

## Rictor Phosphorylation on the Thr-1135 Site Does Not Require Mammalian Target of Rapamycin Complex 2

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### Abstract

In animal cells, growth factors coordinate cell proliferation and survival by regulating the phosphoinositide 3-kinase/Akt signaling pathway. Deregulation of this signaling pathway is common in a variety of human cancers. The PI3K-dependent signaling kinase complex defined as mammalian target of rapamycin complex 2 (mTORC2) functions as a regulatory Ser-473 kinase of Akt. We find that activation of mTORC2 by growth factor signaling is linked to the specific phosphorylation of its component rictor on Thr-1135. The phosphorylation of this site is induced by the growth factor stimulation and expression of the oncogenic forms of ras or PI3K. Rictor phosphorylation is sensitive to the inhibition of PI3K, mTOR, or expression of integrin-linked kinase. The substitution of wild-type rictor with its specific phospho-mutants in rictor null mouse embryonic fibroblasts did not alter the growth factor-dependent phosphorylation of Akt, indicating that the rictor Thr-1135 phosphorylation is not critical in the regulation of the mTORC2 kinase activity. We found that this rictor phosphorylation takes place in the mTORC2-deficient cells, suggesting that this modification might play a role in the regulation of not only mTORC2 but also the mTORC2-independent function of rictor. *Mol Cancer Res*; 8(6); 896–906. ©2010 AACR.

### Introduction

Growth factor signaling plays a decisive role in the regulation of cell proliferation, survival, and differentiation. The deregulation of growth factor signaling pathways is associated with tumorigenesis and is common in human cancers. Binding of growth factors to their specific tyrosine kinase receptors initiates signaling by activating the kinase activity of receptors (1, 2). It results in the autophosphorylation of the receptor cytoplasmic domains and the tyrosine phosphorylation of docking proteins. These tyrosine-phosphorylated sites function as recruitment sites of a wide spectrum of regulatory proteins. Regulated protein/protein interactions are mediated by tyrosine phosphorylation binding Src Homology 2 domains and also by proline-rich bind-

ing SH3 domains (3). The downstream of growth factor receptor crucial signaling controlling cell proliferation and survival is propagated by the recruitment of guanine exchange factors controlling the ras GTPase activity and phosphatidylinositol-3-OH kinase (PI3K; refs. 4, 5). The well-characterized essential effector of PI3K in growth factor signaling is the Akt kinase, also known as protein kinase B.

The activation of PI3K results in the accumulation of phosphatidylinositol-3,4,5-triphosphates, which initiates the recruitment of Akt to the plasma membrane through its pleckstrin homology domain. At this location, Akt is phosphorylated on the Thr-308 and Ser-473 sites required to fully activate Akt (6). The activation loop of Akt on Thr-308 is phosphorylated by phosphoinositide-dependent kinase 1 and is required for the kinase activity of Akt (7-9). The Ser-473 kinase of Akt, named phosphoinositide-dependent kinase 2, which was sought for many years, was only recently identified as the mammalian target of rapamycin complex 2 (mTORC2; ref. 10). Although several candidates were proposed earlier as phosphoinositide-dependent kinase 2 (9, 11), mouse genetic studies confirm the role of mTORC2 as the main Ser-473 kinase of Akt (12-15).

Originally, mTOR was discovered as a target for the lipophilic macrolide rapamycin. Rapamycin is well known as a potent immunosuppressant, as a potential anticancer drug, and also for effectively preventing restenosis after angioplasty. All these antiproliferative effects of rapamycin are related to its specific targeting and inhibition of mTOR, a

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key player of an essential and conserved signaling pathway (16). The biochemical studies identify mTOR as a central component of two distinct and large protein complexes that play different roles in cells (17). Besides mTOR, mLST8 and DEPTOR have been identified as the mTOR-interacting proteins within both complexes. A small adaptor protein mLST8 contains seven WD40 repeats, binds tightly to the kinase domain of mTOR (18, 19), and is required for its kinase activity (20). The recently identified DEPTOR, the DEP domain containing TOR-interacting protein, has been identified as a negative regulator of mTOR (21).

The binding of raptor to mTOR defines assembly of the first complex, known as mTORC1. This complex functions as a nutrient-sensitive kinase complex that regulates protein synthesis by phosphorylating its two substrates, S6K1 and 4EBP1. Rapamycin in a complex with its intracellular receptor FKBP12 specifically binds the FKBP12/rapamycin binding (FRB) domain on mTOR and inhibits the mTORC1 function (22). The FRB domain, a stretch of 100 amino acids, is located at the COOH-terminal half of mTOR. The mTOR kinase domain follows FRB domain, structurally resembles a kinase domain of PI3K but functions as a serine/threonine protein kinase, and is essential for the function of mTOR (16).

The second complex of mTOR, mTORC2, has been initially identified as a regulator of PKC $\alpha$  and cytoskeleton (18, 19). This signaling complex is assembled by mTOR and its essential components rictor and Sin1 (13, 18, 19, 23). Rictor and Sin1 form a heterodimer that determines the mutual stability of both proteins. Rictor remains poorly characterized. The human rictor polypeptide contains 1,708 amino acids but reveals no homology to any known functional domain or protein, although it is conserved in all eukaryotes (10, 18). Initially, rictor's ortholog, *pianissimo*, was identified in *Dictyostelium* as a critical player in chemotaxis and cyclic AMP signal relay (24). Another component, Sin1, might provide more insights into the regulation and function of mTORC2. Two Sin1 functional domains have been proposed: the Raf-like Ras binding domain and a pleckstrin homology domain (25). The Raf-like Ras binding domain points out Ras as a potential up-stream effector of mTORC2, and localization of mTORC2 at the plasma membrane might depend on the pleckstrin homology domain of Sin1. Like rictor's, Sin1's ortholog was initially identified as an important regulator of chemotaxis and, in addition, as a Ras-interacting protein 3 in *Dictyostelium* (26, 27).

In contrast to mTORC1, mTORC2 does not bind the rapamycin/FKBP12 complex, suggesting that the FRB domain on mTOR that is responsible for the binding is not accessible on mTORC2. Nevertheless, prolonged rapamycin treatment causes an indirect effect on mTORC2 by inhibiting the assembly of this complex. In some cell types, mostly lymphoma cells, the prolonged rapamycin treatment causes the inhibition of Akt because of a dramatic effect on the abundance of mTORC2 (28).

The mTORC2 complex carries an important regulatory role in growth factor signaling by mediating the regulation

between PI3K and its crucial downstream effector Akt. The growth factor-dependent regulation of the mTORC2 kinase activity is not understood. The mTORC2 component rictor has been described as a phosphoprotein. In this study, we have characterized the growth factor-dependent phosphorylation of rictor and its regulation.

