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J Immunol 2011; 187:4187-4198; Prepublished online 19 September 2011;
doi: 10.4049/jimmunol.1100367
http://www.jimmunol.org/content/187/8/4187

Supplementary Material http://www.jimmunol.org/content/suppl/2011/09/16/jimmunol.1100367.DC1

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The Journal of Immunology is published twice each month by
The American Association of Immunologists, Inc.,
1451 Rockville Pike, Suite 650, Rockville, MD 20852
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Print ISSN: 0022-1767 Online ISSN: 1550-6606.
The Liver Kinase B1 Is a Central Regulator of T Cell Development, Activation, and Metabolism

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T cell activation leads to engagement of cellular metabolic pathways necessary to support cell proliferation and function. However, our understanding of the signal transduction pathways that regulate metabolism and their impact on T cell function remains limited. The liver kinase B1 (LKB1) is a serine/threonine kinase that links cellular metabolism with cell growth and proliferation. In this study, we demonstrate that LKB1 is a critical regulator of T cell development, viability, activation, and metabolism. T cell-specific ablation of the gene that encodes LKB1 resulted in blocked thymocyte development and a reduction in peripheral T cells. LKB1-deficient T cells exhibited defects in cell proliferation and viability and altered glycolytic and lipid metabolism. Interestingly, loss of LKB1 promoted increased T cell activation and inflammatory cytokine production by both CD4+ and CD8+ T cells. Activation of the AMP-activated protein kinase (AMPK) was decreased in LKB1-deficient T cells. AMPK was found to mediate a subset of mTOR (mammalian target of rapamycin) signaling blocks the differentiation of CD4+ T cells toward inflammatory Th cell lineages (18, 20) while stimulating the development of regulatory T cells (18, 21, 22). Similarly, inhibition of mTOR results in increased Glut1-dependent glucose uptake and glycolysis (2, 3). Glucose availability is essential for the survival, proliferation, and effector function of activated T cells (4, 5). In contrast, quiescent T cells and regulatory T cells rely primarily on mitochondrial oxidative metabolism fueled by lipids and other metabolic substrates to maintain bioenergetic homeostasis and suppressor function (6–8). In addition, a switch from aerobic glycolysis to mitochondrial oxidative pathways is required for the establishment of CD8 T cell memory (9, 10). Thus, metabolic regulation is a crucial factor in T cell function, differentiation, and fate (11, 12).

The signal transduction pathways that regulate T cell metabolism remain poorly characterized. The P13K/Akt signal transduction pathway is a central regulator of glycolytic metabolism in the immune system (13, 14). TCR- and CD28-dependent Akt activation results in increased Glut1-dependent glucose uptake and stimulation of glycolytic activity (13, 15). Akt also stimulates the mammalian target of rapamycin (mTOR), which regulates multiple metabolic pathways including protein translation, lipid synthesis, autophagy, and mitochondrial biogenesis and function in response to growth factor signals (16). mTOR has emerged as an important regulator of T cell differentiation and effector function (17). mTOR activity is required for the full effector function of both CD4+ (18) and CD8+ (19) T cells, and inhibition of mTOR signaling blocks the differentiation of CD4+ T cells toward inflammatory Th cell lineages (18, 20) while stimulating the development of regulatory T cells (18, 21, 22). Similarly, inhibition of mTOR by rapamycin can promote the development of CD8+ T cell memory (9, 10). Identifying the signal transduction pathways that regulate T cell metabolism, and in particular modulators of mTOR activity, may help us understand how metabolic regulation impacts T cell function.

The liver kinase B1 (LKB1) is a serine/threonine kinase that functions as part of an evolutionarily conserved energy-sensing system of Pediatrics, Duke University Medical Center, Durham, NC 27710; Department of Physiology, McGill University, Montreal, Quebec H3G 1Y6, Canada; Goodman Cancer Research Centre, McGill University, Montreal, Quebec H3G 1Y6, Canada; Department of Pharmacology and Cancer Biology, Duke University Medical Center, Durham, NC 27710; Department of Immunology, Duke University Medical Center, Durham, NC 27710; and Sarah W. Stedman Center for Nutrition and Metabolism, Duke University Medical Center, Durham, NC 27710.

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www.jimmunol.org/cgi/doi/10.4049/jimmunol.1100367

pathway to couple cellular bioenergetics to metabolic pathways important for cell growth control, proliferation, polarity, and stress resistance (23). LKB1 was first identified as the tumor suppressor responsible for Peutz-Jeghers syndrome, an autosomal dominant disorder that leads to intestinal hamartomas, mucocutaneous lesions, and an increased risk of spontaneous epithelial carcinomas (24, 25). LKB1 was recently found to have prominent roles in hematopoietic stem cell viability and renewal (26–28), suggesting a prominent function for LKB1 in hematopoietic cells. One of the targets that link LKB1 to cellular metabolism is the serine/threonine kinase AMPK (AMP-activated protein kinase (AMPK), which can act to suppress mTOR activity (29). LKB1-dependent phosphorylation of the α subunit of AMPK at Thr172 stimulates AMPK activity, and LKB1 is essential for AMPK activation under conditions of bioenergetic stress (30–32). From a metabolic standpoint, AMPK promotes ATP conservation by activating pathways of catabolic metabolism and inhibiting anabolic processes that consume ATP (33). AMPK itself has been linked to stress resistance in lymphocytes (34).

