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MAPK, Phosphatidylinositol 3-Kinase, and Mammalian Target of Rapamycin Pathways Converge at the Level of Ribosomal Protein S6 Phosphorylation to Control Metabolic Signaling in CD8 T Cells

Robert J. Salmond,* Juliet Emery,† Klaus Okkenhaug,† and Rose Zamoyska2*‡

Ribosomal protein S6 (rpS6) is a key component of the translational machinery in eukaryotic cells and is essential for ribosome biogenesis. rpS6 is phosphorylated on evolutionarily conserved serine residues, and data indicate that rpS6 phosphorylation might regulate cell growth and protein synthesis. Studies in cell lines have shown an important role for the serine kinase mammalian target of rapamycin (mTOR) in rpS6 phosphorylation, further linking rpS6 to control of cellular metabolism. rpS6 is essential in T cells because its deletion in mouse double-positive thymocyte cells results in a complete block in T cell development; however, the signaling pathway leading to rpS6 phosphorylation downstream of TCR stimulation has yet to be fully characterized. We show that maximal TCR-induced rpS6 phosphorylation in CD8 T cells requires both Lck and Fyn activity and downstream activation of PI3K, mTOR, and MEK/ERK MAPK pathways. We demonstrate that there is cross-talk between the PI3K and MAPK pathways as well as PI3K-independent mTOR activity, which result in differential phosphorylation of specific rpS6 serine residues. These results place rpS6 phosphorylation as a point of convergence for multiple crucial signaling pathways downstream of TCR triggering.

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stimulation of T cells via engagement of the TCR and co-stimulatory receptors induces biochemical signaling pathways that result in a switch from a quiescent state to an activated state. This necessitates an increased acquisition or synthesis of proteins, lipids, and nucleic acids plus an increased production of ATP to sustain the characteristic elevated rates of growth and proliferation, and the acquisition of effector function by activated T cells. A key protein in coupling TCR signals to increased rates of mRNA translation and protein synthesis is the serine/threonine kinase mammalian target of rapamycin (mTOR) (1). Activation of mTOR occurs in T cells in response to multiple stimuli, including extracellular nutrients, cytokines, and TCR/coreceptor engagement, and is thought to be regulated through activation of the PI3K-Akt pathway. mTOR exists in at least two different protein complexes: a rapamycin-sensitive complex with mTORC1 (2, 3) and a rapamycin-insensitive complex with raptor (mTORC1) (2, 3) and a rapamycin-insensitive complex with raptor (mTORC1) (2, 3) and a rapamycin-insensitive complex with raptor (rictor) (4). Rapamycin functions as a potent immunosuppressive drug via inhibition of mTORC1 and subsequent effects on translation (5) and inhibition of lymphocyte proliferation (6). Furthermore, inhibition of mTOR activation during Ag stimulation of T cells in vitro results in anergy, suggesting that mTOR is critical in determining the functional outcome of Ag recognition (7). In addition, recent data have shown that activation of mTOR is important in regulating the expression of the chemokine receptor CCR7 and thereby controlling T cell trafficking in vivo (8).

Important substrates of mTORC1 include ribosomal protein S6 kinase (S6K) (9, 10) and 4E-binding protein 1 (11). Rapamycin-mediated inhibition of S6K phosphorylation and activation or genetic ablation of S6K expression result in translational repression of mRNAs containing a 5′-terminus polyuridylic-acid-rich tract (12). Furthermore, one of the major substrates for S6K, ribosomal protein S6 (rpS6), is a critical determinant of ribosomal biogenesis. Deletion of the S6 gene in mice results in embryonic lethality as a result of a failure to form functional ribosomes, whereas targeted deletion of a floxed S6 allele in the T cell lineage using CD4-Cre completely abrogates T cell development (13). Moreover, whereas deletion of a single floxed S6 allele has no major impact on thymocyte development, T cell proliferation in response to TCR stimulation is completely abrogated as a result of the activation of a p53-dependent cell cycle checkpoint (13).

