2 to stage 3. Our data suggested that strict regulation of the Ras-Erk pathway downstream of iVa 14TCR at checkpoint 2 is essential for iNKT terminal maturation, possibly by ensuring efficient IL-15 signaling and/or proper T-bet-mediated transcription programming. Moreover, the fact that enhanced Ras-Erk activity only affects late stage *i*NKT maturation but not early development suggests that qualitatively and/or quantitatively different TCR signals are involved in these two developmental checkpoints.

We demonstrate that DGK α and ζ perform redundant roles during early development and terminal maturation of iNKT cells. DGK activity regulates both DAG and PA concentrations. Our data suggest that the major impact of DGK α and ζ deficiency on *i*NKT development may be caused by uncontrolled DAG signaling since hyperactivation of either IKK β or KRas can also cause *i*NKT cell developmental defects. CA-IKK β and CA-KRas cause *i*NKT cell developmental defects that can mimic DGK α ζDKO to certain degrees. For example, both CA-IKKβ and DGKαζDKO mice display severe decreases of *i*NKT cells from stage 1 to 3, correlated with increased cell death. Similar to CA-IKKβ mice, ICOS expression in DGKαζDKO iNKT cells and cαβT cells is decreased (supplemental Fig S4A). In addition, stage 2 iNKT cells were relatively enriched in the remaining iNKT of DGKa(DKO mice and a defect in stage 2 to stage 3 maturation can be seen in CA-KRas mice. However, there are obvious differences between DGKa(DKO mice and CA-IKKß or CA-KRas mice. Different from CA-KRas iNKT cells, there is no decrease of T-bet or CD-122 expression on DGKαζDKO stage 2 *i*NKT cells (supplemental Fig S4A). In contrast, CD122 expression is upregulated in CA-IKK β *i*NKT cells (supplemental Fig S4B). Nur77 experssion is slightly increased in DGK $\alpha\zeta$ iNKT cells but not in CA-IKK β iNKT cells. Furthermore, the relative percentages of CD4⁺, CD4⁻, and CD8⁺ populations within *i*NKT cells also appear different among these mice. While these populations in CA-KRas mice are not obviously different from WT mice, the CD4⁺ to the CD4⁻ *i*NKT cell ratio is slightly increased in DGK α (DKO mice. In contrast, the relative percentage of CD4⁺ iNKT cells is decreased while the percentage of CD8⁺ iNKT cells is increased in CA-IKKβ mice (supplemental Fig S4C). Such differences may reflect the fact that DGK α and ζ double deficiency affects both the Ras-Erk1/2 and the PKC0-IKK-NFKB pathways. Furthermore, PA has also been reported to regulate the activities of multiple signaling molecules such as mTOR, Sos, and PI5K (20, 48-50). A reduction of DGK-derived PA could also contribute to the developmental abnormality in DGKaζDKO mice as well as the differences of DGKαζDKO mice to the CA-IKKβ and CA-KRas mice.

The semi-fixed nature of the $iV \alpha$ 14TCR and the existence of likely limited endogenous ligands presented by CD1d to this TCR suggest that $iV \alpha$ 14TCR signaling must be tightly regulated to ensure proper development of *i*NKT cells. Based on our data and other published studies, we propose that DAG signaling is not only essential but also needs to be tightly controlled for normal *i*NKT cell development. Under physiological conditions,

DGK α and ζ may play a redundant role to ensure normal development and homeostasis of *i*NKT cells by tuning down DAG-mediated activation of the PKC θ -IKK-NF κ B and the RasGRP1-Ras-Erk1/2 pathways. Absence of DGK α and ζ activities leads to dysregulated DAG-mediated signaling and defective *i*NKT cell development and homeostasis.