Lymphocyte metabolism is a highly regulated process that plays a key role in the determination of T cell fate and function, and LKB1 is an established regulator of cell metabolism. However, although LKB1 has been shown to be important for thymocyte development (35, 36), its role in peripheral T cell metabolism, effector function, and mTOR regulation is not well defined. In this study, we show that LKB1 is a key regulator of glucose and lipid metabolism in T cells and is essential for both normal T cell development and peripheral T cell function. T cells lacking LKB1 displayed defects in cellular proliferation and viability in response to metabolic stress, yet showed increased activation and inflammatory cytokine production upon TCR stimulation. Moreover, loss of LKB1 in the T cell compartment led to an accumulation of IFN-γ-producing CD8+ and CD4+ T cells in peripheral lymphoid organs. AMPK mediated a subset of LKB1 functions in peripheral T cells; AMPKα1-deficient mice displayed normal thymocyte development and peripheral T cell homeostasis, but AMPKα1+/− CD8+ T cells displayed an activated phenotype with alterations in metabolism and cytokine production similar to LKB1-deficient T cells. Moreover, mTOR complex 1 (mTORC1) activity was elevated in LKB1−/− and AMPKα1-deficient T cells, and elevated IFN-γ production by these T cells could be reversed by rapamycin. Together, these data demonstrate a critical role for LKB1 in the regulation of peripheral T cell function and metabolism through regulation of AMPK-dependent and -independent pathways and mTORC1 signaling.

Materials and Methods

Mice

LKB1 floxed (stkl1-fl/fl) mice, which carry an LKB1 allele with LoxP sites flanking exons 3–6 (37), were obtained from the National Cancer Institute (Frederick, MD). Rag1−/− mice, Lck-Cre mice, CD45.1 congenic mice, and Ub-CreER2 mice were purchased from The Jackson Laboratory (Bar Harbor, MA), and Bcl-xL transgenic mice were obtained from the National Cancer Institute (Frederick, MD). LKB1−/− mice, LCK-Cre mice, and Ub-CreER2 mice were purchased from The Jackson Laboratory (Bar Harbor, MA), and Bcl-xL transgenic mice have been described (4). Mice deficient for AMPKα1 (34) or floxed for AMPKα2 (38) have been described previously. Lck-Cre mice were crossed to the Lck-Cre LKB1 strains to generate LKB1fl/fl Lck-Cre−/− mutants or LKB1−/− Lck-Cre−/−, LKB1−/−/− Lck-Cre−/−, and LKB1−/−/− Lck-Cre−/− controls. Bcl-xL transgenic mice were crossed to the Lck-Cre LKB1 strains to generate LKB1−/−/− Lck-Cre−/− mice that express the Bcl-xL transgene. Mice were bred and maintained under specific pathogen-free conditions at Duke University and McGill University under approved protocols. Experiments were performed using mice between 8 and 20 wk of age.

T cell purification and culture

T cells were purified from spleen and mesenteric lymph nodes by negative selection (StemCell Technologies, Vancouver, BC, Canada), and cells were cultured in IMDM or RPMI 1640 (Mediatech, Washington, DC) supplemented with 10% FBS (Gemini Bio-Products, West Sacramento, CA), 1-glutamine (Invitrogen, Chicago, IL), penicillin-streptomycin (Invitrogen), and 2-ME (Sigma-Aldrich, St. Louis, MO). CD44−/− cells were isolated by negative selection via the addition of biotinylated anti-CD44 added to the enrichment mixture. Where indicated, IL-7 was supplemented into media at a concentration of 10 ng/ml (eBioscience, San Diego, CA). T cell stimulation was induced by culturing purified T cells on anti-CD3ε (clone 145-2C11) and anti-CD28 (clone 37.51)-coated plates (eBioscience) and supplemented with IL-2 (PeproTech, Rocky Hill, NJ). CD4+ T cell differentiation was performed as described previously (7). To activate Cre-ER and excise the floxed LKB1 transgene, isolated T cells were treated with 4-hydroxytamoxifen (0.5 μM in ethanol; Sigma-Aldrich). 2-deoxy-glucose (2-DG), aminooimidazole carboxamide ribonucleotide (AICAR), and rapamycin were obtained from Sigma-Aldrich. T cell proliferation was measured by [3H]thymidine incorporation (1 μCi/ml) 48 h post-activation as previously described (39) or via flow cytometry using CFSE (Molecular Probes, Eugene, OR).

Flow cytometry, viability, and cell size measurements

Single-cell suspensions were stained with fluorescently conjugated Abs against murine CD4, CD8, CD3, Thy1.2, B220, CD19, CD25, CD44, CD45.1, CD45L2L, or CD69 (BD Biosciences, San Jose, CA). Cell viability was assessed via 7-aminofluorescein D (7-AAD; Sigma-Aldrich) or propidium iodide (PI; Molecular Probes) exclusion as previously described (30). Flow cytometry was performed on a FACSscan or LSR II (BD Biosciences) or Gallios (Beckman Coulter, Fullerton, CA) flow cytometer and analyzed with FlowJo software (Tree Star, Ashland, OR). Cell size was determined using a Coulter Z2 particle counter (Beckman Coulter). Bax activation was measured by fixing cells for 5 min with 0.25% paraformaldehyde in PBS, followed by incubation with an Ab specific to aa 12–24 (clone 6A7; BD Biosciences) as previously described (40).