It has long been thought that S6K-mediated serine phosphorylation is critical for rpS6 function, and that the effects of S6K deletion on translation in mice are at least in part a consequence of a failure in rpS6 phosphorylation (14). However, recent analysis of S6KI/2 double-knockout (KO) mice has suggested that, in murine embryonic fibroblasts, there exists an S6K-independent pathway of rpS6 phosphorylation that is mediated by MAPK (12). Furthermore, analysis of knockin mice expressing a nonphosphorylatable version of the rpS6 protein indicates phosphorylation-independent functions of rpS6 in mouse development and in fibroblast growth.
(15). However, the mechanism of TCR-induced rpS6 phosphorylation and its role in T cell responses have not yet been elucidated. Given the critical importance of rpS6 in T cell development and its potential to act as an effector of mTOR/S6K function, we sought to determine the pathways required for rpS6 phosphorylation downstream of TCR engagement. Using TCR transgenic mice, we show that the TCR stimulates robust rpS6 phosphorylation in the absence of CD28 costimulation, and that optimal phosphorylation of rpS6 requires activation of both Lck and Fyn. mTOR and ERK/p90 ribosomal S6K (RSK) MAPK pathways are partially redundant for TCR-induced rpS6 and S6K phosphorylation, and these pathways have distinct influences on phosphorylation of individual rpS6 serine residues. Although the p110α isoform of PI3K contributes to TCR-induced rpS6 phosphorylation, additional PI3K isoforms also participate in this TCR signaling pathway. Furthermore, we demonstrate that PI3K-independent mTOR activity can also facilitate rpS6 phosphorylation in T cells, and show that amino acid signaling may contribute to this pathway. Taken together, these data indicate that TCR-induced mTOR activation can occur through several independent pathways, and that the exquisitely controlled phosphorylation of rpS6 acts as a point of convergence for PI3K, mTOR, and MAPK pathways.

Materials and Methods

Mice

Wild-type (WT) F5 TCR transgenic and inducible Lck (LckΔα/Δα) mice on Lck−/−, Fyn−/−, Rag1−/−, and F3 TCR-transgenic backgrounds have been described previously (16). Lck−/− mice were fed doxycycline (dox) in food (1 mg/g) from birth, and groups of mice were taken off dox for 12 days before analysis. P110α D90A mice (17) were backcrossed to an OT-I TCR transgenic background. Mice were housed under specific pathogen-free conditions in barrier units at the National Institute for Medical Research, the University of Edinburgh, and the Babraham Institute. All procedures were conducted under United Kingdom Home Office and local ethical guidelines.

T cell preparation and stimulation

Single-cell suspensions from lymph nodes of mice were prepared in IMDM supplemented with 10% FCS, penicillin/streptomycin, and 2 mM L-glutamine. For analysis of the role of extracellular amino acids in rpS6 phosphorylation, rpS6 requires activation of both Lck and Fyn. mTOR and ERK/p90 ribosomal S6K (RSK) MAPK pathways are partially redundant for TCR-induced rpS6 and S6K phosphorylation, and these pathways have distinct influences on phosphorylation of individual rpS6 serine residues. Although the p110α isoform of PI3K contributes to TCR-induced rpS6 phosphorylation, additional PI3K isoforms also participate in this TCR signaling pathway. Furthermore, we demonstrate that PI3K-independent mTOR activity can also facilitate rpS6 phosphorylation in T cells, and show that amino acid signaling may contribute to this pathway. Taken together, these data indicate that TCR-induced mTOR activation can occur through several independent pathways, and that the exquisitely controlled phosphorylation of rpS6 acts as a point of convergence for PI3K, mTOR, and MAPK pathways.

Flow cytometry

Flow cytometry was performed using a FACSCalibur flow cytometer (BD Biosciences). Cells were stimulated, as described above, and then fixed at a final concentration of 2% formaldehyde for 20 min at 37°C. Following centrifugation, supernatant was removed, and cells were resuspended in 90% ice-cold methanol and stored at −20°C until analysis. Cells were washed thoroughly in PBS, before being incubated in PBS containing 1% BSA (PBS-1% BSA) for 10 min at room temperature. Cells were stained with anti-phospho-rpS6 Ser235/6 (2F9 or D57.2.2E), anti-phospho-rpS6 Ser240/41 (6H9), or anti-phospho-ERK T202/Y204 (197G2) rabbit mAbs (all Cell Signaling Technology) diluted in PBS-1% BSA for 30 min at room temperature. Cells were washed in PBS before staining with anti-rabbit F(ab′)2–FITC/PE conjugates (Jackson ImmunoResearch Laboratories) and CD8α-allophycocyanin (eBioscience) for 30 min in darkness. Following washing in PBS, at least 10,000 events were captured, and data for gated CD8+ cells were analyzed using FlowJo software (Tree Star).

