**Estradiol and mTORC2 cooperate to enhance prostaglandin biosynthesis and tumorigenesis in TSC2-deficient LAM cells**

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| Citation       | Li, C., P. Lee, Y. Sun, X. Gu, E. Zhang, Y. Guo, C. Wu, et al. 2014. “Estradiol and mTORC2 cooperate to enhance prostaglandin biosynthesis and tumorigenesis in TSC2-deficient LAM cells.” The Journal of Experimental Medicine 211 (1): 15-28. doi:10.1084/jem.20131080. http://dx.doi.org/10.1084/jem.20131080. |
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| Published Version | doi:10.1084/jem.20131080                                                                                                                                                                                                                                                                                                                 |
| Citable link   | http://nrs.harvard.edu/urn-3:HUL.InstRepos:12717476                                                                                                                                                                                                                                                                                      |
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Lymphangioleiomyomatosis (LAM) is a progressive neoplastic disorder that leads to lung destruction and respiratory failure primarily in women. LAM is typically caused by tuberous sclerosis complex 2 (TSC2) mutations resulting in mTORC1 activation in proliferative smooth muscle–like cells in the lung. The female predominance of LAM suggests that estradiol contributes to disease development. Metabolomic profiling identified an estradiol-enhanced prostaglandin biosynthesis signature in Tsc2-deficient (TSC−/−) cells, both in vitro and in vivo. Estradiol increased the expression of cyclooxygenase−2 (COX−2), a rate-limiting enzyme in prostaglandin biosynthesis, which was also increased at baseline in TSC−/− cells and was not affected by rapamycin treatment. However, both Torin 1 treatment and Rictor knockdown led to reduced COX−2 expression and phospho-Akt-S473. Prostaglandin production was also increased in TSC−/− cells. In preclinical models, both Celecoxib and aspirin reduced tumor development. LAM patients had significantly higher serum prostaglandin levels than healthy women. 15-epi-lipoxin-A4 was identified in exhaled breath condensate from LAM subjects and was increased by aspirin treatment, indicative of functional COX−2 expression in the LAM airway. In vitro, 15-epi-lipoxin-A4 reduced the proliferation of LAM patient–derived cells in a dose-dependent manner. Targeting COX−2 and prostaglandin pathways may have therapeutic value in LAM and TSC−/− related diseases, and possibly in other conditions associated with mTOR hyperactivation.
Figure 1. Identification of an estradiol-induced prostaglandin biosynthesis signature in cells and preclinical models. (a) ELT3 cells were treated with 10 nM estradiol for 24 h. Cellular metabolites were profiled by mass spectrometry (n = 5; Metabolon LC-MS/MS). Box plots of PGE$_2$ (6.0–59.6 ng), PGD$_2$ (1.3–7.2 ng), and 6-keto PGF$_{1\alpha}$ (2.5–18.3 ng) are shown. Data show the mean of five sets of independent samples. **, P < 0.01; Welch’s t tests and Wilcoxon rank sum tests. (b) Immunoblot analysis of ELT3 cells treated with estradiol for 2 or 24 h. β-Actin was used as a loading control. (c and d) Secreted PGE$_2$ levels were measured in conditioned media collected from cells treated with estradiol or control at the indicated times. Data were normalized to...
TSC2 mutations in LAM cells and renal angiomyolipoma cells from women with sporadic LAM, but not in normal tissues, has led to the model that LAM cells spread to the lungs via a metastatic mechanism, despite the fact that LAM cells have a histologically benign appearance (Astrandis et al., 2000; Karbowicz et al., 2003; Crino et al., 2006). Genetic and molecular analyses of recurrent LAM after lung transplantation support this benign metastatic model (Karbowicz et al., 2003).

The protein products of TSC1 and TSC2, hamartin and tuberin, respectively, form a heterodimer (Plank et al., 1998; Jaeschke et al. 2002) that inhibits the small GTPase Rheb (Ras homologue enriched in brain), via tuberin's highly conserved GTPase-activating protein domain. Loss of tuberin or hamartin leads to hyperactivation of the mammalian target of Rapamycin complex 1 (mTORC1), in LAM cells, other TSC tumors, and multiple animal models (Manning, 2010). mTORC1 regulates cell growth, protein translation, and metabolism (Düvel et al., 2010). In a randomized MILES (Multicenter International LAM Efficacy of Sirolimus) trial, the mTORC1 inhibitor rapamycin stabilized lung function and improved symptoms in LAM patients (McCormack et al., 2011). However, lung function declined when rapamycin was discontinued.