Cytokine measurements

Intracellular cytokine staining (ICS) was performed using specific fluorochrome-labeled mAbs (eBioscience) and flow cytometry as described (41). In brief, single-cell suspensions of spleen or lymph nodes were stimulated immediately ex vivo with PMA and ionomycin (Sigma-Aldrich) for 4 h. Brefeldin A was added to cultures after 2 h of stimulation. ICS was carried out using a Cytofix/Cytoperm kit (BD Biosciences) following the manufacturer’s protocols. Cytokines in T cell supernatants were measured by capture ELISAs (eBioscience) using paired mAbs and recombinant standards, as previously described (15).

Quantitative real-time PCR

Total mRNA was isolated from mouse T cells using TRIzol (Invitrogen), and cDNA was synthesized from 100 ng total RNA using the Superscript VILO cDNA Synthesis Kit (Invitrogen). Quantitative PCR (qPCR) was performed using SYBR Green qPCR SuperMix (Invitrogen) and an Mx3005 qPCR machine (Agilent Technologies) using the following primers: glut1 forward, 5′-CTG GAC CTC AAA CTT CAT TGT GGG-3′; glut1 reverse, 5′-GGG TGT CTT GTC ACT TGT GCT G-3′; 4E-BP1 forward, 5′-CCG TGG TGG ACA AGA TAA GAG AGA ACC-3′; and b2 reverse, 5′-GGG CAC GTC ACA TTT CCG AGC CAG-3′. All samples were normalized to β-actin mRNA levels.

Immunoblotting

Cell lysate preparation, SDS-PAGE, electrophoretic transfer, immunoblotting, and development using ECL were conducted as described previously (1). To probe for Glut1, cells were lysed for 1 h on ice in PBS plus 1% Triton X-100 and 0.1% SDS containing protease inhibitors (BD Pharmingen). Otherwise, cells were lysed in RIPA buffer or AMPK Lysis Buffer (42) supplemented with protease and phosphatase inhibitors (Sigma-Aldrich). Primary Abs to AMPK (pT172-specific and total), phospho–acetyl-CoA carboxylase (ACC; pS79), p70 S6 kinase (S6K; pT389-specific and total), S6 ribosomal protein (pS235/236-specific and total), 4E-BP1 (pT37/46-specific and total), Bcl-xL, HKII, LDHA, and actin were provided by Cell Signaling Technology (Danvers, MA). Anti-LKB1 mouse mAb (Ley 37D/G6) was obtained from Santa Cruz Biotechnology (Santa Cruz, CA). Glut1 rabbit Ab was obtained from Abcam (Cambridge, MA).

Metabolic assays

Assays for glucose uptake, glycolytic flux, and mitochondrial-dependent β-oxidation of fatty acids were performed as previously described (9, 43, 44).

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Statistical analysis

Data are presented as mean ± SD and were analyzed using paired Student t test. Unless stated otherwise, a confidence level of p < 0.05 was considered statistically significant for all data.

Results

LKB1 is required for T cell development and homeostasis

To understand the role of the serine/threonine kinase LKB1 in T cell function, animals lacking expression of LKB1 in the T cell lineage were generated by crossing mice with LKB1 floxed (LKB1-fl/fl) (37) with mice expressing a Cre recombinase transgene under the control of the proximal Lck promoter (Lck-cre). Cre-expressing LKB1-fl/fl thymocytes and peripheral T cells displayed decreased expression of LKB1 protein as demonstrated by Western blotting (Fig. 1A). Lck-cre+, LKB1-fl/fl mice displayed dramatic reductions in both thymocyte (Fig. 1B) and peripheral T cell (Fig. 1C) numbers compared with control animals that retained endogenous LKB1 expression. Targeted T cell deletion of LKB1 also resulted in an increased proportion of CD4+CD8+ double-negative (DN) thymocytes with accumulation in the DN3 (CD25hi, CD44lo) stage and decreased numbers of double-positive (CD4+CD8+) and CD4+ and CD8+ single-positive thymocytes, suggesting incomplete thymic selection (Fig. 1D). Lck-cre+, LKB1-fl/fl LKB1-deficient mice displayed a decrease in both the proportion (Fig. 1E) and total number (Fig. 1F) of CD4+ and CD8+ peripheral T cells. LKB1-deficient T cells also displayed an increase in T cell size relative to Cre-negative controls (Fig. 1G).