Results

TCR stimulation induces prolonged serine phosphorylation of rpS6

Upon TCR engagement by cognate peptide, an initial wave of tyrosine phosphorylation is followed by the activation of serine/threonine kinases, including MAPK, Akt, and mTOR. Serine/Threonine kinase activity critically regulates many facets of T cell function, including metabolism, survival, and proliferation (19). Ribosomal protein rpS6 is phosphorylated on several different serine residues in response to TCR triggering, and rpS6 phosphorylation has been implicated in the regulation of protein synthesis by serine kinases such as mTOR and S6K. Initial experiments were performed to ascertain the kinetics of TCR-induced rpS6 phosphorylation. CD8+ T cells from Rag1KO F5 TCR transgenic mice were stimulated with cognate peptide from the nucleoprotein of influenza virus A/NT/60/68 (NP68: ASNENMDAM) for varying periods of time, and phosphorylation of rpS6 was assessed by Western blotting using phospho-specific Abs. In addition, the phosphorylation status of a number of kinases potentially involved in the signaling pathway upstream of rpS6 was monitored. The data show that the upstream kinases Akt and ERK were phosphorylated within 5 min of TCR stimulation (Fig. 1). Phosphorylation of Akt and ERK peaked at ~1 h of stimulation, and could still be measured for the full 5 h monitored in the experiment. Initiation of phosphorylation of the ERK target p90 RSK mirrored that of ERK, but the signal appeared to be more sustained (Fig. 1). Similarly, phosphorylation of the mTOR effector p70 S6K was sustained at high levels up to at least 5 h of stimulation (Fig. 1). Finally, rpS6 phosphorylation was assessed using two mAbs specific for distinct phosphorylation sites. In contrast to Akt, ERK, RSK, and S6K, TCR induction of rpS6 phosphorylation was delayed, being undetectable after 5 min of stimulation (Fig. 1). However, once initiated, phosphorylation of both Ser240/41 and Ser421/422 residues was sustained for at least 5 h of stimulation. In the remaining experiments, phosphorylation was measured at up to 3 h of stimulation because at later time points we could not exclude that autocrine cytokine secretion by the F5 cells might contribute to the signaling, thus confusing whether the signals were primarily TCR derived.

Optimal TCR-induced rpS6 phosphorylation requires both Lck and Fyn

Activation of the src family kinases (SFK) Lck and Fyn is critical for TCR signaling. Lck plays a dominant role in initiation of TCR signaling, but Fyn can also contribute to activation of the ERK, MAPK, and PI3K pathways (16, 20). To assess the roles of the two kinases in rpS6 phosphorylation, a LckΔα transgenic mouse system

(TAT-1; in-house hybridoma). Proteins were detected with secondary reagent anti-mouse IRDye 800CW (Rockland) or anti-rabbit Alexa Fluor 680 (Molecular Probes), and visualized using the Odyssey Infrared Imaging System (LI-COR Biosciences).

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was used. As the mice are crossed onto the LckKO background, the expression of Lck protein in Lck\textsuperscript{ind} mice is controlled exclusively by the induction of a tetracycline-responsive transgene by inclusion of dox in the diet (21) (hereafter referred to as LckON). Withdrawal of the mice from dox results in the loss of Lck expression within ~7 days (LckOFF). Groups of Lck\textsuperscript{ind} Rag1\textsuperscript{-/-} Lck\textsuperscript{F5} T cells were removed from dox diet for 12 days, and the response of cells to TCR stimulation was compared with that of cells from mice maintained on dox diet. The three groups of mice analyzed were as follows: 1) dox-fed LckON/FynWT, expressing both Lck and Fyn; 2) dox-fed LckON/FynKO, expressing only Lck; and 3) dox-withdrawn LckOFF/FynWT, expressing only Fyn, allowing the comparison of the responses of cells expressing both SFK or each alone (Fig. 2A). Cells were stimulated for 1 h, and rpS6 phosphorylation was assessed by flow cytometry. The histograms in Fig. 2A demonstrate that either Lck or Fyn alone is sufficient to transduce TCR signals that result in rpS6 phosphorylation. Furthermore, levels of TCR-induced rpS6 phosphorylation were greatest when both kinases were present (Fig. 2, A and C). Importantly, pretreatment of cells with the SFK inhibitor PP2 completely blocked rpS6 phosphorylation in all groups of mice, demonstrating the absolute requirement for SFK activity for activation of this pathway (Fig. 2C).

Next, we assessed TCR-induced phosphorylation of S6K. Phosphorylation of S6K at residue Thr\textsuperscript{389} was completely inhibited by rapamycin and LY294002 (Fig. 2C), as has been previously reported for serum-activated fibroblast cell lines (23). GM-CSF-stimulated neutrophils (24), and BCR-stimulated B cells (27). By contrast, phosphorylation at residues Thr\textsuperscript{421}/Ser\textsuperscript{424} was only partially blocked by inhibition of PI3K, mTOR, or MEK-dependent signaling (Fig. 2C). These data suggest that full activation of S6K following TCR stimulation might require input from both PI3K/mTOR and MAPK pathways.