## Materials and Methods

### Materials

Reagents were obtained from the following sources: protein G-Sepharose from Pierce; rapamycin and LY294002 from LC Laboratories; DMEM/F12 from Life Technologies; insulin-like growth factor I (IGFI) from Peptidech; the fetal bovine serum from Hyclone; Fugene 6 transfection reagent and the complete protease inhibitor cocktail from Roche; DramFect transfection reagent from OZ Biosciences; the antibody to Xpress tag from Invitrogen; the antibodies to phospho-T1135 and phospho-S1177 rictor, phospho-S2448 and phospho-S2481 mTOR, mTOR, Raptor, S6K1, phospho-T389 S6K1, phospho-S473 and phospho-T308 Akt/protein kinase B, and Akt from Cell Signaling Technology; and the antibodies to Rictor, horseradish peroxidase-labeled anti-rabbit, anti-mouse, anti-goat secondary antibodies, and tubulin from Santa Cruz Biotechnology. Lentiviral short hairpin RNAs (shRNA) targeting human mTOR were generated and used as previously described. Integrin-linked kinase (ILK) shRNAs (shRNA) were obtained from Sigma (MISSION shRNA). The retroviral expression plasmids of H-ras (plasmid#18749, pWZL hygro H-ras V12) and PI3K H1047R (plasmid#12524, pBABE puro PI3KCA H1047R) were obtained from Addgene.

### Cell lines and culture

A549, HeLa, MDA-MB-435, and MCF10A were obtained from the American Type Culture Collection. Mouse embryonic fibroblasts (MEF), A549, HeLa, and MDA-MB-435 cells were cultured in DMEM/F12 with 10% fetal bovine serum. MCF10A cells were cultured in DMEM/F12 supplemented with 10  $\mu$ g/mL insulin, 20 ng/mL epidermal growth factor, 0.5  $\mu$ g/mL hydrocortisone, 100 ng/mL cholera toxin, 1 mmol/L CaCl<sub>2</sub>, and 5% horse serum. All of the above cell lines were cultured at a density that allowed cell division throughout the course of the experiment. When indicated, cells were treated with 100 nmol/L rapamycin in growth medium containing 10% FCS for the indicated time. For LY294002 experiments, cells of 60% to 70% confluency were serum starved for 24 hours and incubated with 50  $\mu$ mol/L LY294002 for 1 hour prior the stimulation by 40 ng/mL IGFI for 30 minutes. Mouse embryonic fibroblasts were transfected by the DramFect reagent following the manufacturer's protocol.

### The rictor mutagenesis

The rictor cDNA from the pRK5 plasmid was resubcloned to pcDNA4 with the Xpress tag by using the pcDNA4/HisMax TOPO TA Expression kit from Invitrogen. A large

size of the plasmid (~11 kb) interfered with the PCR-based mutagenesis. To decrease a size of the plasmid to a 6-kb size, the fragment of rictor containing a sequence of the phospho-mutants have been subcloned to pBluescript by BglII and NotI digestion. The primers for mutagenesis were designed based on the QuickChange Primer Design Program available at the Stratagene's Web site. The pBluescript plasmid containing the rictor fragment has been mutagenized with the QuickChange XLII mutagenesis kit (Stratagene). Following the validation of mutations by sequencing, the rictor-mutated fragments were reintroduced back to the Xp-rictor pcDNA4 plasmid by the BglII and NotI digestion.

### Cell lysis and immunoblotting

All cells were rinsed with ice-cold PBS before lysis in buffer containing 40 mmol/L HEPES (pH 7.5), 120 mmol/L NaCl, 1 mmol/L EDTA, 10 mmol/L Na-pyrophosphate, 10 mmol/L sodium glycerophosphate, 50 mmol/L NaF, 1% Triton X-100, and protease inhibitor cocktail (Roche). The scraped lysates were incubated for 20 minutes at 4°C to complete lysis. The soluble fractions of cell lysates were isolated by centrifugation at 13,000 rpm for 10 minutes in a microcentrifuge. Samples of cellular lysates containing the equal total protein concentration were resolved by SDS-PAGE. Resolved proteins on a gel were transferred to polyvinylidene difluoride membranes and were visualized by immunoblotting as previously described (28).

### Mass spectrometric analysis of rictor

In-gel digestions were done according to standard protocols. For this analysis, rictor was purified on a gel by combining 10 rictor immunoprecipitation samples; the protein was visualized by Coomassie staining. Briefly, excised rictor gel bands were washed thrice with 50% acetonitrile/200 mmol/L ammonium bicarbonate. Reduction was done with 10 mmol/L DTT in 100 mmol/L ammonium bicarbonate at 60°C for 30 minutes, and alkylation was performed with 20 mmol/L iodoacetamide in 100 mmol/L ammonium bicarbonate at room temperature for 30 minutes in the dark. Digestion with trypsin (1.0 µg enzyme added; Promega) was done at 30°C overnight. Peptides were extracted from the gel bands thrice with 60% acetonitrile in 0.1% trifluoroacetic acid at 30°C for 30 minutes, and the volume was reduced to 10 µL by vacuum centrifugation.

Nanoliquid chromatography tandem mass spectrometry was done on a LTQ linear ion trap mass spectrometer (Thermo Electron Corp.) coupled with a 1100 series nanoLC system (Agilent Technologies). The nano-liquid chromatography column was a 75 µm ID × 360 µm OD PicoFrit column (New Objective) packed with 3 µm Magic C18 resin (Michrom Bioresources). Mass spectra were acquired over a 90-minute gradient (A, 0.1% formic acid; B, 90% acetonitrile in 0.1% formic acid) by data-dependent acquisition in which the top eight most intense ions per mass spectrometry (MS) scan (mass range of 300–2,000 *m/z*) were selected for collision induced dissociation tandem MS. Dynamic exclusion was enabled with a repeat count of 2, repeat duration of 0.5 minutes, and exclusion duration of 1.5 minutes. Tandem MS spectra were analyzed

using a combination of Spectrum Mill (Agilent Technologies) and manual interpretation.