LKB1-deficient T cells display defects in T cell proliferation and viability

Despite an overall defect in thymic development, limited numbers of peripheral CD4+ and CD8+ T cells were observed in T cell-specific LKB1 mutant animals. To assess their functional status, LKB1-deficient T cells were purified from spleen, activated in vitro using anti-CD3 and anti-CD28 Abs, and T cell proliferation rates measured by thymidine incorporation. As seen in Fig. 2A, T cells from Lck-cre+, LKB1-fl/fl mice displayed decreased proliferative capacity when activated with anti-CD3 Abs alone or in combination with CD28 costimulation. The addition of rIL-2 led to a partial rescue in proliferation of LKB1-deficient (LKB1-fl/fl, Lck-cre+) T cells (Supplemental Fig. 1A), but did not fully rescue T cell proliferation. To assess whether enhanced apoptosis could underlie the defective proliferation of LKB1-deficient T cells, we assessed levels of viability dye exclusion using PI. CFSE dilution profiles demonstrated that the majority of viable LKB1-deficient cells remained CFSEbright (Fig. 2B). However, LKB1-null T cells also displayed reduced viability relative to control T cells following activation (Fig. 2C). Although we cannot exclude cell death that occurred at the time of cell division, these data indicate that viable LKB1-deficient T cells exhibited delays in initiating cell division in response to TCR stimulation.

FIGURE 1. LKB1 is required for T cell development and peripheral homeostasis. A, LKB1 protein expression in LKB1-expressing (Lck-cre−) or LKB1-deficient (Lck-cre+) thymocytes and T cells. Total thymocytes and purified peripheral T cells were lysed and immunoblotted with Abs against LKB1 and actin. B and C, Summary of thymocyte (B) and peripheral T cell (C) counts in control (Lck-cre−, black bars) and LKB1 mutant (Lck-cre+, open bars) mice. Data are presented as means ± SEM for a minimum of 10 mice per genotype. D, Representative flow plots for expression of CD4 and CD8 on total thymocytes (top panel) and CD4 and CD8 expression on CD4/CD8 DN thymocytes (lower panel) from control (LKB1-fl/fl, Lck-cre−) or LKB1 mutant (LKB1-fl/fl, Lck-cre+) animals. Numbers represent the percentage of cells in the indicated quadrant. E, Representative flow plots for B220 versus Thy1.2 expression (upper panel) and CD4 versus CD8 expression on total splenocytes (lower panel) from animals of the indicated genotypes. F, Summary of peripheral CD4 and CD8 T cell numbers from control (black bars) or LKB1 mutant (open bars) animals. G, Resting T cell size as measured by Coulter counter (Beckman Coulter). Black bars represent control T cells; open bars represent LKB1-deficient T cells.
deficient T cells compared with controls (Supplemental Fig. 1C) of glycolysis (9), promoted increased rates of cell death of LKB1-deficient T cells, lacking LKB1 displayed increased rates of glucose uptake and glycolysis were assessed in LKB1-deficient T cells. T cells from mice with conditional and inducible deletion of LKB1 resulted in a pronounced increase in apoptosis following metabolic stress in LKB1-null T cells (Fig. 2F).

Because altered development may have influenced activation of peripheral LKB1-deficient T cells, we examined proliferation following inducible deletion of LKB1 in mature peripheral T cells. T cells from LKB1-fl/fl, Ub-Cre-ER<sup>+</sup> or LKB1-fl/fl, Ub-Cre-ER<sup>−</sup> animals were cultured with rIL-7 and 4-hydroxytamoxifen for 4 d to promote deletion of the floxed LKB1 alleles in Ub-Cre-ER<sup>+</sup> T cells, and then T cells were labeled with CFSE and stimulated with anti-CD3 and anti-CD28 Abs for 48 h. CFSE dilution profiles showed that T cells with acute deletion of LKB1 displayed reduced levels of cell division (Supplemental Fig. 1B).

LKB1 is an important regulator of cellular stress responses (45) and plays an essential role in the maintenance of hematopoietic stem cell viability (27). To test whether loss of LKB1 could influence T cell viability, LKB1-deficient or control thymocytes and peripheral T cells were cultured in the presence of the glycolytic inhibitor 2-DG, and cell viability was assessed. Although the viability of control cells was largely unaffected by 2-DG treatment (10 mM), LKB1-deficient thymocytes (Fig. 2E) and T cells (Fig. 2F) displayed increased levels of cell death. Withdrawal of IL-2, which reduces glucose metabolism similar to the direct inhibition of glycolysis (9), promoted increased rates of cell death of LKB1-deficient T cells compared with controls (Supplemental Fig. 1C). In addition, treatment of activated LKB1-null T cells with 2-DG (Fig. 2G) or withdrawal from IL-2 (Supplemental Fig. 1D) promoted increased activation of the proapoptotic Bax protein, demonstrating an increase in apoptosis following metabolic stress in LKB1-null T cells.

**LKB1 regulates T cell metabolism**

Activated effector T cells rely heavily on glucose metabolism to survive, proliferate, and support specific effector functions (4, 5, 46). To evaluate the influence of LKB1 loss on T cell metabolism, the rates of glucose uptake and glycolysis were assessed in LKB1-deficient T cells. T cells lacking LKB1 displayed increased rates of glucose uptake (Fig. 3A) and glycolytic flux (Fig. 3B) relative to control T cells, consistent with findings suggesting that LKB1 is required to regulate glucose metabolism in metabolic tissues (47). LKB1-deficient T cells displayed elevated expression of both glt1 and hexokinase 2 mRNA (Fig. 3C), as well as elevated Glut1 and hexokinase 2 protein levels (Fig. 3D, 3E). Glut1 protein expression was increased both at baseline and following TCR stimulation in the LKB1-null T cells as compared with controls (Fig. 3D).