TCR-induced rpS6 phosphorylation is dependent on the combined activity of the PI3K, mTOR, and MEK pathways

Previous studies have shown that MAPK and S6K contribute to phosphorylation of rpS6 in murine embryonic fibroblasts (12). Furthermore, full activation of S6K is critically dependent on its phosphorylation at multiple Ser and Thr residues (22). S6K Thr\textsuperscript{389} phosphorylation in serum-stimulated cell lines is inhibited by blockade of PI3K or mTOR pathways (23), whereas MAPK pathways may contribute to phosphorylation of S6K at additional Thr and Ser residues (24). Rapamycin-mediated inhibition of phosphorylation of Thr\textsuperscript{421}/Ser\textsuperscript{424} sites in S6K is likely to be indirect, because dephosphorylation of Thr\textsuperscript{389} affects the accessibility of these sites to other kinases (22). To assess the role of the PI3K, mTOR, and MAPK pathways in TCR-induced S6K and rpS6 phosphorylation, F5 T cells were pretreated with pharmacological inhibitors, and then stimulated for varying time periods with NP68 peptide. The inhibitors used were the mTOR/P13K inhibitor LY294002, the MEK inhibitor U0126, and the mTOR inhibitor rapamycin. Although CD28 costimulation augments PI3K activation at the immunological synapse, anti-CD3 can induce robust phosphorylation of Akt in CD28\textsuperscript{-/-} cells (25). In the present work, we used CTLA4-Ig to block CD28 signaling.

Phosphorylation of signaling molecules was assessed after stimulation of F5 T cells with cognate NP68 peptide for the times specified. Western blots of whole-cell lysates were probed with phospho-specific and loading control Abs, as indicated. Images were obtained using the Odyssey LI-COR Infrared Imaging System and in all cases, blots represent one of at least three replicate experiments.

**FIGURE 1.** TCR triggering induces sustained rpS6 phosphorylation. Phosphorylation of signaling molecules was assessed after stimulation of F5 T cells with cognate NP68 peptide for the times specified. Western blots of whole-cell lysates were probed with phospho-specific and loading control Abs, as indicated. Images were obtained using the Odyssey LI-COR Infrared Imaging System and in all cases, blots represent one of at least three replicate experiments.

Phosphorylation of signaling molecules was assessed after stimulation of F5 T cells with cognate NP68 peptide for the times specified. Western blots of whole-cell lysates were probed with phospho-specific and loading control Abs, as indicated. Images were obtained using the Odyssey LI-COR Infrared Imaging System and in all cases, blots represent one of at least three replicate experiments.
To assess the effects of the inhibitors on rpS6 phosphorylation, FACS experiments were performed, because this analysis allows assessment of both the numbers of cells that respond in the presence of the inhibitor (percentage of positive cells), as well as the extent of rpS6 phosphorylation per cell. The latter can be obtained by measuring the mean fluorescence index (MFI). For both types of analyses, values were calculated relative to the maximal control values obtained following stimulation of cells with peptide in the absence of inhibitor. There was maximal inhibition of only \( \frac{30\%}{30\%} \) in the numbers of rpS6 phospho-Ser235/6-positive cells after stimulation with peptide for 0.5 or 3 h following treatment with LY294002, rapamycin, or UO126 (Fig. 4A and supplementary Fig. 1). However, the extent of rpS6 Ser235/6 phosphorylation in positive cells was reduced by all three inhibitors, as assessed by the reduction in MFI, an effect most clearly seen after 3 h of stimulation (Fig. 4B and supplementary Fig. 1). However, the extent of rpS6 Ser235/6 phosphorylation in positive cells was reduced by all three inhibitors, as assessed by the reduction in MFI, an effect most clearly seen after 3 h of stimulation (Fig. 4B and supplementary Fig. 1). In this regard, the MFI in individual cells was \( \frac{50\%}{50\%} \) lower on average in cells treated with any one of the three inhibitors as compared with peptide alone.

Interestingly, dissimilar results were obtained when we assessed rpS6 Ser240/4 phosphorylation in which markedly different effects of the inhibitors were observed. Following inhibition of mTOR and/or PI3K with LY294002 or rapamycin treatment, numbers of rpS6 phospho-Ser240/4-positive cells were reduced by \( \frac{40 – 60\%}{40 – 60\%} \), whereas inhibition of MEK with UO126 had no effect on the numbers of positive cells, despite control ERK phosphorylation being completely inhibited (data not shown). Furthermore, the MFI of rpS6 phospho-Ser240/4 staining in positive-gated cells was reduced by \( \frac{50\%}{50\%} \) by rapamycin (Fig. 4B and supplementary Fig. 1). LY294002 had a similar inhibitory effect when assessed after 30 min, but this reduction in MFI had disappeared by 3 h of peptide stimulation. In contrast, there was a consistent increase in the levels of rpS6 phospho-Ser240/4 staining in cells pretreated with UO126, suggesting that the MEK/ERK pathway might also negatively regulate rpS6 phosphorylation.