### Immunoprecipitations and kinase assays

For immunoprecipitation experiments, the lysis buffer contained 0.3% CHAPS instead of 1% Triton to preserve the integrity of the mTOR complexes. As previously described (10), 4 µg of rictor antibodies were added to the cleared cellular lysates (1 mg protein content in 700 µL) and incubated with rotation for 90 minutes, followed with 1 hour of incubation with 20 µL of a 50% slurry of protein G-Sepharose. Immunoprecipitates captured with protein G-Sepharose were washed four times with the CHAPS-containing lysis buffer and once with the rictor-mTOR kinase buffer [25 mmol/L HEPES (pH 7.5), 100 mmol/L potassium acetate, and 2 mmol/L MgCl<sub>2</sub>]. For kinase reaction, immunoprecipitates were incubated in a final volume of 15 µL for 20 minutes at 37°C in the rictor-mTOR kinase buffer containing 500 ng inactive Akt1-glutathione *S*-transferase and 500 mmol/L ATP. The reaction was stopped by the addition of 200 µL of the ice-cold Enzyme Dilution buffer [20 mmol/L MOPS (pH 7.0), 1 mmol/L EDTA, 0.3% CHAPS, 5% glycerol, 0.1% 2-mercaptoethanol, 1 mg/mL bovine serum albumin]. After a quick spin, the supernatant was removed from the protein G-Sepharose, and a 15-µL portion was analyzed by immunoblotting for phospho-Ser473 Akt and Akt level detection. The pelleted G-agarose beads were also analyzed by immunoblotting to determine the levels of rictor and mTOR in the immunoprecipitates.

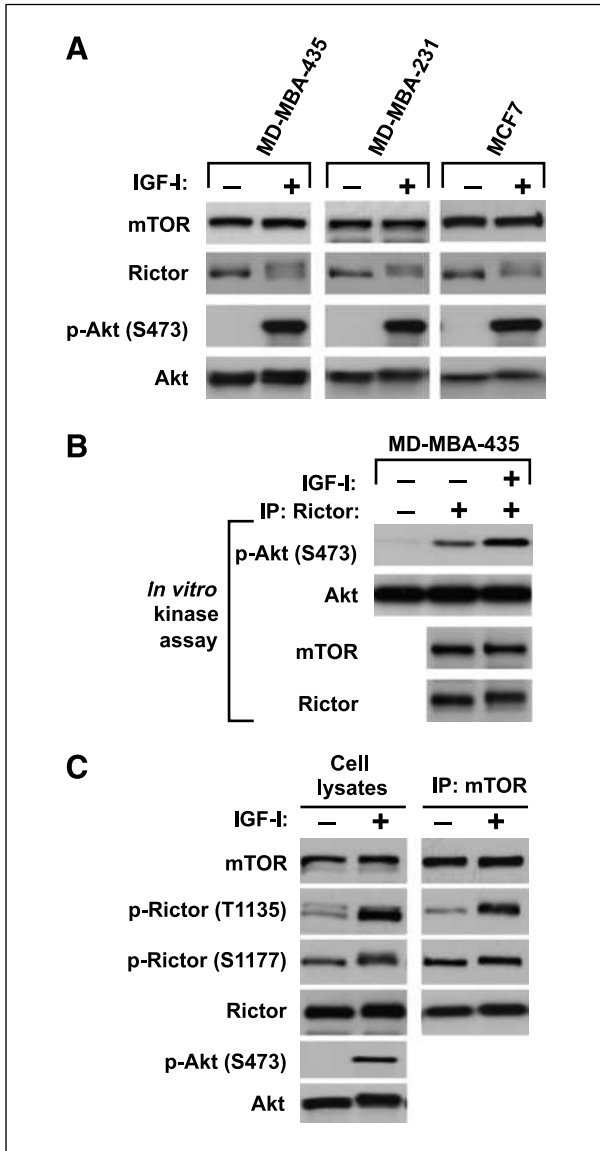
### Retroviral vector, retroviral production, and infection

The retroviral vectors used as plasmids were propagated in and purified from XL-10 Gold bacterial cells and cotransfected together with the Δ VPR and VSVG plasmids into actively growing cells as previously described (18). The day prior transfection, human embryonic kidney 293T cells ( $1.2 \times 10^6$ ) were plated on 6-cm plates in 3 mL DMEM supplemented with 10% fetal bovine serum. Retroviruses were harvested 48 hours after transfection and spinned at 3,000 *g* for 15 minutes to eliminate any remaining human embryonic kidney 293T cells. The day prior infection, cells to be infected were seeded in six-well dishes. The viral supernatant was added at a ratio of 1:1 to the culture medium in the presence of polybrene (8 µg/mL), and the cells were spinned at 1,800 rpm for 45 minutes to increase the infection rate. Cells were incubated with the retroviruses for the following 24 hours. A second infection was done following the same protocol the next day. After an additional 24 hours of recovery in normal medium, infected cells were passaged and selected with puromycin (2.5 µg/mL for 3–4 d).

## Results

### Identification of the growth factor-dependent rictor phosphorylation in cancer cells

The kinase activity of mTORC2 as the Ser-473 regulatory kinase of Akt is dependent on growth factor signaling



**FIGURE 1.** Rictor phosphorylation associates with the IGF1-dependent stimulation of the mTORC2 kinase activity. **A**, the IGF1-dependent rictor phosphorylation. The serum starved MDA-MB-231, MDA-MB-435, and MCF7 cells for 24 h were stimulated by IGF1 (40 ng/mL) for 20 min. The lysates were analyzed by immunoblotting for indicated proteins and phosphorylation of Akt. **B**, the mTORC2 kinase assay. The rictor immunoprecipitates (IP) from the serum-starved or IGF1-stimulated MDA-MB-435 cells were used in a kinase assay with a full-length wild-type Akt1 as a substrate. Immunoblotting was used to detect the phosphorylation of Akt on Ser-473 and the levels of mTOR, Rictor, and Akt1 in the kinase assay. In a first lane of the Akt immunoblots, Akt1 was used in a kinase assay to detect a basal phosphorylation of the substrate. **C**, detection of the IGF1-dependent phosphorylation site of rictor. The serum-starved MDA-MB-435 cells with or without the IGF1 stimulation were lysed and analyzed by immunoblotting for the indicated proteins and phosphorylation states by the phospho-specific rictor and Akt antibodies (left). In parallel, the mTOR-associated rictor phosphorylation was analyzed in the mTOR immunoprecipitates (right).

(10, 23). Rictor, as a component of mTORC2, has been initially characterized as a phosphoprotein (18). The growth factor–dependent phosphorylation of rictor has been studied in three cancer cell lines sensitive to the IGF1 stimulation. We detected a robust phosphorylation of Akt on the Ser-473 site following the growth factor stimulation in the MDA-MB-435, MDA-MB-231, and MCF7 cells. We also found that the protein mobility of rictor in a gel changed to a slower migratory form in the IGF1-stimulated cells compare with its mobility in the serum-starved cells (Fig. 1A). A slower migratory form of rictor is dependent on its phosphorylation (18, 29). Activation of mTORC2 as the regulatory Akt kinase takes place following the stimulation of cells with IGF1 as shown by performing the *in vitro* mTORC2 kinase assay (Fig. 1B), in which mTORC2 has been purified by the immunoprecipitation of rictor from the cellular lysates of MDA-MB-435 cells shown in Fig. 1A. These observations indicate that the growth factor–dependent activation of mTORC2 as the Ser-473 kinase of Akt is associated with the rictor phosphorylation.