Supplementary Material

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Abbreviations

α-Galcer	α-galactosyl ceramide
DAG	Diacylglycerol
DGK	DAG kinase
IKK	IkB kinase
iNKT	invariant natural killer T cell
iVa14TCR	invariant Va14-Ja18 T cell receptor

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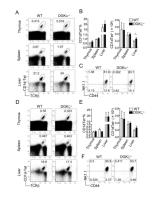


Figure 1.

*i*NKT cell developmental in mice deficient of either DGK α or ζ Thymocytes, splenocytes, and liver mononuclear cells from DGK $\alpha^{-/-}$ (A–C) or DGK $\zeta^{-/-}$ (D–F) mice and age/sexmatched WT controls were isolated, counted, and subjected to flow cytometry analysis. FACS plots shown are representative of five mice per group. (A) and (D), Flow cytometry of total thymocytes, splenocytes, and liver mononuclear cells stained with CD1d-Tet and anti-TCR β . (B) and (E), Percentage (left) and number (right) of live CD1d-Tet⁺TCR β ⁺ cells in thymus, spleen, and liver (mean, s.e.m.). *, p<0.05 (student t-test). (C) and (F), Expression of CD44 vs. NK1.1 on live CD1d-Tet⁺CD24⁻ gated thymocytes.

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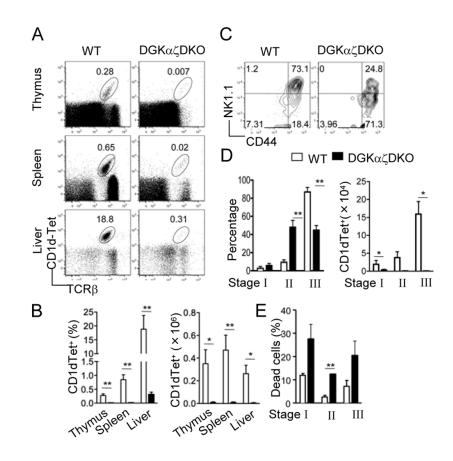


Figure 2.

Severe *i*NKT cell developmental defects in DGK α ζDKO mice Thymocytes, splenocytes, and liver mononuclear cells from age- and sex-matched DGK α ζDKO mice and WT controls were subjected to flow cytometric analysis. Data shown are representative of five mice per group. (A) Flow cytometry of cells stained with CD1d-Tet and anti-TCR β . (B) Percentage (left) and number (right) of live CD1d-Tet⁺ TCR β ⁺ cells (mean, s.e.m.). (C) Expression of CD44 vs. NK1.1 on live CD1d-Tet⁺CD24⁻ gated thymocytes. (D) Percentage (left) and number (right) of CD1d-Tet⁺CD24⁻ live thymocytes in different *i*NKT developmental compartments (mean, s.e.m.). (E) Percentage of cell death (defined by positive Live-Dead[®] staining) in different *i*NKT developmental compartments (mean, s.e.m.). *, p<0.05; **, p<0.01; ***, p<0.001.

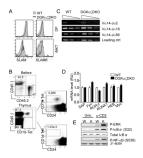


Figure 3. *i*NKT cell developmental defects in DGKaζDKO mice are cell-intrinsic and correlated with elevated DAG-mediated signaling

(A) Expression of SLAM (CD150) and SLAM6 (Ly108) on *i*NKT cells and DP thymocytes and TCR from WT and DGK $\alpha\zeta$ DKO mice. Data are representative of three mice per group. (B) Left top panel, expression of CD45.1 and CD45.2 on mixed WT and DGK $\alpha\zeta$ DKO bone marrow cells before adoptive transfer. Left bottom panel, CD45.1 and CD1d-Tet staining on total live thymocytes from recipient mice 7–8 weeks after bone marrow reconstitution. Right panels, CD1d-Tet and CD24 staining on CD45.1⁺ WT (top) and CD45.1⁻ DGK $\alpha\zeta$ DKO (bottom) live thymocytes from recipient mice. Data are representative of three experiments. (C) Semi-quantitative PCR analysis of sorted CD4⁺CD8⁺ thymocytes from WT and DGK $\alpha\zeta$ DKO mice with primers for V α 14-J α 2, V α 14-J α 18, V α 14-J α 56, and CD14 (loading control). (D) Real-time PCR analysis of mRNA expression of various proteins in sorted CD4⁺CD8⁺ thymocytes from WT and DGK $\alpha\zeta$ DKO mice. (E) Western blotting analysis with indicated antibodies of WT (W) and DGK $\alpha\zeta$ DKO (K) thymocytes left unstimulated (Uns.) or stimulated with anti-CD3.