We have previously shown that lipid oxidation can function as an alternate metabolic pathway in resting and memory T cells when glucose uptake is low or reduced or when cytokine availability is limiting (9). Thus, we assessed whether IL-2-dependent control of lipid metabolism was altered in LKB1-deficient T cells. Following cytokine withdrawal, which leads to downregulation of the glucose transporter Glut1 and reduced glycolysis (44), control T cells displayed an increase in their rate of lipid oxidation; however, the induction of lipid oxidation induced by IL-2 withdrawal was impaired in LKB1-deficient T cells (Fig. 3F). Collectively, these data suggest that LKB1 functions to coordinate glucose and lipid metabolism in T cells, and loss of LKB1 leads to deregulated metabolic function.

**Loss of LKB1 results in the accumulation of activated inflammatory T cells**

Given the disrupted metabolic and proliferative capacity of LKB1-deficient T cells, we next examined the effect of LKB1 loss on T cell effector function. Despite possessing fewer T cells overall, Lck-cre<sup>+</sup>, LKB1-fl/fl animals displayed increased numbers of CD4<sup>+</sup> and CD8<sup>+</sup> T cells with an activated phenotype (CD4<sup>+</sup> CD62L<sup>lo</sup>) (Fig. 4A). Both the CD4<sup>+</sup> and CD8<sup>+</sup> T cell populations from Lck-cre<sup>+</sup>, LKB1-fl/fl mice displayed a higher proportion of CD44-expressing cells (Supplemental Fig. 2A). Moreover, both conditional and inducible deletion of LKB1 resulted in a pronounced increase in the surface expression of activation markers.
CD25, CD44, and CD69 following TCR ligation (Supplemental Fig. 2B, 2C). Given the heightened activation state of LKB1-null T cells, we next examined cytokine production by T cells lacking LKB1. Peripheral T cells from LKB1-fl/fl; Lck-Cre+ or LKB1-fl/fl; Lck-Cre− control animals were isolated, stimulated with anti-CD3 and anti-CD28 Abs and IFN-γ and IL-17A in culture supernatants was measured. Despite lower overall levels of proliferation (Fig. 2A), LKB1-deficient T cells displayed elevated IFN-γ and IL-17A production relative to control T cells (Fig. 4B). We next isolated naive (CD44lo) CD4+ and CD8+ T cells from LKB1 mutant and control mice and examined TCR-induced cytokine production by individual T cell subsets. LKB1-deficient CD8+ T cells produced increased amounts of IFN-γ and IL-17A upon activation relative to LKB1-expressing T cells (Fig. 4C). LKB1-deficient CD4+ T cells also displayed a slight enhancement in IFN-γ production (Supplemental Fig. 2D). Finally, we assessed the capacity of naive CD4+ LKB1-null T cells to differentiate into Th1, Th2, or Th17 effector cells in vitro. T cells lacking LKB1 displayed enhanced differentiation toward Th1 and Th17 CD4+ T cell lineages (Fig. 4D).

We next analyzed whether LKB1 deficiency could alter the number of cytokine-producing T cells in vivo. Total splenocytes or lymph node cells were isolated from Lck-cre−, LKB1-fl/fl animals or littermate controls, stimulated immediately ex vivo with PMA and ionomycin, and the presence of IFN-γ and IL-2–producing cells was measured by ICS. Peripheral CD8+ (Fig. 4E) and CD4+ (Fig. 4F) T cells from T cell-specific LKB1-null animals were enriched for IFN-γ–producing cells as determined by ICS. In particular, a significant increase in the level of IFN-γ/IL-2–double-positive CD8+ T cells was observed in LKB1 T cell-deficient animals (Fig. 4E), suggesting that LKB1 functions as a negative regulator of IFN-γ–producing T cells in vivo.

**Bcl-xL rescues decreased thymocyte and peripheral T lymphocyte cellularity caused by LKB1 deficiency**

In principle, deletion of LKB1 at the DN stage of thymocyte development may promote low T lymphocyte cellularity (Fig. 1) due to either inefficient thymocyte differentiation or reduced viability. The antiapoptotic Bcl-2 family protein Bcl-xL is a key regulator of thymocyte viability (48), and reduced Bcl-xL levels have been linked to LKB1 deficiency (35). Indeed, thymocytes with deletion of both alleles of LKB1 gene displayed decreased levels of Bcl-xL protein (Fig. 5A). To assess whether restoring Bcl-xL levels could rescue the defect in T cell development in T cell LKB1-deficient mice, we generated Lck-cre−, LKB1-fl/fl mice that also expressed a T cell-specific Bcl-xL transgene and analyzed the central and peripheral T cell compartments of these mice by flow cytometry. Transgenic expression of Bcl-xL rescues total thymocyte cellularity in T cell-specific LKB1-deficient mice to wild-type levels and increased splenic T cell cellularity above wild-type levels regardless of LKB1 status (Fig. 5B).