We found that the growth factor–dependent regulation of the mTORC2 activity by IGF1 is linked to the phosphorylation of its component rictor, although the function of this phosphorylation in the mTORC2 signaling is unknown. To identify the rictor phosphorylation sites, mass spectrometric analysis was carried out on the immunopurified rictor samples from the stimulated cells. Based on the alterations of MS readings of the distinct rictor's peptides, Thr-1135 and Ser-1177 have been identified with a high probability as rictor phosphorylation sites (Supplementary Fig. S1). To study a role of the rictor phosphorylation on this site, rictor phospho-specific antibodies have been developed. The specificity of the antibodies was validated by analyzing their binding to the immunopurified rictor proteins with the appropriate phospho-mutants. The phospho-specific antibodies did not recognize their mutated epitopes (Supplementary Fig. S2A). Most importantly, we found that the detection of rictor by the rictor phospho-Thr-1135 antibody was greater in the cellular extracts of MDA-MB-435 cells stimulated by IGF1 than it was in the unstimulated serum-starved cells (Fig. 1C, a left). This finding confirmed that the rictor phosphorylation takes place on the Thr-1135 site following a stimulation of cells with IGF1, whereas the Ser-1177 site was most likely steadily phosphorylated because it did not reveal a considerable change in the antibody binding following the IGF1 stimulation.

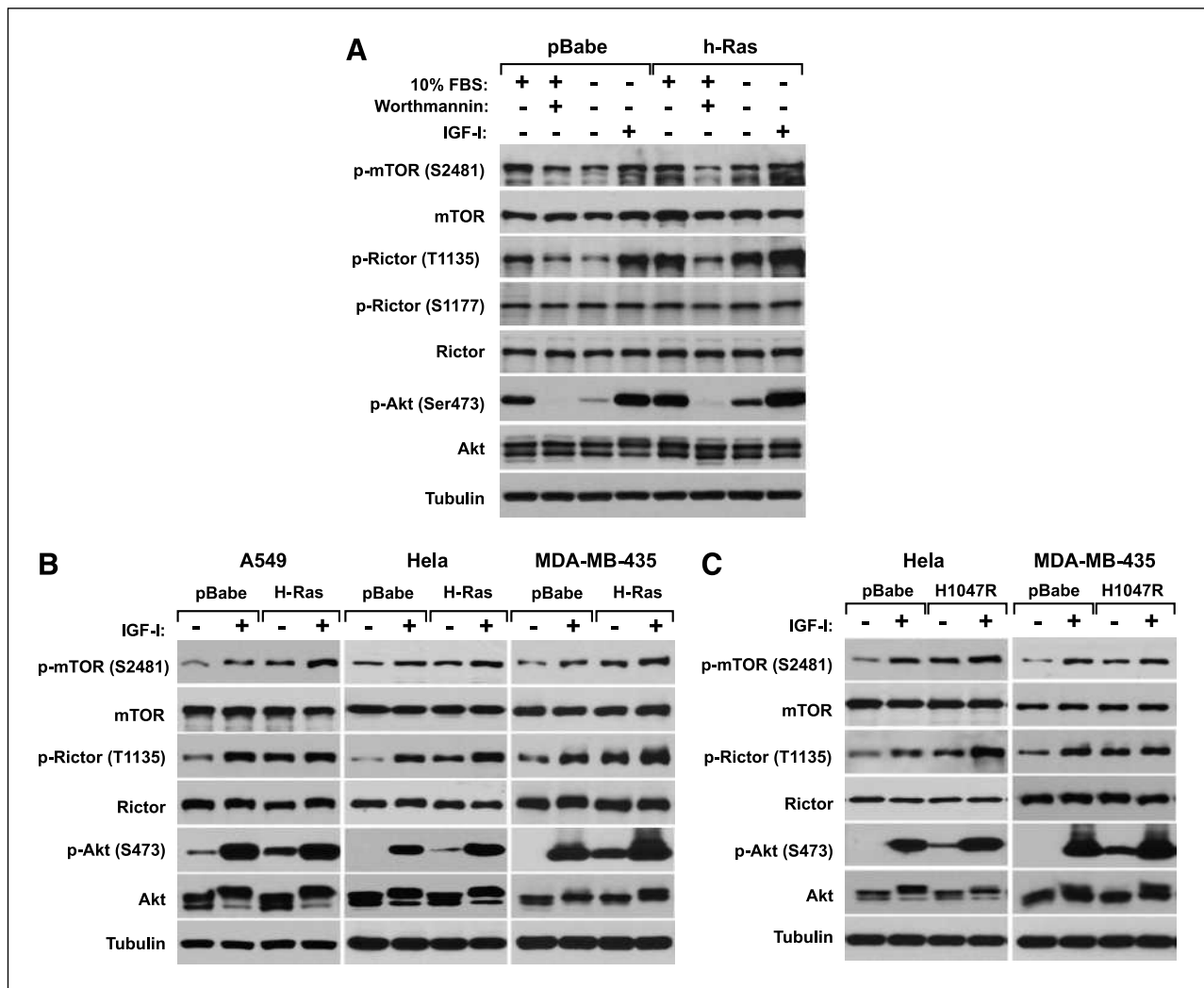
After detecting rictor phosphorylation in total cellular lysates, we studied the phosphorylation of rictor within the mTORC2 complex. We purified mTORC2 by immunoprecipitating mTOR from cells in experimental conditions known to preserve the complex (18). We found that the mTORC2 component rictor was phosphorylated in response to the IGF1 stimulation on the Thr-1135 site, but the phosphorylation on Ser-1177 was not affected (Fig. 1C, a right). In our following studies, we focused only on the rictor Thr-1135 site because we did not identify any conditions that regulate the Ser-1177 site. Thus, we found a similar pattern of the rictor phosphorylation in the total

cellular extracts and the immunopurified mTORC2. The rictor phosphorylation in total cellular extracts represents the rictor phosphorylation within the mTORC2 complex, and the phosphorylation state of Thr-1135 can be applied as the indirect activity marker of this kinase complex.