The female predominance of LAM strongly suggests that estradiol contributes to disease pathogenesis (Henske and McCormack, 2012; McCormack et al., 2012). We have demonstrated that estradiol treatment increases levels of circulating tumor cells and pulmonary metastases of TSC2-deficient cells in a xenograft model of LAM (Yu et al., 2009). Other studies have demonstrated that estradiol induces COX-2–mediated prostaglandin synthesis (Egan et al., 2004). COX-2 is a rate-limiting enzyme catalyzing the conversion of arachidonate to prostaglandins. COX-2 overexpression has been documented in human tumors, and prostaglandins may contribute to cancer development (FitzGerald and Patrono, 2001; Müller, 2004; Wang et al., 2007; Wang and Dubois, 2010). In this study, we discovered that estradiol enhances prostaglandin production by TSC2-deficient cells. Furthermore, loss of TSC2 increases COX-2 and prostaglandin biosynthesis in a rapamycin-insensitive but Torin 1-sensitive and Rictor-dependent manner, suggesting an mTORC1-independent but mTORC2-dependent mechanism. We also showed that loss of TSC2 leads to alterations in the cellular distribution of EGFR, and this appears to be the mechanism by which it causes increased PG biosynthesis. Celecoxib reduced renal tumor incidence in a spontaneous-arising Tsc2+/- mouse tumor model, and aspirin suppressed tumor progression in a xenograft tumor model. This study indicates that targeting COX-2 with aspirin or related drugs may have therapeutic benefit in LAM and TSC-related diseases.

RESULTS
Identification of an estradiol–induced prostaglandin biosynthesis signature in TSC2-deficient cells in vitro and in vivo
To examine the possible effects of estradiol on metabolic pathways in TSC2-deficient rat uterus–derived (ELT3) cells, we performed a metabolomic screen. A significant increase in prostaglandins including PGE2, PGD2, and 6-keto-PGF1α was seen in estradiol-treated cells (Fig. 1 a). Furthermore, estradiol increased p44/42–MAPK T202/Y204 phosphorylation, COX-2 expression, and PGE2 levels in TSC2-deficient cells at 2 and 24 h (Fig. 1, b and c). Analysis of LAM patient–derived TSC-deficient 621–101 cells (Yu et al., 2004) showed that estradiol also increased PGE2 levels at 24 h (Fig. 1 d), confirming the results in the TSC2-deficient ELT3 cells.

To define the impact of estradiol on activation of signaling pathways, we first compared the basal levels of phospho-S6, phospho-MAPK, and phospho-Akt S473 for the TSC2+/- and TSC2-/- cells. TSC-deficient cells exhibited lower levels of phospho-Akt S473 and higher levels of phospho-MAPK and phospho-S6, relative to TSC-addback cells (TSC2+; Fig. 1 e). We next performed a time-course analysis of the effect of estradiol on activation of these pathways in both TSC-deficient and TSC-addback LAM-derived cells. We found that estradiol activated Akt S473 within 6 h, MAPK (T202/Y204) at 2, 4, 6, 8, and 24 h, but not S6 in TSC2-deficient cells (Fig. 1 f, left). In comparison, estradiol stimulated Akt S473 and MAPK (T202/Y204) to a lesser degree in TSC2-addback cells (Fig. 1 f, right). Our data indicate that estradiol activates MAPK and Akt pathways in the absence of TSC2.

To determine whether the effect of estradiol on cells is dependent on TSC defects, we examined the levels of COX-2 using immunoblotting in estradiol-stimulated TSC2-deficient and TSC2-addback cells. Estradiol treatment did not affect COX-2 expression in TSC2-addback LAM patient–derived cells (Fig. 1 g). To address how estradiol exerts its action on COX-2 expression and prostaglandin production, we examined
Figure 2. TSC2 negatively regulates COX-2 expression and prostaglandin production in a rapamycin-insensitive but Torin 1 and mTORC2-dependent manner in vitro. (a) Simplified prostaglandin biosynthesis pathway. (b) Re-analysis of previously published expression array data (Lee et al., 2010). Bar graph of the transcript levels of PTGS2 (COX-2) and PTGIS (prostacyclin synthase) in TSC2-deficient (TSC2−) and TSC2-addback (TSC2+) LAM patient-derived cells treated with rapamycin (Rapa) or Vehicle for 24 h. Data show the mean of three sets of independent samples. (c) Real-time RT-PCR analysis of the transcript levels of PTGS2 and PTGIS in TSC2-deficient LAM patient-derived cells relative to TSC2-addback cells treated with 20 nM rapamycin.
the activation of p44/42–MAPK and PI3K–Akt, which are known pathways promoting COX-2 expression (Wang and Dubois, 2010). We found that estrogen activates both p44/42–MAPK and PI3K–Akt in TSC2-deficient cells, assayed by phosphorylation at T202/T204 and S473 sites, respectively, but not in TSC2-addback cells (Fig. 1, g and h). Inhibition of p44/42–MAPK using PD98059 or PI3K–Akt using PI-103 blocked estrogen-enhanced COX-2 expression (Fig. 1, i and j). Collectively, these data indicate that estradiol activates COX-2 expression via p44/42–MAPK and PI3K–Akt pathways.