None of the inhibitors used alone completely inhibited rpS6 phosphorylation, suggesting that the PI3K, mTOR, and MEK pathways were partially redundant in inducing rpS6 phosphorylation upon TCR triggering. We therefore reasoned that to completely block rpS6 phosphorylation, combinations of the inhibitors might be more effective. Combining LY294002 and rapamycin failed to completely block RSK, S6K Thr421/Ser424, and rpS6 phosphorylation (Fig. 5A), indicating that these inhibitors act on a downstream pathway that is common to PI3K and mTOR. By contrast,
inhibiting the MEK/ERK pathway together with either PI3K and/or mTOR using a combination of UO126 with either LY294002 or rapamycin completely prevented phosphorylation of rpS6, S6K, and RSK (Fig. 5A). Similarly, pretreatment with the SFK inhibitor PP2 completely blocked TCR-induced rpS6, S6K, and RSK phosphorylation, confirming a critical role for the upstream kinases Lck and Fyn (Fig. 5A). These data demonstrate convergence of the mTOR and MAPK pathways at the level of both rpS6 and S6K phosphorylation. Full activation of S6K appears to require phosphorylation at a number of important residues, including Thr389 and Thr421/Ser424 (24). There- ther addition of rapamycin, indicating that S6K and rpS6 phosphorylation is partly mTOR dependent, but PI3K independent (Fig. 5D). As before, a combination of rapamycin and UO126 or LY294002 and UO126 completely inhibited rpS6 phosphorylation (Fig. 5D). Thus, complete inhibition of TCR-induced rpS6 and S6K phosphorylation is achieved by simultaneously blocking mTOR- and MEK-dependent signaling, and whereas PI3K activity contributes to the upstream signaling pathway(s), it appears to act indirectly on S6K and rpS6 phosphorylation through mTOR and/or MEK.

A potential complication in the use of LY294002 is that this compound inhibits both mTOR and PI3K at nearly identical concentrations (28). Therefore, it is unclear whether a given effect is due to inhibition of PI3K or mTOR or both. Wortmannin, a structurally distinct PI3K inhibitor, can also directly inhibit mTOR, but only at doses 10- to 100-fold higher than those required for PI3K inhibition (28). We compared the ability of wortmannin and LY294002 to block S6K and rpS6 phosphorylation. Pretreatment of F5 cells with either inhibitor blocked TCR-induced Akt phosphorylation, indicating equivalent inhibition of PI3K-dependent pathways (Fig. 5B). In contrast, wortmannin had little effect on S6K Thr389/Ser424 phosphorylation (Fig. 5B). Furthermore, a combination of wortmannin and UO126 failed to block all S6K or rpS6 phosphorylation (Fig. 5, C and D). Importantly, the remaining phospho-S6K and rpS6 signal was blocked completely by the
FIGURE 5. Complete blockade of rpS6 phosphorylation requires inhibition of both mTOR- and MEK-dependent pathways. A, F5 T cells were pretreated with combinations of LY294002 (LY), rapamycin (Rap), UO126 (UO), and PP2 before stimulation with NP68 for 1 h, and Western blots of total cell lysates were performed, as described. B, Wortmannin (wort) is a less potent inhibitor of S6K phosphorylation than LY294002. Cells were pretreated with the indicated inhibitors for 30 min before stimulation with NP68 peptide for 1 h. mTOR-dependent, MEK/PI3K-independent rpS6 (C) and S6K (D) phosphorylation could be demonstrated in F5 T cells pretreated with combinations of inhibitors, as indicated, and stimulated with NP68 peptide for 1 h. C, Intracellular staining for rpS6 and FACS was performed. Filled histograms represent levels of phospho-rpS6 staining in control, unstimulated cells, whereas overlays represent cells stimulated with NP68 in the presence of inhibitors. D, Western blots of total cell lysates were probed with pS6K and S6K Abs. E, F5 T cells pretreated with rapamycin (Rap) were cultured in conventional RPMI 1640 or amino acid-free (No AA) RPMI 1640 culture medium and stimulated with NP68 peptide for 30 min. Intracellular phospho-rpS6 staining and FACS analysis were performed. For parts C and E, values in upper right of histograms represent percentage of gated phospho-rpS6-positive cells (upper value) and MFI of gated phospho-rpS6-positive cells (lower values). All Western blots and FACS histograms are representative of three experiments.
amino acid-free conditions, clearly indicating a link between amino acid signaling and mTOR activation. By contrast, similar levels of phospho-rpS6 Ser235/236 were induced in cells cultured in either conventional or amino acid-free conditions, suggesting that amino acid-induced mTOR activation was less critical. These data indicate a role for extracellular amino acids in TCR-induced rpS6 phosphorylation, and suggest that in T cells, PI3K-independent mTOR activation might occur through amino acid signaling.