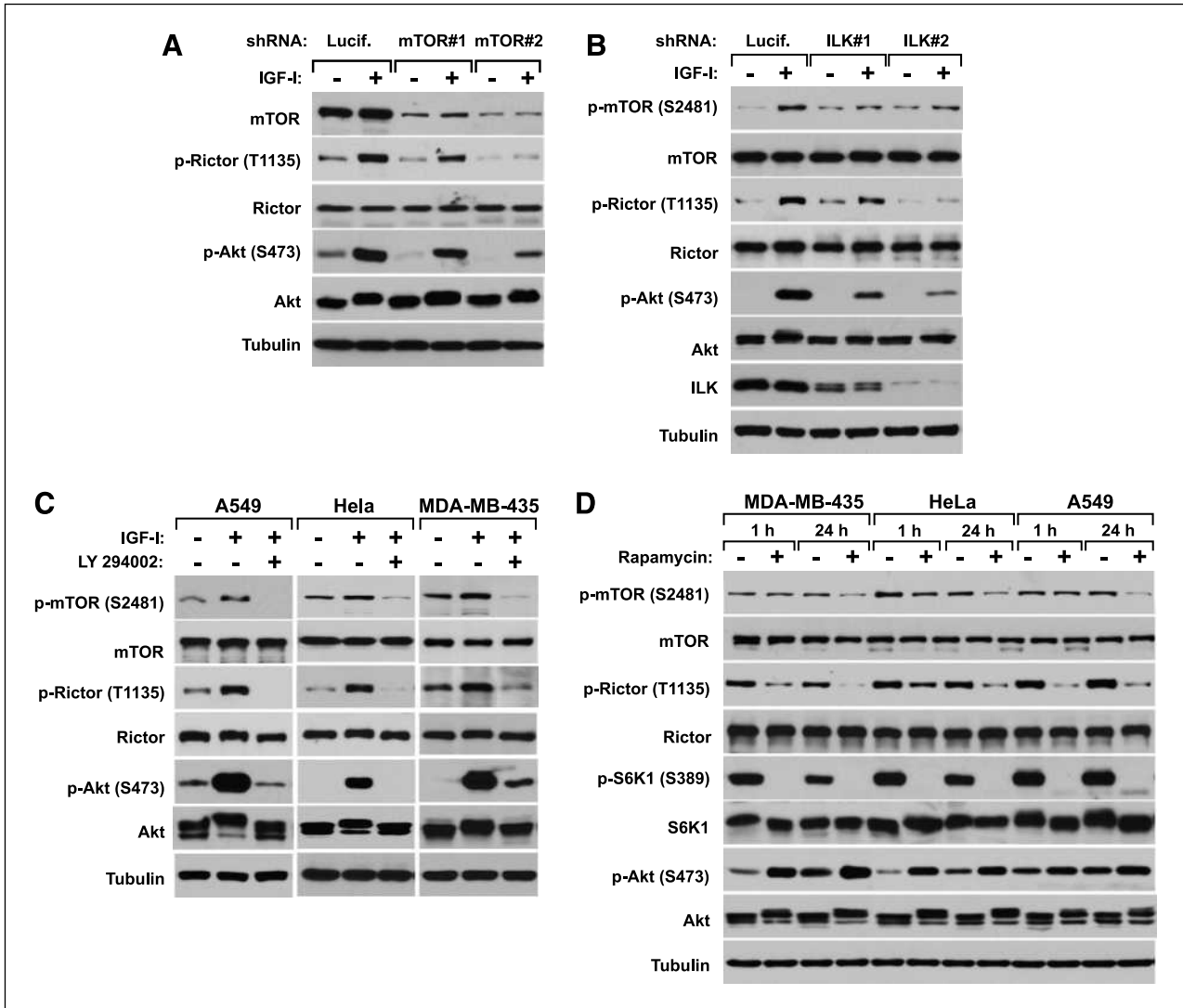
### Deregulation of the rictor Thr-1135 phosphorylation by the oncogenic forms of ras and PI3K

Our studies indicate that the rictor phosphorylation is dependent on growth factor signaling and PI3K pathway. It is known that some oncogenes cause constitutive activa-

tion of this important signaling pathway that gives an advantage for cancer cells in proliferation and survival (5, 30). The small GTPase Ras couples growth factor receptor signaling to extracellular signal-regulated kinase (mitogen-activated protein kinase) and PI3K pathways. The constitutively active form of ras is known as a common and potent oncogene that causes the growth factor-independent activation of the PI3K pathway (31, 32). In our next study, we analyzed the effect of the ras oncogene on the phosphorylation of rictor on the Thr-1135 site in the nontumorigenic MCF-10A human breast epithelial cell



**FIGURE 2.** The mTORC2 signaling upregulation by the *ras* or *PI3K* oncogenes is associated with the rictor T1135 phosphorylation. A loss of the growth factor-dependent rictor phosphorylation caused by the oncogenic form of H-ras. The oncogenic form of H-ras and empty vector as a control have been constitutively expressed in the nontumorigenic MCF10A cells (A) or in A549, HeLa, and MDA-MB-435 cells (B) based on the retroviral expression system. The transduced cells were selected and, following the indicated treatments, were lysed and analyzed by immunoblotting for the indicated proteins and phosphorylation states by the phospho-specific rictor, mTOR, and Akt antibodies. As indicated, cells were growing in 10% serum with or without Wortmannin at 100 nmol/L concentration for 1 h. In parallel, cells were serum starved for 24 h or stimulated by IGF1 (40 ng/mL) for 30 min. C, expression of the oncogenic PI3K is sufficient in stimulation of the rictor Thr-1135 phosphorylation. The constitutively active form of the PI3K catalytic unit p110 (H1047R) has been constitutively expressed in A549, HeLa, and MDA-MB-435 cells based on the retroviral pBabe expression vector. The pBabe empty vector was used as control. The transduced and selected cells were starved for 24 h and stimulated or not with IGF for 30 min at the concentration of 40 ng/mL.



**FIGURE 3.** Regulation of the rictor T1135 phosphorylation. A, the phosphorylation of rictor on the Thr-1135 site is mTOR dependent. MDA-MB-435 cells were infected with lentiviruses expressing shRNA-targeting luciferase (control) and mTOR following a serum starvation for 24 h and stimulation by IGF-I (40 ng/mL) for 30 min. The cells were lysed and the equal amount of protein lysates were analyzed by Western blotting by the indicated antibodies. B, the ILK knock down inhibits the phosphorylation of rictor on the Thr-1135 site. MDA-MB-435 cells were infected with lentiviruses expressing shRNA-targeting luciferase (control) and ILK following a serum starvation for 24 h and stimulation by IGF-I (40 ng/mL) for 30 min. C, the growth factor-dependent phosphorylation of rictor is prevented by inhibition of PI3K. The MDA-MB-435, A549, and HeLa cells were serum starved for 24 h. Where indicated, cells were preincubated or not with the PI3K inhibitor LY294002 at 50 mmol/L concentration for 1 h and stimulated with IGF-I (40 ng/mL) for 30 min. D, the rictor phosphorylation is rapamycin dependent. The MDA-MB-435, A549, and HeLa cell lines were grown in the growth medium containing 10% serum with or without rapamycin at 100 nmol/L concentration for the indicated periods of time.