To determine the effect of estradiol on cellular metabolism in vivo, we used xenograft tumors of TSC2-deficient ELT3 cells (Yu et al., 2009) from placebo or estradiol-implanted ovariectomized female mice, in which p44/42–MAPK phosphorylation was evident (Fig. 1 k). A metabolomic screen showed that levels of PGE$_2$, PGD$_2$, and 6-keto-PGF$_{1α}$ was significantly increased in xenograft tumors from mice treated with estradiol (Fig. 1 l). Estradiol-treated mice bearing ELT3 xenograft tumors also exhibited higher levels of urinary PGE$_2$, relative to placebo controls (Fig. 1 m). These data demonstrate that estradiol stimulates prostaglandin biosynthesis by TSC2-deficient cells in vitro and in vivo.

### Table 1. Rapamycin-insensitive up-regulation of PTGS2 and PTGIS expression in TSC-deficient LAM patient-derived cells are not affected by rapamycin treatment compared to TSC2-addback cells

| Gene    | Protein                  | Fold change TSC$^-$/vehicle versus TSC$^+$/vehicle | Fold change TSC$^+$-rapamycin versus TSC$^+$/vehicle | Fold change TSC$^-$/rapamycin versus TSC$^+$/vehicle |
|---------|--------------------------|----------------------------------------------------|-----------------------------------------------------|-----------------------------------------------------|
| PTGS2   | COX-2                    | 2.1 ($P = 0.0004$)                                  | 1.3 ($P = 0.05$)                                     | 2.8 ($P = 0.0006$)                                   |
| PTGIS   | Prostacyclin synthase (PGIS) | 40.4 ($P = 0.000001$)                              | 1.5 ($P = 0.0006$)                                  | 61.1 ($P = 0.000003$)                                |

**TSC2 negatively regulates COX-2 expression and prostaglandin production in vitro and in vivo**

Prostaglandins are products of prostaglandin-endoperoxide synthases (PTGSs) 1 and 2, or more commonly known as COX-1 and COX-2 (Fig. 2). COX-1 and COX-2 convert arachidonic acids released from membrane phospholipids into PGH$_2$. Prostacyclin (PGI$_2$) is produced by prostacyclin synthase (PTGIS) from PGH$_2$ (Fig. 2 a). To define the molecular mechanisms responsible for estradiol-enhanced COX-2 expression and prostaglandin production, we analyzed our previous expression array of TSC2-deficient LAM patient-derived cells (Lee et al., 2010) and found that both COX-2 (PTGS2) and prostacyclin synthase (PTGIS) expression were significantly increased, by 2- and 40-fold, respectively (Fig. 2 b and Table 1), in TSC2-deficient cells relative to TSC2-addback cells. To validate the findings of the expression array, we first performed real-time RT-PCR analysis; TSC2-deficient LAM patient-derived cells exhibited a 102-fold increase of PTGS2, and a 15-fold increase of PTGIS ($P < 0.0001$; Fig. 2 c). Importantly, rapamycin treatment did not affect the levels of PTGS2, but increased the levels of PTGIS by 6.6-fold ($P < 0.05$; Fig. 2 c), consistent with the changes identified in the expression array profile (Lee et al., 2010; Fig. 2 b).

We next examined the protein levels of COX-2 and PTGIS using immunoblotting analysis. COX-2 protein levels were higher in TSC2-deficient cells compared with TSC2-addback 621–101 cells (Fig. 2 d). Rapamycin treatment suppressed phosphorylation of the ribosomal protein p70S6 (S6), but did not affect the level of COX-2 expression, although it altered the migration of COX-2 (Fig. 2 d). COX-2 occurs as 72- and 74-kD isoforms, with the larger form a result of glycosylation (Sevigny et al., 2006). LAM cells treated with tunicamycin, an inhibitor of N-acetylglucosamine transferases, showed a marked reduction in the slower migrating form of COX-2, but showed similar production of PGE$_2$ (Fig. 2 e). This implies that this gel shift of COX-2 is caused by increased glycosylation.

Prostacyclin synthase (PTGIS) catalyzes the conversion of PGH$_2$ to prostacyclin (PGI$_2$). PTGIS protein levels were markedly higher in TSC2-deficient cells compared with TSC2-addback 621–101 cells (Fig. 2 f). Rapamycin treatment suppressed phosphorylation of the ribosomal protein p70S6 (S6), and decreased PTGIS levels in TSC2-deficient cells to a minor extent, but had no appreciable effect on TSC2-addback cells (Fig. 2 f), suggesting that TSC2 also regulates PTGIS expression independent of mTORC1.

