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The RAS-related GTPase RHOB confers resistance to EGFR-tyrosine kinase inhibitors in non-small-cell lung cancer via an AKT-dependent mechanism

Olivier Calvayrac1,2,†, Julien Mazières1,2,3,4,†, Sarah Figaro1, Claire Marty-Detraves1, Isabelle Raymond-Leotron4, Emilie Bousquet3, Magali Farella1,5, Estelle Clermont-Taranchon6, Julie Milia2,3, Isabelle Rouquette6, Nicolas Guibert1,3, Amélie Lusque7, Jacques Cadranel8, Nathalie Mathiot8, Ariel Savina9, Anne Pradines1,5 & Gilles Favre1,2,5,**†

Abstract

Although lung cancer patients harboring EGFR mutations benefit from treatment with EGFR-tyrosine kinase inhibitors (EGFR-TKI), most of them rapidly relapse. RHOB GTPase is a critical player in both lung carcinogenesis and the EGFR signaling pathway; therefore, we hypothesized that it could play a role in the response to EGFR-TKI. In a series of samples from EGFR-mutated patients, we found that low RHOB expression correlated with a good response to EGFR-TKI treatment while a poor response correlated with high RHOB expression (15.3 versus 5.6 months of progression-free survival). Moreover, a better response to EGFR-TKI was associated with low RHOB levels in a panel of lung tumor cell lines and in a lung-specific tetracycline-inducible EGFRL858R transgenic mouse model. High RHOB expression was also found to prevent erlotinib-induced AKT inhibition in vitro and in vivo. Furthermore, a combination of the new-generation AKT inhibitor GSK94 with erlotinib induced tumor cell death in vitro and tumor regression in vivo in RHOB-positive cells. Our results support a role for RHOB/AKT signaling in the resistance to EGFR-TKI and propose RHOB as a potential predictor of patient response to EGFR-TKI treatment.

Keywords RHOB; EGFR; TKI; AKT; resistance

Introduction

Epidermal growth factor receptor (EGFR) is the main oncogenic driver in non-small-cell lung cancer (NSCLC), occurring in 10–50% of the patients depending on their origins. EGFR-tyrosine kinase inhibitors (EGFR-TKI) are widely used to treat metastatic NSCLC in patients bearing EGFR-activating mutations, which are most commonly the L858R point mutation and the deletion of exon 19 (Rosell et al, 2012). Sixty–seventy percent of the EGFR-mutated patients respond to therapy, 20% have a stable disease, and 15% develop primary resistance. However, despite this high response rate, all patients usually relapse with a median delay of 12 months. Among the few identified mechanisms of primary resistance, low expression levels of the pro-apoptotic protein BIM have been revealed as a good predictor of nonresponsiveness to targeted therapy in EGFR-mutated cells and patients (Faber et al, 2011), and similar observations have been reported for the RAS GTPase-activating protein NF1 (de Bruin et al, 2014). Many mechanisms of acquired resistance have been elucidated so far, such as the T790M gatekeeper mutation (Nguyen et al, 2009), amplification of either the MET oncogene (Engelman et al, 2007) or HER2 (Takezawa et al, 2012), or epithelial-to-mesenchymal transition (EMT) (Thomson et al, 2005). These have led to the development of new-generation drugs (Cross et al, 2014) that are given sequentially after EGFR-TKI failure. Resistance mechanisms to EGFR-TKI could be mediated by a bypass reactivation of one or several key proliferation and survival signaling pathways downstream from EGFR, mainly PI3K (phosphatidylinositol 3-kinase)/AKT (Engelman et al, 2007), MEK...
levels on EGFR signaling using dedicated cell lines and a mouse model. We then analyzed the consequences of modulating RHOB tumor tissue levels predicted patient response rate to EGFR-TKI and demonstrated that low-RHOB patients and samples with moderate or high staining as high-RHOB patients (Fig 1A). Tumor tissues and completed follow-up files were available for all these patients (Fig 1B and Appendix Table S1). Median progression-free survival (PFS) was 12.06 months (95% CI [8.11; 13.99]) for the whole population (Fig EV1A). We observed an impressive clinical response to EGFR-TKI in patients with low RHOB expression, suggesting that RHOB could predict EGFR-TKI sensitivity, as exemplified in Fig 1C. PFS was not statistically different between the RHOB (0) and RHOB (+) groups and between the RHOB (+) and RHOB (+++) groups (Fig EV1B), allowing us to group RHOB (0) with (+) and RHOB (+++) with (+++). This suggests that there is a RHOB threshold that defines the EGFR-TKI response, with a clear cut-off between weak and moderate RHOB expression. Indeed, median PFS was 15.3 months (95% CI [13.1; 18.2]) for patients with low RHOB expression (0 and +) and 5.6 months (95% CI [3.6; 6.4]) for patients with high RHOB expression (++ and ++++) (P < 0.0001; Fig 1D). As an alternative method, we determined RHOB mRNA expression in a subset of tumors, and we observed a significant correlation between RHOB mRNA expression (determined by RT-qPCR) and RHOB protein staining (determined by IHC) (Appendix Fig S1A–C). PFS analysis showed that both methods of detection gave similar results on the predictive role of RHOB in response to EGFR-TKI.