The p110δ PI3K isoform contributes to TCR-induced rpS6 phosphorylation

Wortmannin and LY294002 inhibit all classes of PI3K. It has been shown that the p110δ isoform represents the major class IA PI3K activity activated by the T and B cell Ag receptors (30). However, the class IB isoform p110γ may contribute to certain PI3K-dependent processes in T cells (31), and, of relevance to the current work, the class III PI3K vps34 has been reported to be involved in the activation of mTOR in response to nutrients (32). To assess the role of p110δ in TCR-induced rpS6 phosphorylation, we used mice that express a catalytically inactive knockin version of the kinase (17). P110δ D910A mutant mice were backcrossed to the MHC class I-restricted OT-I TCR transgenic background. Preliminary experiments using pharmacological inhibitors confirmed that OT-I and F5 TCR transgenic T cells used similar signaling pathways to induce rpS6 phosphorylation in response to their cognate peptides, although OT-I cells appeared somewhat more sensitive to PI3K and mTOR inhibition than F5 cells (Fig. 6C and data not shown). Next, levels of rpS6 phosphorylation following peptide stimulation were compared for WT and p110δ D910A OT-I cells. Fewer D910A OT-I cells phosphorylated rpS6 in response to SIINFEKL peptide than control cells; numbers of phospho-rpS6 Ser235/236-positive cells were reduced by ~30% (Fig. 6A), whereas numbers of phospho-rpS6 Ser240/244-positive cells were reduced by ~25% (Fig. 6B). Incubation of WT cells with the p110δ-specific inhibitor IC87114 reduced numbers of phospho-rpS6-positive cells, but had no effect on D910A OT-I cells. Interestingly, wortmannin inhibited rpS6 phosphorylation to a similar extent in both WT and D910A cells (Fig. 6). Taken together, these data indicate that p110δ PI3K contributes ~50% of the PI3K-dependent component, leading to TCR-induced rpS6 phosphorylation, and therefore suggests that other PI3K isoforms also contribute to this pathway.

Peptide-induced ERK phosphorylation was also reduced by ~30% in D910A OT-I cells as compared with WT OT-I cells (Fig. 6C). Furthermore, wortmannin inhibited ERK phosphorylation in both WT and p110δ D910A OT-I cells, suggesting that p110δ together with additional PI3K isoforms influence MAPK signaling. These data indicate that PI3K is important for maximal activation of the Ras/ERK pathway in T cells.

MEK-dependent phosphorylation of rpS6, but not S6K, requires RSK

Given that we saw a significant contribution of the MEK/ERK pathway to rpS6 phosphorylation, we asked whether this occurred through activation of the kinase RSK, which is known to be downstream of ERK. To accomplish this aim, we used a recently described highly specific RSK inhibitor, BI-D1870 (33). Upstream events such as F5 TCR-induced ERK phosphorylation were not blocked by preincubation with BI-D1870, because the inhibitor functions to block the catalytic site of RSK (Fig. 7). Similarly, Akt phosphorylation was completely unaffected by BI-D1870 (Fig. 7). However, RSK phosphorylation was somewhat reduced following incubation of cells with BI-D1870. Importantly, the combination of inhibiting RSK and mTOR with BI-D1870 and rapamycin, but not either inhibitor
alone, completely blocked rpS6 phosphorylation, indicating that RSK is responsible for the MEK-dependent phosphorylation of rpS6 (Fig. 7). However, BI-D1870 had no effect on TCR-induced S6K phosphorylation either alone or in combination with rapamycin. These data indicate that another MEK-dependent kinase is responsible for the UO126-inhibitable phosphorylation of S6K Thr421/Ser424 (Fig. 3).

Finally, we undertook experiments to determine whether the TCR-induced signaling pathways leading to rpS6 phosphorylation were similar for CD4 T cells. Mixed lymph node cultures were pretreated with BI-D1870 and/or rapamycin, and then stimulated for 3 h with anti-CD3 Ab. As was the case for F5 T cells, a combination of inhibition of RSK and mTOR, but not either pathway alone, completely blocked CD3-induced rpS6 phosphorylation in gated polyclonal CD4+ and CD8+ T cells (supplementary Fig. 2).

Discussion
Phosphorylation of ribosomal protein rpS6 on evolutionarily conserved serine residues occurs in all cell types and in response to a wide range of stimuli. In the current work, we have extensively characterized the signaling pathways that are required for rpS6 phosphorylation following TCR engagement in CD8+ TCR transgenic T cells. The data indicate that rpS6 phosphorylation acts as a point of convergence for multiple TCR-induced signaling pathways. We show that both of the SFK expressed in T cells, Lck and Fyn, contribute to the induction of sustained rpS6 phosphorylation, via the activation of mTOR- and MAPK-dependent pathways (Fig. 8). The convergence of these critical signaling pathways at the level of rpS6 suggests that these phosphorylation events represent an important mechanism for regulating CD8+ T cell responses.