Expression of Bcl-xL also restored the positive selection of CD4+ and CD8+ T cells in the thymus (Fig. 5C) and circumvented the developmental block at the DN3 (CD25loCD44lo) stage of thymocyte development caused by targeted deletion of LKB1 in thymocytes (Fig. 5D).
One explanation for the accumulation of activated T cells in T cell-specific LKB1-null animals is increased homeostatic T cell proliferation brought on by the reduced T cell compartment in these mice. To test this possibility, CFSE-labeled CD45.1 congenic donor T cells were adoptively transferred into either LKB1-deficient hosts or various control mice, and the level of homeostatic proliferation was assessed by CFSE dye dilution 1 wk posttransfer. Minimal levels of homeostatic proliferation by the CD45.1 donor T cell population were detected in LKB1-fl/fl, Lck-Cre+, Bcl-xL-Tg mice, with significant levels of T cell division observed only in Rag1−/− hosts (Supplemental Fig. 3A). Moreover, LKB1-dependent thymic cellularity was restored by expression of a Bcl-xL transgene (Fig. 5B), which permitted the direct examination of LKB1-deficient peripheral T cell function in the absence of lymphopenia. Despite equivalent cell numbers as control Bcl-xL transgenic animals, LKB1-deficient T cells expressing Bcl-xL continued to display elevated CD44 expression at baseline, as well as increased CD44, CD25, and CD69 expression upon stimulation (Supplemental Fig. 3B). Similarly, LKB1-deficient T cells expressing Bcl-xL displayed increased IFN-γ production upon T cell activation relative to control Bcl-xL-transgenic T cells (Fig. 5E). Thus, transgenic expression of Bcl-xL reversed the developmental and homeostatic defects, but not the activated T cell phenotype, in T cell-specific LKB1-deficient mice (Fig. 5), suggesting a cell-intrinsic role for LKB1 in the regulation of T cell activation.

**AMPKα1 regulates T cell viability and metabolism, but not TCR-mediated proliferation**

The most well-defined physiological target of LKB1 is the serine/threonine kinase AMPK (45). Phosphorylation of AMPKα at Thr172 and phosphorylation of its downstream target ACC occurs rapidly following TCR stimulation (Fig. 6A). As seen in Fig. 6B, LKB1-deficient T cells (LKB1-fl/fl, Lck-cre+) displayed impaired AMPKα and ACC phosphorylation following stimulation with the AMPK agonist AICAR, in agreement with previous work suggesting that T cells lacking LKB1 are defective for AMPKα and possibly AMPK signaling. We next examined the effects of AMPKα1 loss on T cell viability and metabolism. Activated T cells from AMPKα1-deficient
or control animals were cultured in the absence of IL-2 (Fig. 6D) or subjected to metabolic stress by 2-DG treatment (Fig. 6E) and cell viability measured. Similar to LKB1 deficiency, AMPKα1−/− T cells displayed reduced viability relative to control cells in response to these stresses (Fig. 6D, 6E). However, the expression of Bcl-xL protein was equivalent in both AMPKα1−/− and control T cells (Fig. 6F). Similar to LKB1-deficient T cells, AMPKα1−/− T cells displayed a 3-fold increase in the basal glycolytic rate of resting T cells ex vivo (Fig. 6G) and increased levels of glut1 and hko2 mRNA (Fig. 6H). AMPKα1-deficient T cells also displayed elevated expression of hexokinase 2 protein (Fig. 6I). Thus, loss of AMPK activity appears to phenocopy the effect of LKB1 deficiency on T cell metabolism (Fig. 3).

**AMPKα1 regulates CD8+ T cell activation and cytokine production**

To assess the effect of AMPKα1 loss on T cell effector function, we measured the level of activation and cytokine production of AMPKα1-deficient T cells following TCR stimulation. CD8+ T cells from AMPKα1−/− mice displayed elevated CD44 expression both prior to and following anti-CD3 and anti-CD28 stimulation (Fig. 7A). Similar to LKB1-deficient T cells, increased levels of secreted IFN-γ and IL-17A (Fig. 7B) were detected in AMPKα1−/− cultures following TCR stimulation. To ensure that these effects were not due to the presence of previously activated cells, naive (CD44−) CD4+ and CD8+ T cells were isolated and activated with anti-CD3 and anti-CD28 Abs, and supernatants were analyzed for cytokine production by ELISA. Interestingly, AMPKα1−/− CD8+ T cells displayed elevated IFN-γ and IL-17 production (Fig. 7C), whereas IFN-γ production by AMPKα1−/− CD4+ T cells did not differ significantly from control cells (Supplemental Fig. 4C). Elevated production of IFN-γ by AMPKα1−/− CD8+ T cells was also detected by intracellular cytokine staining (Fig. 7D). We next induced naive AMPKα1−/− CD4+ T cells to differentiate into Th1, Th2, and Th17 effector cells and observed no discernible difference in cytokine production between AMPKα1-deficient or control CD4+ T cells (Fig. 7E). Altogether, these data suggest that, in contrast to LKB1 (Fig. 4), AMPKα1 specifically regulates the production of inflammatory cytokines by CD8+ but not CD4+ T cells.