To determine the functional impact of altered expression COX-2 and PTGIS on prostaglandin production, secreted or vehicle for 24 h. Data show the mean of three sets of independent samples. (d–f) Immunoblot analyses of tuberin, PTGIS, phospho-S6 (S235/236), and COX-2 protein in LAM patient–derived cell treated with 20 nM rapamycin (Rapa), 1 μg/ml tunicamycin (TN), or rapamycin plus tunicamycin, for 24 h. Results are representative of three different experiments. (e and g) Secreted prostaglandin levels were quantified in conditioned media collected from LAM patient–derived cells treated with 20 nM rapamycin (Rapa), 1 μg/ml tunicamycin (TN), or rapamycin plus tunicamycin, for 24 h ($n = 3$; ELISA). Results are representative of three sets of independent samples per group. (h) ELT3 cells were treated with 20 nM rapamycin (Rapa) or control for 24 h. Immunoblot analysis of COX-2 and phospho-S6 (S235/236) is representative of three different experiments. (i) Secreted prostaglandin levels were quantified in conditioned media collected from ELT3 cells treated with rapamycin or control. Data were normalized to control group ($n = 3$; ELISA). Results are representative of three sets of independent samples per group. (j) HeLa, OVCAR-5, and U2OS cells were treated with 20 nM rapamycin for 24 h. Immunoblot analysis of COX-2 and phospho-S6 (S235/236) is representative of three different experiments. (k) Secreted prostaglandin levels were quantified in conditioned media collected from cells treated with rapamycin or control, data were normalized to control group ($n = 3$; ELISA). Results are representative of three sets of independent samples per group. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.005$; Student’s t test.
levels of PGEM (a stable PGE₂ metabolite), 6-keto-PGF₁α (a stable prostacyclin PGI₂ metabolite), and PGE₂ were measured from TSC2-deficient LAM patient-derived cells treated with rapamycin or control. Levels of PGE₂, 6-keto-PGF₁α, and PGE₂ were all significantly higher in TSC2-deficient cells relative to TSC2-addback cells, and were also insensitive to rapamycin treatment (Fig. 2 g). Similar results on COX-2 expression were also seen in TSC2-deficient ELT3 cells (Fig. 2 h). PGE₂ levels were elevated by 2.5-fold in ELT3 cells in comparison to TSC2-addback cells, and this was again not affected by rapamycin treatment (Fig. 2 i). To determine whether this phenomenon of rapamycin-insensitive prostaglandin production was seen in other cancer cells with intact TSC2 levels but mTORC1 activation, we examined HeLa, U2OS, and OVCAR5 cells. Although PGE₂ production was variable among these cell lines, rapamycin did not affect COX-2 expression or PGE₂ production, although it did reduce phospho-S6 (Fig. 2, j and k). Together, these data indicate that up-regulation of COX-2 and prostaglandin production is rapamycin-insensitive in cells with mTORC1 activation.

To determine whether TSC2 regulates COX-2 and prostaglandin production in vivo, we used xenograft tumors from mice inoculated with TSC2-deficient ELT3-V3 (vector-control) cells and TSC2-addback ELT3-T3 cells. COX-2 levels were significantly higher in the ELT3-V3 xenograft tumors with elevated phospho-S6 relative to TSC2-addback ELT3-T3 tumors (Fig. 3 a). In addition, levels of PGE₂ in xenograft tumors were significantly higher in mice with the ELT3-V3 tumors in comparison to mice with the TSC2-addback ELT3-T3 tumors (Fig. 3 b). Moreover, urinary PGE₂ level was significantly higher in mice with the ELT3-V3 tumors in comparison to mice with the TSC2-addback ELT3-T3 tumors (Fig. 3 c). Similar results on PGTIS expression were also observed in xenograft tumors of TSC2-deficient ELT3 cells (Fig. 3 d). Urinary 6-keto-PGF₁α levels were also significantly higher in mice with the ELT3-V3 tumors in comparison to mice with the TSC2-addback ELT3-T3 tumors (Fig. 3 e). Together, these data indicate that up-regulation of COX-2 and prostaglandin production is rapamycin-insensitive in cells with mTORC1 activation.

mTORC2 is a critical mediator of COX-2 expression and prostaglandin biosynthesis in TSC2-deficient cells