line (Fig. 2A). Constitutive expression of the oncogenic H-ras in MCF10A cells increased the basal phosphorylation level of rictor on the Thr-1135 site in cell growth culture conditions (medium containing 10% serum) and also following stimulation by IGF-I. In H-ras-expressing cells, this phosphorylation remained highly sensitive to PI3K inhibition by wortmannin, but most importantly, it was resistant to serum starvation. The rictor phosphorylation was similar to the Akt Ser-473 phosphorylation, indicating that the rictor Thr-1135 site is a matching read-out of the PI3K-

dependent mTORC2 activity. This finding is also supported by the mTOR Ser-2481 phosphorylation, a known mTORC2 activity marker. This study was extended into three different growth factor-dependent cancer cell lines (A549, HeLa, and MDA MB-435) and revealed similar results (Fig. 2B). In addition to the ras oncogene, constitutive expression of the oncogenic form of PI3K also caused upregulation of the Akt pathway that was associated with the hyperphosphorylation of rictor and mTOR in serum-starved and growth factor-stimulated cell culture

conditions (Fig. 2C). It points out that the activation of the PI3K activity is sufficient for the activation of the mTORC2 signaling as evaluated by both mTORC2 activity markers.

### Regulation of the rictor Thr-1135 phosphorylation

Within the known components of the mTORC2 complex, only mTOR carries the functional kinase domain (16, 17). In our next experiment, we addressed whether the rictor Thr-1135 phosphorylation is dependent on mTOR. A partial knock down of mTOR by the shRNA#1 detects a weak effect on the phosphorylation of Akt that also partially inhibits the rictor Thr-1135 phosphorylation. The second mTOR shRNA expression carried a stronger effect on the expression of mTOR and, in addition, the stimulation of Akt that also caused a dramatic effect on the rictor phosphorylation (Fig. 3A). These data indicate that mTOR as a central component of both mTOR complexes controls the rictor Thr-1135 phosphorylation.

In addition to the PI3K pathway, the ILK has been characterized as an important regulator of Akt (33-35). Moreover, ILK has been shown to directly interact with rictor (36). In our study, we found that both rictor Thr-1135 and mTOR Ser-2481 phosphorylation sites are dependent on ILK (Fig. 3B). Although the ILK knock down was toxic in the studied cells, the levels of rictor and mTOR were not affected. In accordance with the previous studies (34, 35), we detected a low phosphorylation of Akt in the ILK knocked down cells stimulated by growth factor. Under these conditions, we found that the rictor and mTOR phosphorylation were inhibited. We observed that more efficient knock down of ILK had a stronger effect on the rictor but not on mTOR phosphorylation. This implies that compared with the mTOR Ser-2481 site, the rictor Thr-1135 site is more sensitive to ILK inhibition.

Recently, the hydrophobic Ser-2481 site of mTOR has been identified as an mTORC2 activity marker (37). We also found the mTOR phosphorylation on Ser-2481 only in the IGFI-stimulated mTORC2 but not on mTORC1. In contrast, the mTOR Ser-2448 site was phosphorylated on both complexes (Supplementary Fig. S3). Our study identified the rictor Thr-1135 phosphorylation site as a new activity marker of mTORC2. In our following experiments, we analyzed the regulation of the rictor Thr-1135 phosphorylation in parallel with the mTOR Ser-2481 site. First, we addressed whether the growth factor-dependent rictor phosphorylation is dependent on PI3K activity. We observed that in three cancer cell lines, pre incubation of cells with the PI3K inhibitor LY 294002 completely abrogated the IGFI-induced phosphorylation not only of Akt on Ser-473, but also rictor on Thr-1135 and mTOR on Ser-2481 (Fig. 3C). This indicates that similar to the mTOR Ser-2481 site, the rictor Thr-1135 phosphorylation site is dependent on the PI3K pathway and linked to the activity of mTORC2.

It is known that mTORC2 is sensitive to prolonged rapamycin treatment that leads to the inhibition of the

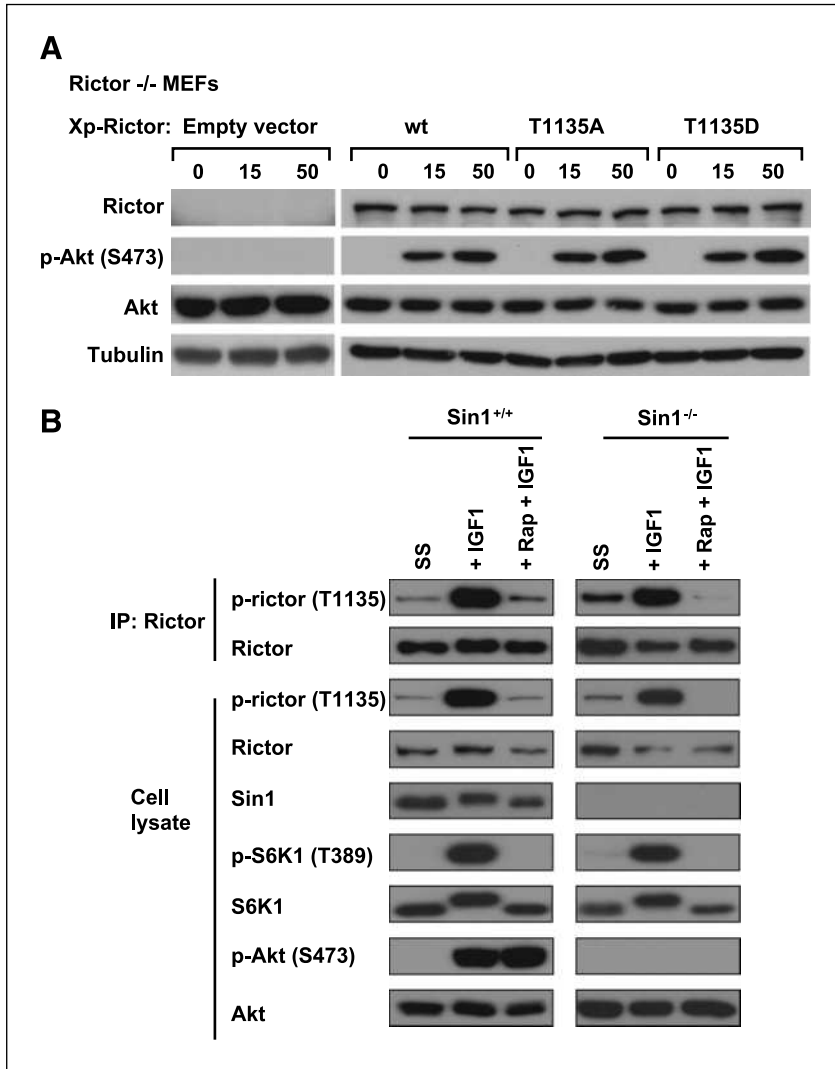
mTORC2 assembly and rictor phosphorylation (28, 29). In our next experiment, we studied the effects of short-term (1 h) and long-term (24 h) rapamycin treatments on rictor phosphorylation in three human cancer cell lines. Rapamycin by targeting mTORC1 inhibits the activity of S6K1 as detected by its dephosphorylation on the Thr-389 site (Fig. 3D). Elimination of the negative feedback loop on the PI3K pathway by inhibiting the rapamycin-dependent S6K1 kinase is known to associate with the upregulation of a basal PI3K-dependent phosphorylation of Akt on Ser473 (38-40), as we detected following the 1- and 24-hour rapamycin treatments. A decrease of the mTOR Ser-2481 phosphorylation has been detected only at the prolonged but not short-term rapamycin treatment that correlates well with the indirect effect of rapamycin on mTORC2. Interestingly, the rictor phosphorylation on Thr-1135 was sensitive to rapamycin within the short-term (1 h) rapamycin treatments (Fig. 3D). Our finding indicates that the rictor Thr-1135 phosphorylation is sensitive to acute rapamycin treatment. In contrast to mTORC1, mTORC2 is not directly targeted by the rapamycin/FKBP12 complex, suggesting insensitivity of mTORC2 to an acute rapamycin treatment (28). One potential mechanism of this regulation might be linked to the mTORC1-dependent phosphorylation of the rictor Thr-1135 site that points out on S6K1 as a kinase candidate. Indeed, three groups have recently reported that the rictor Thr-1135 site is phosphorylated by S6K1 (41-43), which explains a sensitivity of this site to an acute treatment of rapamycin.