Activation of mTOR following TCR triggering is thought to be important for the greatly increased rate of protein synthesis that is required for T cell growth and proliferation (34). In this regard, mTOR regulates the expression of CD98, which in turn allows increased uptake of amino acids from the extracellular environment (35), whereas phosphorylation of the translational repressor 4E-binding protein by mTOR facilitates initiation of translation (11). A recent study has highlighted the importance of mTOR signaling for CD4 Th cell differentiation; mTOR-deficient T cells fail to differentiate to Th1, Th2, or Th17 effector cells (36). Interestingly, Ahmed and colleagues (37) have reported that mTOR is an important regulator of CD8 T cell differentiation and that, surprisingly, rapamycin has a positive effect on the generation of memory CD8 T cells in both mice and nonhuman primates. In addition, it
has become clear that in some circumstances Ag-induced CD8 T cell proliferation is partly resistant to rapamycin treatment (38, 39). The ERK/RSK MAPK pathway also regulates many aspects of T cell biology. For example, ERK activation is critical for positive selection of double-positive thymocytes in the thymus (40), whereas RSK2-deficient T cells demonstrate delayed cell cycle entry and IL-2 production upon TCR stimulation (41). However, the role of rpS6 phosphorylation in mediating mTOR and/or ERK/RSK function is much less clear. Analysis of knockin mice that express a rpS6 protein in which all phosphorylatable serines are substituted for alanine (rpS6\textsuperscript{K\textasciitilde}) has shown that rpS6 phosphorylation is dispensable for global protein synthesis, and in some cell types might even be inhibitory (15). These data indicate that mTOR-dependent protein synthesis must proceed independently of the ability of mTOR to mediate rpS6 phosphorylation. However, certain aspects of mTOR function do appear to be mediated by rpS6 phosphorylation because rpS6\textsuperscript{K\textasciitilde} murine embryonic fibroblasts have a reduced cell size that is not affected by rapamycin (15). The immune phenotype of rpS6\textsuperscript{K\textasciitilde} mice has yet to be described; analysis of T cell development and responses in these mice and comparison with the phenotypes of mice deficient in upstream kinases will be highly informative.

Our analysis of the effects of pharmacological inhibitors on signaling in F5 T cells indicated some subtle, but important differences in TCR-induced pathways leading to rpS6 phosphorylation as compared with those previously published for other cell types and stimuli. Furthermore, the results emphasize the importance of validating the drug sensitivity of phosphorylation events in each cellular system. For example, in F5 T cells, rapamycin and LY294002 had a small effect on TCR-induced rpS6 Ser\textsuperscript{235/6} phosphorylation, but a marked effect on rpS6 Ser\textsuperscript{240/4} phosphorylation. However, we could still clearly detect phosphorylation at both sites in rapamycin-treated cells. By contrast, previous studies indicated that, in the HEK293 cell line, serum-induced phosphorylation of rpS6 residues Ser\textsuperscript{240/4} was abolished by rapamycin (42). Similarly, Pende et al. (12) reported that insulin- and epidermal growth factor-factor-induced rpS6 Ser\textsuperscript{240/4} phosphorylation was completely blocked in rapamycin-treated hepatocytes. A number of studies have suggested a role for MAPK in rpS6 Ser\textsuperscript{235/6} phosphorylation (12, 42), and indeed, we find that TCR-induced phosphorylation at these sites is mediated by both RSK and S6K. By contrast, rpS6 Ser\textsuperscript{235/6} phosphorylation is sometimes used as a specific readout of mTORC1 activity (43). Our data emphasize the fact that care should be taken in the interpretation of individual phosphorylation events, because multiple pathways may intersect at the same phosphosite. Previous work by Roux et al. (42) showed that, in vitro, Rsk1 and Rsk2 efficiently phosphorylated rpS6 at Ser\textsuperscript{235/6} residues, but not Ser\textsuperscript{240/4}. However, our data using the RSK inhibitor BI-D1870 indicate that, in T cells, mTOR-independent rpS6 Ser\textsuperscript{240/4} phosphorylation is mediated by RSK (or an RSK-dependent downstream kinase). It is also worthy of note that subtle differences were also apparent in the effects of inhibitors on TCR-induced rpS6 phosphorylation in F5 as opposed to OT-1 cells. Specifically, OT-1 cells were more sensitive to PI3K or mTOR inhibition than F5 cells (data not shown). These data suggest that distinct TCRs may differentially use specific pathways to engage downstream effectors. Nonetheless, in both cell types, maximal TCR-induced rpS6 phosphorylation required input from both PI3K/mTOR and MAPK pathways.