To identify additional molecular determinants responsible for rapamycin-insensitive COX-2 expression and prostaglandin biosynthesis, we first treated Tsc2⁻/⁻ p53⁻/⁻ MEFs with Torin 1, a potent ATP-competitive mTORC1 and mTORC2 inhibitor for 24 h. Torin 1 decreased the level of COX-2 and phosphorylation of S6 (S235/236) and 4EBP1. Interestingly, cells treated with LY294002, a PI3K inhibitor, for 24 h exhibited reduced level of COX-2. However, rapamycin treatment did not affect the level of COX-2 (Fig. 4 a). Our data suggest that mTORC2 might play a role in mediating COX-2 expression. To further test the impact of mTORC2 on COX-2 expression,
Figure 4. mTORC2 regulates COX-2 expression via PI3K–AKT pathway in TSC2-deficient cells. (a) Tsc2+/+ p53−/− MEFs were treated with 20 nM rapamycin, 250 nM Torin 1, or 20 µM LY294002 for 24 h. Levels of COX-2, 4EBP1, and phospho-S6 (S235/236) were assessed by immunoblot. (b and c) Tsc2+/+ p53−/− MEFs were transfected with Rictor shRNA or control shRNA, and then selected with puromycin to obtain stable cells. Control shRNA or with Rictor shRNA-Tsc2+/+ p53−/− MEFs were treated with vehicle or 20 nM rapamycin for 24 h. Levels of COX-2, COX-1, phospho-S6 (S235/236), and phospho-Akt (S473) were assessed by immunoblot. (d) LAM patient–derived cells (TSC̶) cells were treated with 20 nM rapamycin, or 250 nM Torin 1, or
Tuberin inhibits COX-2 in TSC | Li et al.

Results are representative of six sets of independent samples per group. *, P < 0.05; Student’s t test.

Inhibition of COX-2 suppresses renal tumorigenesis and inhibits the progression of xenograft tumor of TSC2-deficient cells in preclinical models

To determine the efficacy of inhibition of COX-2 in vivo, first, we used the COX-2–specific inhibitor Celecoxib to treat Tsc2<sup>−/−</sup> mice, which develop spontaneous renal cystadenomas at age of 4 mo. We found that treatment with Celecoxib strongly suppressed microscopic renal lesions in Tsc2<sup>−/−</sup> mice by ~50% after 4 mo of treatment (0.1% wt/wt in chow) relative to vehicle control (Fig. 5, a and b). These data indicate that COX-2 is responsible for renal tumorigenesis.

We next assessed the possible benefit of aspirin in a xenograft tumor model of TSC2-deficient ELT3-luciferase-expressing cells. Aspirin treatment for 3 wk decreased the intensity of bioluminescence (Fig. 5, c and d), and decreased the tumor
Figure 5. Inhibition of COX-2 suppresses renal tumorigenesis and inhibits the progression of xenograft tumor of TSC2-deficient cells in preclinical models. (a and b) Tsc2^{-/-} mice were treated with either vehicle or Celecoxib (0.1% in mouse chow) for one month, and then sacrificed for analysis at the end of treatment. Renal cystadenoma histology and microscopic kidney tumor scores were assessed. (a) Microscopic kidney tumor scores are plotted on a linear scale (P = 0.0002). Data are analyzed from 16 vehicle and 11 Celecoxib treatment groups. (b) Two cystadenomas are shown. Results are representatives of 11 or 16 mice per group. Bar, 100 µM. (c–g) Female CB17-scid mice were inoculated with ELT3-luciferase cells subcutaneously. Mice were treated with either vehicle or aspirin (100 mg/kg/day in the drinking water) for 3 wk (n = 9). Results are representative of five to eight mice per group.
Evidence for COX-2 activation in vivo in LAM

We then examined whether these in vitro and xenograft model findings were relevant to human LAM. Accordingly, LAM lungs were found to express higher levels of COX-2 (PTGS2) in comparison with control lungs (Fig. 6 a). Furthermore, immunohistochemistry analyses showed that COX-2 expression was specifically increased in pulmonary LAM nodules (arrows), which also expressed both smooth muscle actin and phospho-S6 (Fig. 6 b). To examine the functional effects of COX-2 expression in LAM, 15-epi-lipoxin A4 (LXA4), a product of aspirin-acetylated COX-2, was measured in exhaled breath condensate (EBC) from three LAM subjects (Table 2). LXA4 was detected in EBCs and the levels were increased with aspirin (Fig. 6 c). LXA4 decreases proliferation of A549 cells (Human lung adenocarcinoma; Clària et al., 1996) and also reduced the growth of LAM patient–derived 621–101 cells at 100 nM (Fig. 6 d). In a separate experiment, the 15-epi-LXA4 integrity was confirmed by UV-Vis spectrophotometry to ensure the presence of the diagnostic tetraene chromophore and accurate quantitation and HPLC to ensure that only a single peak was present without evidence for isomerization (Fig. 6 e). We next performed a dose–response of LXA4 and found that LXA4 at 500 nM exhibited the strongest inhibitory effect on cell growth (Fig. 6 e).