Rictor is an essential component of mTORC2. Our initial characterization of the rictor Thr-1135 phosphorylation site indicates that this site is highly regulated and also dynamic in response to the cell growth conditions. We found that similar to the mTOR Ser-2481 site, the rictor phosphorylation is dependent on growth factor signaling pathway. This site is responsive to growth factor stimulation, PI3K activity, rapamycin, and expression of mTOR or ILK. The only difference we found in the behavior of both these sites is a sensitivity of the rictor Thr-1135 site to the short-term (1 h) rapamycin treatment, whereas inhibition of the mTOR Ser-2481 site is detected only following a prolonged (24 h) treatment.

### Functional studies of the Thr-1135 site by mutagenesis

Following the confirmation of rictor phosphorylation on the Thr-1135 site, we studied its functional role on the growth factor-dependent activation of mTORC2. In pursuing this task, we developed the phospho-specific rictor mutants by substituting the phospho sites to alanine or aspartic acid. To eliminate any interference from the endogenous rictor, the wild-type and phospho-mutant rictor isoforms were expressed in the rictor null MEFs previously described (12). In the rictor null cells, we did not detect any traces of rictor expression and the growth factor-dependent phosphorylation of Akt on the Ser-473 site (Fig. 4A). The wild-type rictor expression in these cells reconstituted the rictor-dependent function of

**FIGURE 4.** Characterization of the rictor Thr-1135 phosphorylation. A, the functional study of the rictor T1135 phosphorylation site. Reconstitution of the mTORC2 signaling in rictor null MEFs by expressing the wild-type and phospho-rictor mutants (T1135A and T1135D). Following 48 h after transfection, cells were lysed and cell extracts were analyzed by immunoblotting for the indicated proteins and phosphorylation state of Akt on the Ser-473 site. B, the rapamycin-sensitive rictor phosphorylation does not require mTORC2. The wild-type and Sin1 KO MEFs were serum starved overnight. As indicated, the cells were stimulated by IGF1 (50 ng/mL) for 20 min or treated with rapamycin (50 ng/mL) for 15 min before the stimulation of cells with the growth factor. The cells were lysed and analyzed as described in A.



mTORC2 as the growth factor-dependent Ser-473 kinase of Akt. Following the IGF1 stimulation of the transfected cells, the phosphorylation of Akt on the Ser-473 site occurred in a growth factor-dependent manner. In parallel, similar levels of the phospho-rictor mutants were expressed and their effect on the regulation of Akt was assessed. Prevention of the rictor Thr-1135 phosphorylation by a substitution of this site to alanine did not alter the mTORC2-dependent phosphorylation of Akt in the MEF cells. At the same time, mimicking a constitutive phosphorylation of rictor on Thr-1135 by mutating this site to aspartic acid did not cause any detectable changes on the phosphorylation of Akt (Fig. 4A). We also did not detect any effect on the phosphorylation of Akt by expressing the phospho-Ser-1177 rictor mutants (Supplementary Fig. S2B). The double rictor mutant preventing the phosphorylation of both Thr-1135 and Ser-1177 sites also did not have a substantial effect on the regulation of Akt (data not shown). These data indicated that the mutations on the identified rictor phosphorylation sites did

not carry a substantial effect on the growth factor-dependent activation of mTORC2 that correlates well with the recent report by Treins et al. (43) on the functional characterization of the rictor Thr-1135 site.

Our data described in Fig. 4A indicate that the phosphorylation of rictor on the Thr-1135 site is not essential in the regulation of growth factor-dependent regulation of the mTORC2 activity as the regulatory kinase of Akt. If this rictor phosphorylation is dispensable in regulation of mTORC2, this modification of rictor might play a role in the mTOR-independent function of rictor. In our next experiment, we studied whether rictor phosphorylation on Thr-1135 occurs in the mTORC2-deficient cells. Similar to rictor, Sin1 is also required for the assembly and functional integrity of mTORC2. The Sin1 knock out (KO) cells have been characterized as the mTORC2-deficient cells, in which rictor without its binding partner Sin1 becomes an unstable protein and does not bind mTOR (13). To attain the comparable levels of rictor in wild-type and Sin1 KO MEFs, the total protein lysate concentration of



the mutant was increased twice. We found that in wild-type MEFs following IGF1 stimulation, both mTORC1 and mTORC2 were responsive to growth factor as detected by the phosphorylation of their substrates S6K1 and Akt (Fig. 4B, left), in which only the mTORC1-dependent phosphorylation of S6K1 was detected in Sin1 KO cells (Fig. 4B, right). Importantly, in both cell types, we have detected the growth factor-dependent phosphorylation of rictor on the Thr-1135 site as shown by the analysis of the immunopurified rictor or total cell lysates. This rictor phosphorylation was associated with the mTORC1-dependent activation of S6K1 and was highly sensitive to rapamycin (Fig. 4B). Our study indicates that the rapamycin-dependent rictor Thr-1135 phosphorylation does not require the assembly of rictor to the mTORC2 complex or its interaction with Sin1, and implies a role of this phosphorylation in regulation of the mTORC2-independent function of rictor that remains to be elucidated.