In F5 T cells, the MEK inhibitor U0126 had interesting context-dependent effects on phosphorylation of rpS6 Ser\textsuperscript{240/4}. When the mTOR pathway was inhibited by the use of rapamycin, the addition of U0126 completely blocked TCR-induced rpS6 Ser\textsuperscript{240/4} phosphorylation, indicating a positive role for the MEK/ERK/RSK pathway. In contrast and somewhat unexpectedly, preincubation of F5 cells with U0126 alone consistently resulted in elevated levels of phospho-rpS6 Ser\textsuperscript{240/4} staining in cells upon TCR stimulation. These data suggest that the MAPK pathway may also play a role in feedback inhibition of rpS6 phosphorylation in T cells. Recent data have shown that ERK can phosphorylate the inhibitor-2 protein and thereby activate the Ser/Thr phosphatase protein phosphatase 1 (44). One possibility then is that following TCR triggering, in addition to facilitating the phosphorylation of rpS6, the MAPK pathway might also activate a phosphatase that dephosphorylates rpS6 Ser\textsuperscript{240/4}. In this scenario, when MEK is inhibited by treating cells with U0126, the dominant effect on rpS6 Ser\textsuperscript{240/4} is removal of a negative regulator and, hence, phosphorylation mediated via mTOR and S6K is elevated. Further investigations are required to test this hypothesis. However, it should be noted that we did not detect equivalent increases in rpS6 Ser\textsuperscript{240/4} phosphorylation in the presence of U0126 in peptide-stimulated OT-I cells (data not shown), further emphasizing the fact that different TCRs engage downstream signaling pathways in a nonidentical manner. Nevertheless, recent evidence has suggested that many kinases may be involved in both positive and negative feedback of TCR signaling. For example, Fyn can transduce TCR signals to the MAPK and PI3K pathways (16, 20), both of which most likely contribute to Fyn-dependent rpS6 phosphorylation (see Fig. 2). However, Fyn is also involved in feedback inhibition of TCR signaling through phosphorylation of the transmembrane adapter phosphoprotein associated with glycosphingolipid-enriched domains that recruits Csk and results in phosphorylation and inhibition of Lck function (45). Feedback inhibition of TCR signaling by Fyn is implicated in the induction of T cell anergy (46, 47), and it is possible that MAPK-dependent inhibition of rpS6 Ser\textsuperscript{240/4} phosphorylation also has important functional consequences.

A role for the class IA p110\textsubscript{PI3K} isoform was indicated by data showing reduced TCR-induced rpS6 phosphorylation in knockin p110\textsubscript{PI3K} D910A OT-I cells as compared with WT OT-I cells, and a similar effect on rpS6 phosphorylation was observed in WT cells incubated in the presence of p110\textsubscript{PI3K}-specific inhibitor IC87114. However, wortmannin was a more potent inhibitor of rpS6 phosphorylation than IC87114 and had additional inhibitory effects in p110\textsubscript{D910A} cells. PI10\textsubscript{D910A} has been shown to be the most important class IA PI3K in T cells, and TCR-induced Akt phosphorylation is largely ablated in D910A mice (48). Experiments showed that treatment of cells with an inhibitor of class IB p110\textsubscript{y} PI3K had only a small effect on TCR-induced rpS6 phosphorylation, and a combination of p110\textsubscript{D} and p110\textsubscript{y} inhibitors was less effective than use of the pan-PI3K inhibitor wortmannin (data not shown). Taken together, these data indicate that multiple isoforms of PI3K contribute to TCR-induced rpS6 phosphorylation. It is worthy of note that PI3K activation most likely contributes to TCR-induced rpS6 phosphorylation at several levels, as follows: 1) through the activation of mTOR via Akt, and 2) through a positive role in the activation of the Ras/ERK pathway (see Fig. 6C) (48).

The present work also shows that TCR-induced activation of mTOR and S6K is at least in part independent of PI3K activity. In this regard, PI3K- and MEK-independent rpS6 phosphorylation (i.e., not inhibited by the combination of wortmannin and U0126) was completely blocked by rapamycin. Recently, Donahue and Fruman (49) reported PI3K-independent mTOR activation in B cells stimulated either through the BCR or with LPS. Amino acid signaling pathways are known to induce mTOR activation independently of PI3K activity (29), and our experiments showed that extracellular amino acids present in the culture medium played a role in rpS6 phosphorylation.
Studies have shown that the mTOR, PI3K, and MAPK pathways regulate many aspects of T cell biology, including growth, proliferation, survival, and differentiation; however, the role of rpS6 phosphorylation in these processes is unclear. The small cell size and elevated rates of protein synthesis of fibroblasts from rpS6−/− mice indicate an important role for rpS6 phosphorylation in cell growth (15). In future studies, a full analysis of the T cell phenotype in rpS6−/− mice will allow the function of TCR-induced rpS6 phosphorylation to be ascertained.

Disclosures

The authors have no financial conflict of interest.

References