**LKB1-AMPKα1–dependent control of mTORC1 regulates IFN-γ production**

A major downstream effect of LKB1-AMPK signaling is the inactivation of the mTOR pathway (45). To determine the influence of reduced LKB1 signaling on mTORC1 activity, LKB1-null T cells were stimulated with anti-CD3 and anti-CD28 for 24 h, and phosphorylation of the downstream mTORC1 targets S6K, rS6, and 4EBP1 were assessed by Western blot. T cells lacking LKB1 expression displayed elevated S6K, rS6, and 4EBP1 phosphorylation following activation (Fig. 8A). Similar increases in S6K, rS6, and 4EBP1 phosphorylation were observed in T cells...
lacking AMPKα1 (Fig. 8B). Baseline phosphorylation of rS6 and 4EBP1 was also elevated in unstimulated AMPKα1−/− T cells (Fig. 8B). Inhibition of mTORC1 signaling by the addition of rapamycin to T cell cultures ablated the effect of LKB1- or AMPKα1-deficiency on enhanced IFN-γ production (Fig. 8C, 8D). Thus, LKB1 and AMPKα1 appear to play a key role in suppressing mTORC1 signaling, and elevated mTORC1 activity appears to promote the enhanced cytokine production by LKB1 and AMPKα1-deficient T cells.

**Discussion**

LKB1 functions at the center of a signaling axis that couples cellular bioenergetics and environmental stimuli with cell growth control and metabolism. In this study, we demonstrate that LKB1 plays a critical role in regulating T cell development and peripheral T cell function. Animals lacking LKB1 in the T cell compartment displayed a block in thymocyte development at the DN3 stage, resulting in decreased thymic cellularity and a reduced peripheral T cell compartment. LKB1-deficient T cells displayed defective proliferation in response to TCR and costimulatory signals, were increasingly susceptible to apoptosis induced by metabolic stressors or cytokine withdrawal, and displayed perturbations in glucose and lipid metabolism. Surprisingly, LKB1-deficient T cells that did not reach the periphery, either naturally or through forced expression of Bcl-xL to block aberrant cell death due to the lack of LKB1, displayed an activated phenotype characterized by increased ex-
expression of activation markers and elevated production of inflammatory cytokines. In particular, loss of LKB1 enhanced IFN-\(\gamma\) and IL-17 production by CD8\(^+\) T cells and promoted enhanced differentiation of CD4\(^+\) T cells toward Th1 and Th17 effector subtypes. In contrast, loss of AMPK\(\alpha\)1, a prominent downstream target of LKB1, only partially recapitulated the phenotype of LKB1-deficient T cells. AMPK\(\alpha\)1\(^{-/-}\) T cells displayed similar defects in T cell viability and metabolism, whereas T cell development and proliferative responses were normal. Although IFN-\(\gamma\) and IL-17 production by AMPK\(\alpha\)1\(^{-/-}\) T cells was also enhanced, this was largely due to deregulated CD8\(^+\) T cell function in the absence of AMPK\(\alpha\)1. The mTORC1 pathway was hyperactivated in both LKB1- and AMPK\(\alpha\)1-deficient T cells, and inhibition of this pathway by rapamycin was sufficient to block elevated IFN-\(\gamma\) production by these cells. Together our results establish the LKB1--AMPK signaling axis as a critical regulator of peripheral T cell viability and metabolism and a negative regulator of T cell inflammatory cytokine production through regulation of mTORC1 activity (Fig. 8E).

The present study, coupled with lines of evidence from other groups, indicates that LKB1 plays a multifaceted role in T cell development and peripheral function. Our data support previous work focused largely on the role of LKB1 in thymocyte development (36) and thymocyte survival (35) and suggest that LKB1 is a cell-autonomous factor essential for T cell development. We also demonstrate that LKB1 functions largely to regulate thymocyte viability, as both thymocyte cellularity and the impaired DN to double-positive transition are restored when apoptosis is blocked in T cell-specific LKB1-null mice by transgenic overexpression of Bcl-xL. This suggests that LKB1 is not essential for the T cell differentiation process itself, but rather may function to support cell survival during thymocyte development. Indeed, thymocytes and T cells lacking LKB1 display increased susceptibility to apoptosis induced by metabolic stress or cytokine withdrawal. Collectively, our data suggest that loss of LKB1 in T cells decreases overall T cell fitness leading to decreased viability, similar to that observed in hematopoietic stem cells (26–28). It is important to note, however, that the LKB1 mouse strain used in this study, which targets exons 3–6 of the stk11 gene for LKB1 (37), is different from the animals used by Tamas et al. (50), which targets exons 4–7 and results in the generation of a hypomorphic mutation that decreases LKB1 expression in the absence Cre recombinase. Consequently, one cannot rule out the possibility that hypomorphic LKB1 expression in other tissues, such as thymic epithelium, could contribute to the phenotypes previously described (36). Together, however, these data suggest that LKB1 functions to couple environmental cues to T cell survival either through the regulation of cellular metabolism and bioenergetics and/or Bcl-xL levels.

AMPK is one of the key physiological effectors downstream of LKB1. However, our data suggest that LKB1 exerts effects on T cell biology through both AMPK-dependent and -independent
AMPKα1 was largely dispensable for thymocyte development and T cell proliferation, both LKB1 and AMPKα1 mutant T cells displayed defects in glucose and lipid metabolism and stress-induced apoptosis, suggesting these biological processes are regulated through a common pathway. Similarly, LKB1 and AMPKα1 both function as negative regulators of inflammatory cytokine production. However, AMPK appears only to regulate CD8+ T cell activation and cytokine production, whereas LKB1 influences both CD4+ and CD8+ T cell function. AMPKα1 is just 1 out of 13 enzymes of the AMPK-related family of kinases activated by LKB1 and, as such, may only represent a fraction of LKB1-dependent processes in T cells.