## Discussion

The mTORC2 signaling complex functions as the regulatory Ser-473 kinase of Akt; therefore, the main known function of this kinase complex is to mediate a signaling between PI3K and its important downstream effector Akt. How growth factor signaling regulates mTORC2 is not known, and in this study, we show that the activation of mTORC2 is coupled to a specific phosphorylation of its component rictor. Initially, rictor was identified as a phosphoprotein; later, the rapamycin-dependent phosphorylation of rictor was also reported (18, 29). These studies were based on changes of the rictor protein mobility in a gel. Previously, specific rictor phosphorylation sites have not been identified and characterized. In this report, we show that rictor is specifically phosphorylated on the Thr-1135 site and that this phosphorylation is coupled to the growth factor-dependent activation of mTORC2.

Based on our characterization of the rictor Thr-1135 phosphorylation, we identified that this phosphorylation is coupled to growth factor signaling and is also a rapamycin-dependent site of rictor. First, similar to mTORC2 activity and its substrate Akt phosphorylation, this rictor site is dephosphorylated in serum-starved cells and is highly responsive to growth factor stimulation. Second, the oncogenic factors activating the ras/PI3K pathway and mTORC2 signaling cause the growth factor-independent phosphorylation of rictor on Thr-1135. Third, the rictor phosphorylation is similar to the mTORC2-dependent Akt phosphorylation as being sensitive to inhibition of PI3K, mTOR, and ILK. Moreover, the identified regulation of the rictor Thr-1135 phosphorylation correlates well with the mTOR Ser-2481 phosphorylation, which was recently identified as an mTORC2 activity marker (37).

We have shown that expression of the oncogenic form of ras or PI3K caused the growth factor-independent activation of the mTORC2 signaling. Earlier, it has been proposed that the activation of mTORC2 might take place by a binding of ras to the putative ras binding domain on

the mTORC2 component Sin1 (13, 23). We found that the ras-induced upregulation of the mTORC2 activity is highly sensitive to the inhibition of PI3K. This finding indicates that the ras-dependent activation of mTORC2 is PI3K dependent, suggesting insufficiency of the constitutively active form of ras in a direct activation of mTORC2. Ras is a critical intermediate in coupling a signaling between growth factor receptor and PI3K, whereas the ras binding domain of PI3K is required for ras-driven tumorigenesis (44). This binding domain might function as a link in growth factor- and ras-dependent activation of mTORC2.

Prolonged rapamycin treatment inhibits the assembly of mTORC2, and we detected that both mTORC2 phosphomarkers, rictor Thr-1135 and mTOR Ser-2481 sites, are sensitive to the long-term (24 h) treatment of rapamycin. This effect of the drug well correlates with the reported long-term effect of rapamycin on the mTORC2 assembly (28). Surprisingly, the rictor Thr-1135, but not the mTOR Ser-2481, phosphorylation site was affected within the short-term (1 h) rapamycin treatment. It is a first observation describing the effects of rapamycin on mTORC2 within a short-term treatment. In the previous work, it has been proposed that only prolonged, but not short-term, rapamycin treatment affects mTORC2 by interfering with the assembly of this complex (28). It is possible that the rictor Thr-1135 phosphorylation is dependent on mTORC1 that is a directly targeted by rapamycin. This finding is coherent with the recent reports from three laboratories that identified the mTORC1 substrate S6K1 as a kinase of rictor on the Thr-1135 site (41-43). This finding indicates that activation of the mTORC1/S6K1 signaling coordinates a rictor function by phosphorylating it specifically at least within one site that explains a high sensitivity of this rictor phosphorylation to rapamycin.

In this study, we addressed a role of the rictor Thr-1135 phosphorylation on the activation of mTORC2 by transiently expressing the wild-type rictor and its phospho-specific mutants in the rictor null cells. We did not detect any substantial effect of the rictor phospho-mutants on the mTORC2 signaling. It is possible that a constitutive expression of rictor and its mutants will be appropriate for a long-term analysis of the role of these phospho-mutants on mTORC2 and will lead to the understanding of the functional role of this phosphorylation site. Our study of the rictor Thr-1135 phosphorylation site revealed that the alteration of this site is not sufficient to affect the growth factor-dependent activation of the mTORC2 signaling that correlates well with the report from the Downward group (43). The reports from the Manning and Roux groups (41, 42) indicated a weak stimulation of the mTORC2 function by a substitution of rictor by the T1135A phospho-mutant as detected by the Akt phosphorylation. One potential explanation in this variation of the phospho-rictor mutant studies might be linked to application of the different rictor KO MEFs. The spontaneously immortalized rictor KO MEFs (12) have been studied by the Downward group and in our work, whereas

the Manning and Roux groups have applied the double rictor and p53 KO MEFs (15). Nevertheless, the rictor Thr-1135 phosphorylation site is conserved in vertebrates and most likely carries an important role in regulation of mTORC2 by providing the phosphorylation-dependent binding site to 14-3-3 proteins (41, 43).

The recent reports characterizing the rictor Thr-1135 phosphorylation have been focused on its role in the regulation of the mTORC2 function. We found that the rictor Thr-1135 phosphorylation takes place not only within the rictor assembled within the mTORC2 complex but also in the mTORC2-deficient cells. We believe that rictor also carries the mTORC2-independent function that is supported by the work describing a role of rictor in regulation of cell morphology by binding to unconventional myosin Myo1c (45). It has been described that the mTOR-independent binding of rictor to Myo1c is independent on growth factor signaling, suggesting that the rictor Thr-1135 phosphorylation is not involved in the regulation of the rictor and Myo1c interaction.

In summary, we show that following growth factor stimulation and activation of the PI3K/mTOR/Akt pathway, the mTORC2 component rictor is specifically phosphorylated on the Thr-1135 site. This phosphorylation is controlled by the mTORC1/S6K1 signaling and is highly sensitive to rapamycin. A regulation of the mTORC2 function by the mTORC1 signaling through the phosphorylation of rictor by S6K1 is an attractive

regulatory mechanism in coordination of the two branches of the mTOR pathway. Under the experimental settings presented in this work, the rapamycin-dependent rictor phosphorylation was not essential in the regulation of the mTORC2 function as the regulatory kinase of Akt. We found that the rictor Thr-1135 phosphorylation takes place in the mTORC2-deficient cells, implying a role of this phosphorylation in regulation of the mTORC2-independent rictor function that remains to be characterized.

## Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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