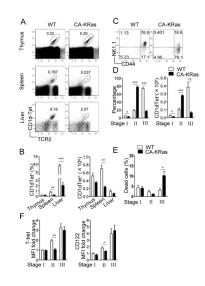


Figure 4.

Impaired *i*NKT cell terminal maturation caused by enhanced Ras signaling Thymocytes, splenocytes, and liver mononuclear cells from age- and sex-matched CA-KRas mice and WT controls were subjected to flow cytometric analysis. Data shown are representative of five mice per group. (A) Flow cytometry of cells stained with CD1d-Tet and anti-TCR β . (B) Percentage (left) and number (right) of live CD1d-Tet⁺TCR β^+ cells (mean, s.e.m.). (C) Expression of CD44 vs. NK1.1 on live CD1d-Tet⁺CD24⁻ gated thymocytes. (D) Percentage (left) and number (right) of CD1d-Tet⁺CD24⁻ live thymocytes in different *i*NKT developmental compartments (mean, s.e.m.). (E) Percentage of cell death in different *i*NKT developmental compartments (mean, s.e.m.). (F) Fold change in mean fluorescence intensity (MFI) of intracellular T-bet (left) and surface CD122 (right) staining in various subsets of CD1d-Tet⁺CD24⁻ thymocytes (mean, s.e.m.). *, p<0.05; **, p<0.01, ***, p<0.001.

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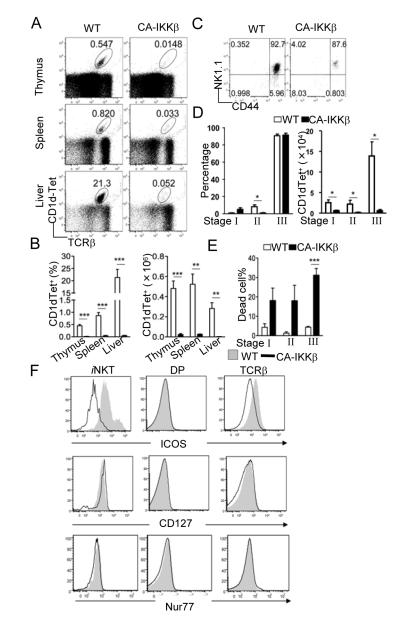


Figure 5. *i***NKT cell developmental defects in thymocytes expressing constitutively active IKK** β Thymocytes, splenocytes, and liver mononuclear cells from age- and sex-matched CA-IKK β mice and WT controls were subjected to flow cytometric analysis. Data shown are representative of five mice per group. (A) Flow cytometry of cells stained with CD1d-Tet and anti-TCR β . (B) Percentage (left) and number (right) of live CD1d-Tet⁺ cells (mean, s.e.m.). (B) Percentage (left) and number (right) of live CD1d-Tet⁺ TCR β ⁺ cells (mean, s.e.m.). (C) Expression of CD44 vs. NK1.1 on live CD1d-Tet⁺CD24⁻ gated thymocytes. (D) Percentage (left) and number (right) of CD1d-Tet⁺CD24⁻ live thymocytes in different *i*NKT developmental compartments (mean, s.e.m.). (F) ICOS, CD127, and Nur77 expression in *i*NKT cells, DP thymocytes, and TCR β ⁺ thymocytes. *, p<0.05; **, p<0.01; ***, p<0.001.