We first determined whether RHOB expression in primary lung tumors is predictive of the response to EGFR-TKI in EGFR-mutated patients. We performed RHOB immunohistochemistry analysis on 96 lung tumor biopsies collected before any treatment from a series of EGFR-mutated lung adenocarcinoma. Patients received EGFR-TKI treatment (erlotinib, n = 43; gefitinib, n = 51; afatinib, n = 2) as first-line (n = 63), second-line (n = 28), third-line (n = 3), or fourth-line (n = 2) therapy. According to the intensity of the staining, we defined four levels: null: 0; weak: +; moderate: ++; and high: +++ (Fig 1A). Samples with null or weak staining were considered as low-RHOB patients and samples with moderate or high staining as high-RHOB patients (Fig 1A). Tumor tissues and completed follow-up files were available for all these patients (Fig 1B and Appendix Table S1). Median progression-free survival (PFS) was 12.06 months (95% CI [8.11; 13.99]) for the whole population (Fig EV1A). We observed an impressive clinical response to EGFR-TKI in patients with low RHOB expression, suggesting that RHOB could predict EGFR-TKI sensitivity, as exemplified in Fig 1C. PFS was not statistically different between the RHOB (0) and RHOB (+) groups and between the RHOB (+) and RHOB (+++) groups (Fig EV1B), allowing us to group RHOB (0) with (+) and RHOB (+++) with (+++). This suggests that there is a RHOB threshold that defines the EGFR-TKI response, with a clear cut-off between weak and moderate RHOB expression. Indeed, median PFS was 15.3 months (95% CI [13.1; 18.2]) for patients with low RHOB expression (0 and +) and 5.6 months (95% CI [3.6; 6.4]) for patients with high RHOB expression (++ and ++++) (P < 0.0001; Fig 1D). As an alternative method, we determined RHOB mRNA expression in a subset of tumors, and we observed a significant correlation between RHOB mRNA expression (determined by RT-qPCR) and RHOB protein staining (determined by IHC) (Appendix Fig S1A–C). PFS analysis showed that both methods of detection gave similar results on the predictive role of RHOB in response to EGFR-TKI.

We first investigated this hypothesis in patients carrying mutated EGFR who had been treated with EGFR-TKI and demonstrated that RHOB tumor tissue levels predicted patient response rate to EGFR-TKI therapy. We then analyzed the consequences of modulating RHOB levels on EGFR signaling using dedicated cell lines and a mouse model of inducible lung-specific EGFR<sup>L858R</sup>-driven tumors (Politi et al., 2006). The results presented here demonstrate that RHOB expression is predictive of EGFR-TKI response and suggest that an EGFR-TKI–AKT inhibitor combination may provide a clinical advantage to prevent resistance to EGFR-TKI in RHOB-positive tumor patients.