One striking aspect of the activated T cell phenotype of LKB1 mutant mice is the appearance of enhanced cytokine-producing CD8+ T cells with diminished proliferative capacity. LKB1 has previously been shown to be a negative regulator of cell cycle entry (52), so loss of proliferative capacity with LKB1 loss in T cells runs counter to other cellular systems. One possible explanation for the increased activation of LKB1-null T cells could be homeostatic proliferation driven by lymphopenia due to the reduced T cell compartment in Lck-Cre+, LKB1-fl/fl mice (53, 54). However, expression of a Bcl-xL transgene rescues T cell numbers in LKB1 mutant mice but does not affect the heightened activation profile of or cytokine production by LKB1-deficient T cells. Moreover, the observation that AMPKα1-deficient animals display normal T cell development but enhanced T cell activation and cytokine production upon stimulation suggests that lymphopenia may not drive the activated phenotype of LKB1-deficient cells. Rather, altered LKB1/AMPK-dependent processes such as cellular metabolism or deregulated signaling downstream of LKB1 (i.e., increased mTORC1 activity) may drive T cell activation and cytokine production. Again, the complete scope of LKB1-dependent processes in T cells may only partially depend on AMPK, with AMPKα1 coupling LKB1 to the regulation of effector cytokine production while being dispensable for proliferation (Fig. 8E).

Our data suggest that regulation of mTORC1 signaling downstream of LKB1/AMPK is critical for inflammatory cytokine production. mTORC1 activity is elevated in LKB1- and AMPKα1-deficient T cells and rapamycin can reverse the elevated IFN-γ production by these T cells. Thus, LKB1–AMPK signaling represents a novel mechanism for regulation of mTORC1-dependent effector functions in T cells. Increased mTORC1 activity appears to generally influence T cell viability and effector function. T cell-specific deletion of Tsc1, a tumor suppressor that lies downstream of LKB1–AMPK signaling, results in increased mTORC1 activity and is required for the maintenance of T cell metabolism.
viability and quiescence (55–57). Whether LKB1–AMPK signaling influences T cell function through control of metabolism remains unclear. Increased glucose uptake, such as that observed in LKB1- and AMPKα1-deficient T cells, can enhance T cell activation and cytokine production (5). Thus, the increase in glucose metabolism associated with loss of LKB1–AMPK signaling may drive a feed-forward loop that promotes the development of proinflammatory effector T cells, resulting in the accumulation of activated IFN-γ-producing cells. The engagement of alternate metabolic pathways such as lipid oxidation (9), which is defective in LKB1- and AMPKα1-deficient T cells, may also contribute to this process. The activation of mTORC1 signaling, either through PI3K/Akt-mediated signal transduction or suppression of LKB1–AMPK activity, as shown in this study, appears to favor the development of inflammatory effector T cells.

Our data add to the growing body of evidence that AMPK signaling can influence inflammatory processes (58, 59).

The signal transduction pathways that regulate LKB1 and AMPK activity in T cells remain unclear. LKB1 is considered to have constitutive kinase activity and may be limited by the availability and/or localization of its substrates (23). More recent data have suggested that LKB1 is phosphorylated by Lck following TCR stimulation and associates with downstream TCR signaling components linker for activation of T cells and phospholipase Cγ1 (60). AMPK itself can be activated by other kinases in addition to LKB1, including CaMKK2 (61, 62), which may promote AMPK activation downstream of TCR stimulation (49). TCR activation stimulates the PI3K/Akt/mTOR pathway to promote Glut1 cell-surface trafficking and glycolysis, but upregulation of this metabolic pathway following TCR ligation takes several hours (5, 63). AMPK is rapidly activated following TCR stimulation (49) and thus may function to promote rapid increases in ATP generation through alternative metabolic pathways prior to the induction of glycolysis. Alternatively, the increased metabolic demands of T cell activation may promote metabolic stress conditions that in turn activate AMPK via LKB1. Developing and resting T cells require extrinsic signals mediated through the TCR and IL-7R to maintain glucose metabolism (4, 64), and these receptors may signal through LKB1 to regulate basal T cell metabolism. Further work must be done to characterize the signaling pathways both upstream and downstream of LKB1.

Together, our data establish LKB1 as a critical regulator of T cell development and peripheral T cell function. Our data suggest that inhibition of the LKB1–AMPK signaling axis disrupts T cell metabolism and promotes the development of proinflammatory T cells through hyperactivation of mTORC1 signaling. Deficiency in LKB1 or AMPKα1 leads to a reciprocal phenotype to mTOR deficiency (17), supporting the model that these pathways act in opposition as critical regulators of T cell metabolism and function. Thus, manipulation of LKB1–AMPK signaling may provide a new means by which to modulate inflammation and autoimmunity.

Acknowledgments

We thank Benoit Viollet for the generous gift of AMPKα1 and AMPKα2-deficient mice, Erika Pearce and Pamela Ohashi for critical reading of the manuscript, and members of the Rathmell and Jones Laboratories for helpful discussion and feedback.

Disclosures

The authors have no financial conflicts of interest.

References