Urinary PGE2 levels were measured in 29 LAM patients and in 18 healthy women; however, these levels were not significantly different between two groups (Fig. 6 f). Because renal prostaglandin production can significantly influence urinary prostaglandin levels, we next measured PGE2 and 6-keto-PGF1α levels in sera from 14 LAM patients and 13 healthy women. The mean serum PGE2 level of LAM patients (27.8 ± 1.8 pg/ml) was higher than that of healthy women (19.6 ± 1.4 pg/ml; P = 0.0021; Fig. 6 g). In addition, the mean serum 6-keto-PGF1α level of LAM patients (192.2 ± 64.9 pg/ml) was also higher compared with the mean in healthy women (82.6 ± 6.3 pg/ml; P = 0.0006; Fig. 6 h).

DISCUSSION

LAM is a neoplastic disorder in which smooth muscle-like cells with biallelic inactivation of TSC2 leads to hyperactivation of mTORC1. This fundamental mechanistic insight led to the recent reported success in treating LAM patients with rapamycin. However, mTORC1-independent effects of TSC2 loss are also known (Yu and Henske, 2010; Neuman and Henske, 2011). The marked female predominance of LAM suggests that estradiol promotes disease progression. In this study, we identified an estradiol-induced prostaglandin metabolic signature in TSC2-deficient ELT3 cells in vitro and in vivo. Prostaglandins, synthesized via COX-1/COX-2, appear to play important roles in cancer progression (FitzGerald and Patrono, 2001; Müller, 2004; Wang et al., 2007; Wang and Dubois, 2010), although their precise role is still hotly debated. Estradiol-dependent prostaglandin production has been studied in other models. Estradiol activated COX-2 and increased prostacyclin synthesis in mouse aortic smooth muscle cells (Egan et al., 2004). Increased levels of PGE2 causes enhanced aromatase expression and local estradiol production in breast tissue (Subbaramaiah et al., 2012). However, the relationship between prostaglandins and TSC/LAM has not been investigated previously. Remarkably, we found that estradiol enhances the expression of COX-2 and induces production of PGE2 in TSC2-deficient cells in vitro and in vivo. Furthermore, we identified a novel function of TSC2 as a negative regulator of COX-2 expression and prostaglandin biosynthesis. Interestingly, this regulation appears to be rapamycin-insensitive but sensitive to Akt inhibition and Rictor knockdown, suggesting that COX-2 may be regulated by Akt in TSC2-deficient cells.

We also demonstrated that COX-2 is abundant in LAM lesions, and that serum levels of PGE2 are elevated in LAM patients. Collectively, our data suggest that COX-2 may play an important role in LAM pathogenesis.

NS398 and aspirin are direct enzyme inhibitors of COX-2 and/or COX-1. As expected, we have found that cells treated with NS398 or aspirin exhibited reduced levels of PGE2 (Fig. 4 k), consistent with this inhibition. However, we also found that both NS398 and aspirin decreased the levels of COX-2 protein. Although this was initially surprising to us, multiple experiments confirmed this effect, and our results are in agreement with previous reports that COX-2 protein expression is reduced by classical nonsteroidal antiinflammatory drugs (NSAIDs), including aspirin and NS398 (Takada et al., 2004; Galamb et al., 2010). Therefore, we think that both enzymatic inhibition and reduction in expression of COX-2 occurs in response to NS398 and aspirin treatment. Aspirin, the prototypical NSAID, covalently modifies both COX-1 and COX-2 by acetylation. We demonstrated that aspirin treatment significantly reduced the growth of xenograft tumors of TSC2-deficient ELT3 cells, and led to reduced urinary levels of PGE2 and 6-keto-PGF1α, which is consistent with
Although aspirin-acetylated COX-2 inhibits prostaglandin formation, the enzyme is not completely inactivated. Rather, aspirin-acetylated COX-2 catalyzes the conversion of arachidonate to prostaglandins. Furthermore, xenograft tumors from aspirin-treated mice exhibited higher levels of apoptosis compared with vehicle treatment (Fig. 5 f).
to 15-epi-LXA₄ (Clària et al., 1996). In this manner, aspirin both inhibits prostaglandin production and triggers the formation of 15-epi-LXA₄, a potent inhibitor of malignant cell proliferation (Clària et al., 1996). 15-epi-LXA₄ was present in EBCs from LAM patients, and was increased with oral aspirin ingestion. 15-epi-LXA₄ also decreased LAM-patient–derived cell proliferation (Fig. 6, d and e). Together, these findings suggest that aspirin may have rapamycin-independent beneficial effects in LAM.