**Results**

**RHOB expression predicts the response to EGFR-TKI in patients harboring EGFR-activating mutations**

We first determined whether RHOB expression in primary lung tumors is predictive of the response to EGFR-TKI in EGFR-mutated patients. We performed RHOB immunohistochemistry analysis on 96 lung tumor biopsies collected before any treatment from a series of EGFR-mutated lung adenocarcinoma. Patients received EGFR-TKI treatment (erlotinib, n = 43; gefitinib, n = 51; afatinib, n = 2) as first-line (n = 63), second-line (n = 28), third-line (n = 3), or fourth-line (n = 2) therapy. According to the intensity of the staining, we defined four levels: null: 0; weak: +; moderate: ++; and high: +++ (Fig 1A). Samples with null or weak staining were considered as low-RHOB patients and samples with moderate or high staining as high-RHOB patients (Fig 1A). Tumor tissues and completed follow-up files were available for all these patients (Fig 1B and Appendix Table S1). Median progression-free survival (PFS) was 12.06 months (95% CI [8.11; 13.99]) for the whole population (Fig EV1A). We observed an impressive clinical response to EGFR-TKI in patients with low RHOB expression, suggesting that RHOB could predict EGFR-TKI sensitivity, as exemplified in Fig 1C. PFS was not statistically different between the RHOB (0) and RHOB (+) groups and between the RHOB (+) and RHOB (+++) groups (Fig EV1B), allowing us to group RHOB (0) with (+) and RHOB (+++) with (+++). This suggests that there is a RHOB threshold that defines the EGFR-TKI response, with a clear cut-off between weak and moderate RHOB expression. Indeed, median PFS was 15.3 months (95% CI [13.1; 18.2]) for patients with low RHOB expression (0 and +) and 5.6 months (95% CI [3.6; 6.4]) for patients with high RHOB expression (++ and ++++) (P < 0.0001; Fig 1D). As an alternative method, we determined RHOB mRNA expression in a subset of tumors, and we observed a significant correlation between RHOB mRNA expression (determined by RT-qPCR) and RHOB protein staining (determined by IHC) (Appendix Fig S1A–C). PFS analysis showed that both methods of detection gave similar results on the predictive role of RHOB in response to EGFR-TKI.

We first investigated this hypothesis in patients carrying mutated EGFR who had been treated with EGFR-TKI and demonstrated that RHOB tumor tissue levels predicted patient response rate to EGFR-TKI therapy. We then analyzed the consequences of modulating RHOB levels on EGFR signaling using dedicated cell lines and a mouse model of inducible lung-specific EGFR<sup>L858R</sup>-driven tumors (Politi et al., 2006). The results presented here demonstrate that RHOB expression is predictive of EGFR-TKI response and suggest that an EGFR-TKI–AKT inhibitor combination may provide a clinical advantage to prevent resistance to EGFR-TKI in RHOB-positive tumor patients.

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previously described mouse model of inducible lung-specific EGFR<sup>L858R</sup>-driven tumors crossed into a Rhob wild-type, heterozygous, or null genetic background (Calvayrac et al., 2014). To evaluate the effect of RHOB loss on erlotinib sensitivity, we performed a 4-day treatment with erlotinib at 12.5 mg/kg/day that did not show objective response in the initially described mouse model (Politi et al., 2006). In these conditions, erlotinib treatment induced a strong anti-tumoral response in EGFR<sup>L858R/Rhob<sup>+/−</sup> and EGFR<sup>L858R/Rhob<sup>−/−</sup> mice, whereas no significant tumor shrinkage was observed in EGFR<sup>L858R/Rhob<sup>+/−</sup> mice (Fig 2A). Erlotinib induced a significant decrease in tumor/total lung surface ratios in Rhob-deficient and heterozygous mice (Fig 2B), and lungs of these mice were almost clear of tumor cells after treatment. In addition, cell proliferation, measured by the Ki67-positive cell ratio, decreased in Rhob<sup>+/−</sup> and Rhob<sup>−/−</sup> mice but not in Rhob<sup>+/+</sup> mice (Fig 2C and D). Moreover, caspase-3 cleavage was detected after 24 h of treatment in EGFR<sup>L858R/Rhob<sup>−/−</sup> but not in EGFR<sup>L858R/Rhob<sup>+/−</sup> mice, suggesting a strong and rapid apoptotic response to erlotinib in Rhob-deficient mice (Fig 2E). These observations with EGFR-mutated driven lung tumors in mice confirm our data obtained with patients, showing that low RHOB expression is associated with a good response to EGFR-TKI.