LAM is often a progressive disease which leads to respiratory failure and death in the absence of lung transplantation. The recent demonstration that rapamycin has clinical benefit in LAM is a major success. However, not all patients respond to rapamycin, and upon rapamycin withdrawal, lung function decline resumes (McCormack et al., 2012). Hence, lifelong treatment of LAM patients with rapamycin may be required to maintain benefit, with unknown long-term toxicities. Our findings suggest that aspirin and/or other COX-1/COX-2 inhibitors may have significant benefit in slowing LAM progression. The well-known side-effect and toxicity profile of these drugs make them attractive candidates for long-term therapy in LAM patients. It is also possible that other neoplastic conditions associated with mTOR hyperactivation could be responsive to these agents. Further preclinical and clinical investigation is warranted to explore these possibilities.

**MATERIALS AND METHODS**

**Cell culture and reagents.** ELT3 cells (Eker rat uterine leiomyoma–derived cells; Howe et al., 1995a,b) and LAM patient–derived 621–101, 621–102, and 621–103 cells were cultured in IIA complete medium. 

**Expression array analysis.**

**Microscopic kidney tumor scores.** Mouse kidneys were removed rapidly after euthanasia and fixed overnight in 10% formalin. Kidneys were then prepared for histological evaluation in stereotypical fashion by cutting the kidney into sections at 1-mm sections.

**Microscopic kidney tumor scores were determined in a semiquantitative fashion by a single blinded observer.** The set of 1-mm sections were prepared as H&E-stained 8-μm sections. Each tumor or cyst identified was measured to determine its length and width in two dimensions, as well as the percentage of the lumen filled by tumor (this was 0% for a simple cyst, and 100% for a completely filled, solid adenoma). These measurements were converted into a measurement of tumor volume per lesion using the following formula: tumor volume = maximum (tumor percent, 5)/100 × 3.14159/6 × 1.64 × (tumor length × tumor width) **1.5** (Auricchio et al., 2012). The total tumor volume per kidney was then equal to sum of the tumor volume of each lesion identified. Comparisons between sets of mice for tumor measurements were made using the nonparametric Mann-Whitney test in Prism (GraphPad Software, Inc.).

**Bioluminescent reporter imaging.** 10 min before imaging, animals were injected with luciferin (120 mg/kg; i.p.; Xenogen). Bioluminescent signals were recorded using the Xenogen IVIS System. Total photon flux of tumors was analyzed as previously described (Yu et al., 2009).

**Confocal microscopy.** ELT3 cells and LAM-derived cells were plated on glass coverslips in 12-well tissue culture plates overnight. Cells were serum starved overnight, and then treated with 20 nM rapamycin for 24 h. Cells were rinsed with PBS twice, fixed with warm 4% paraformaldehyde, permeabilized with 0.2% Triton X-100, blocked in 3% BSA/PBS for 1 h, incubated with primary antibody 1% BSA in PBS for 1 h at room temperature, and then incubated with secondary antibodies for 1 h. Images were captured with a FluoView FV-10i Olympus Laser Point Scanning Confocal Microscope.

**Expression array analysis.** Re-analysis of previously published expression array data (GEO accession no. GSE16944; Lee et al., 2010) was performed using the online tool GEO2R. Transcript levels of PTGS2 (COX-2; ID: 238018) and PTGSl (prostaglycerin synthase; ID: 454010) were compared between TSC2-deficient and TSC2-addback (TSC2+) cells, or rapamycin- and vehicle-treated TSC2-deficient cells.
Quantitative RT-PCR. RNA from cultured cells and xenograft tumors was isolated using RNeasy Mini Kit (QIAGEN). Gene expression was quantified using One-Step qRT-PCR kits (Invitrogen) in the Applied Biosystems Step One Plus Real-Time PCR System and normalized to β-actin.

Immunoblotting and antibodies. Cells were lysed in m-PER buffer (Thermo Fisher Scientific). The following antibodies were used: COX-1, COX-2, EGF-R, phospho-p44/42-MAPK (T202/Y204), phospho-S6 (S235/236), phospho-Akt (S473), cleaved caspase 3, and cleaved PARP (Cell Signaling Technology); tuberin and e-Myc (Santa Cruz Biotechnology, Inc.); smooth muscle actin (BioGenes); β-actin (Sigma-Aldrich); and Alexa Fluor 488 goat anti–rabbit IgG (H+L) antibody (Invitrogen).

Metabolomic profiling. 100 µg of frozen biopsy tissue was submitted to Metabolon, Inc. for sample extraction and analysis. In brief, Metabolon performed cold methanol extraction of mechanically digested tissue samples and these extracts were split into three aliquots. The reproducibility of the extraction protocol was assessed by the recovery of xenobiotic compounds spiked into every tissue sample before extraction. These aliquots were processed and characterized by one of the three analytical methods previously described (Evans et al., 2009): UHPLC-ESI-MS/MS in the positive ion mode, UHPLC-ESI-MS/MS in the negative ion mode, and stable isotope dilution followed by GC-El-MS. Chromatographic timelines were standardized using a series of xenobiotics that elute at specified intervals throughout each chromatographic run. The technical variability of each analytical platform was assessed by repeated characterization of a pooled standard that contained an aliquot of each sample within the study. Metabolon’s global screening platform utilizes a nontargeted approach (Evans et al., 2009). For LC-MS/MS, after peak identification and quality control filtering (signal greater than 3x background, retention index within a prespecified platform–dependent window, quant ions to library match within 0.4 m/z, and the MS/MS forward and reverse scores), the metabolites’ relative concentrations were obtained from median-scaled day–block normalized data for each compound. In vitro data were normalized to total protein levels as measured by Bradford assay. Eicosanoids identified by the Metabolon platform in this study were measured by LC-MS/MS run in the negative mode. Fragmentation of the molecule’s quasi ion generated a pattern of ions that matched in mass and relative intensities to a purified standard as described by DeHaven et al. (2010). In this study, the data were derived using a nontargeted method that does not incorporate labeled standards. However, in cases where targeted methods have been created and used to validate Metabolon screening platform, the results from the screening platform have shown a high degree of correlation with the targeted/absolute quantification methods and clinical measurements, when available (Sreekumar et al., 2009; Zhang et al., 2011).

Cell viability assay. Cell viability was determined by MTT assay (Sigma-Aldrich).

Short hairpin RNA (shRNA) down-regulation. 293T packaging cells were transected with Rictor shRNA or non-targeting shRNA vectors using Mirus Trans-IT TKO Transfection reagent (Mirus). Tsc22Δ/Δ p53−/− MEFs were infected with lentivirus containing Rictor shRNA, or non-Targeting shRNA. Cells were harvested 48 h after transfection and then selected against puromycin. Stable clones were harvested for future experiments.

Immunohistochemistry. Sections were deparaffinized, incubated with primary antibodies and biotinylated secondary antibodies, and counterstained with Gill’s Hematoxylin.

Quantification of prostaglandin levels. Levels of PGEM (a stable metabolite of PGE2), 6-keto-PGF1α (a stable metabolite of prostacyclin), and creatinine were measured using ELISA kits (Cayman Chemical). Levels of secreted prostaglandins were normalized to vehicle control and expressed as fold change. Urinary levels of prostaglandins were normalized to creatinine levels and expressed as nanograms per milliliter.

Statistical analyses. Statistical analyses were performed using Student’s t test when comparing two groups for in vitro and in vivo studies. Welch’s t tests and Wilcoxon rank sum tests were performed for metabolomic profiling. Two-way ANOVA test was performed in xenograft tumor–aspirin studies. Mann-Whitney tests were used for prostaglandin quantification in clinical data.

We are grateful for Dr. C. Walker (Texas A&M Health Science Center) for providing ELT3 cells, Ms. E. Peters (The Center for LAM Research and Clinical Care – Brigham and Women’s Hospital) for human specimen acquisition, Mr. B. Ith, and Dr. M. Perrella for specimen preparation, Dr. C. Jiang (Peking Union Medical College, China) for providing access to research facility, and Dr. I. Rosas for providing non-LAM lung tissues. We thank Dr. A. Choi for valuable discussion and critical review of the manuscript. We gratefully acknowledge LAM patients and healthy volunteers for their valuable contribution to this study.

A. Cubi and X. Gu are LAM Foundation postdoctoral fellows. J. Li is a Tuberous Sclerosis Alliance postdoctoral fellow. J. Blenis is a LAM Foundation established investigator. This study is supported by The LAM Foundation, The Adler Foundation, The LAM Treatment Alliance [to E.P. Henske], National Institutes of Health Grant GM51405 [to J. Blenis], the National Heart Lung and Blood Institute grants HL68669 [to B.D. Levy] and HL118760 [to E.P. Henske], the National Cancer Institute grants 1PO1CA210864 [to D. Kwiatkowski] and HU008216 [to J.J. Yu], the Department of Defense Exploratory Idea Development Award (W81XWH-12-1-0442 to J.J. Yu), and Biomedical Research Institute-BiW Microgrants to C.L. and J.J. Yu.

B.D. Levy is an inventor on patents on lipoxins assigned to Brigham and Women’s Hospital, some of which are licensed for clinical development. The interests of B.D. Levy were reviewed and are managed by the Brigham and Women’s Hospital and Partners HealthCare in accordance with their conflict of interest policies. The other authors have no conflicting financial interests.

Submitted: 24 May 2013
Accepted: 9 December 2013

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