The modulation of RHOB expression determines the level of resistance to erlotinib in EGFR-mutated lung cancer cell lines

To further confirm that RHOB expression impacts on the response to EGFR-TKI treatment, we downregulated or
overexpressed RHOB by RNA interference and adenoviral transduction, respectively, in several EGFR-mutated human lung cancer cell lines. Interestingly, and in accordance with our previous results, RHOB downregulation hypersensitized HCC4006 cells to erlotinib (Fig 3A) while its overexpression protected them (Fig 3B). To avoid any possible siRNA off-target effects, siRNA-transfected cells were transduced with a RHOB-expressing adenovirus. Figure 3C shows that RHOB overexpression completely

Figure 2. RHOB loss of expression increases sensitivity to erlotinib in mice with EGFR<sup>858R</sup>-driven lung tumors.

A Representative H&E staining of whole lungs from EGFR<sup>858R</sup>/Rhob<sup>-/-</sup>, EGFR<sup>858R</sup>/Rhob<sup>+/+</sup>, and EGFR<sup>858R</sup>/Rhob<sup>+</sup>/placebo mice treated or not with erlotinib (12.5 mg/kg/day) for 4 days. Scale bars: 5 mm.

B Quantification of the tumor/lung ratio. n = 7 for each group except for EGFR<sup>858R</sup>/Rhob<sup>-/-</sup> placebo (n = 6).

C, D Representative Ki67 immunostaining of EGFR<sup>858R</sup>/Rhob<sup>-/-</sup>, EGFR<sup>858R</sup>/Rhob<sup>+/+</sup>, and EGFR<sup>858R</sup>/Rhob<sup>+</sup>/placebo mice treated or not with erlotinib (12.5 mg/kg/day) for 4 days (scale bars: 50 μm), and the corresponding quantification (D). Three independent zones per mouse lung were used for quantification. n = 21 (seven mice) for each group except for EGFR<sup>858R</sup>/Rhob<sup>-/-</sup> placebo (n = 18; six mice).

E Immunostaining of cleaved caspase-3 in lung tumors from EGFR<sup>858R</sup>/Rhob<sup>+/+</sup> or EGFR<sup>858R</sup>/Rhob<sup>-/-</sup> mice treated for 24 h with erlotinib at 12.5 mg/kg. Black arrows point apoptotic cells. Scale bars: 50 μm.

Data information: **P < 0.001 versus placebo; ***P < 0.0001 versus placebo. Data are expressed as mean ± SEM, P-values were determined by Mann-Whitney two-tailed t-test.
reversed the effect of RHOB downregulation on erlotinib sensitiv-
ity. Similar results were obtained with several cell lines harboring
either an exon 19 deletion (HCC827 and HCC2935) (Figs 3D and
E, and EV2A–C) or an exon 21 L858R point mutation (H3255)
(Figs 3F and EV2D), which together account for more than 85%

of all activated EGFR mutations found in human lung cancers.
Moreover, a gradual increase in RHOB expression, obtained
through RHOB recombinant adenoviral transduction, gradually
increased the erlotinib IC50 values in HCC4006 (Fig 3G) and
HCC827 cells (Appendix Fig S2). These findings clearly demons-
strate that RHOB expression levels determine the resistance of
EGFR-mutated cells to erlotinib.

RHOB-induced resistance to erlotinib involves the AKT pathway

To investigate the mechanisms underlying the involvement of RHOB
in the resistance to erlotinib treatment, we analyzed the potential
role of RHOB in cell survival. We first tested a panel of EGFR-
mutated cell lines for their ERK and AKT phosphorylation status,
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contrast, when RHOB was overexpressed in the four EGFR-mutated cell lines, EGFR and ERK phosphorylation was still downregulated by erlotinib whereas AKT remained fully phosphorylated (Fig 4A), and no effect was observed on EGFR WT cells (Fig EV3). Consistent with this, erlotinib more potently inhibited AKT phosphorylation in Rhob−/− lung tumor mice compared to Rhob+/+ mice, while erlotinib inhibited ERK phosphorylation in both mouse models (Fig 4B).

These results demonstrate that RHOB prevents erlotinib-induced AKT dephosphorylation, suggesting that the RHOB/AKT axis might characterize the effect of erlotinib on ERK and AKT pathways in both characterizing the effect of RHOB overexpression onto HCC4006 (Fig 4C) and normalizing according to total protein levels. RHOB overexpression was also monitored by Western blotting.

B Representative immunostaining of phospho-AKT (Ser473) and phospho-ERK1/2 and their total protein amounts in lung tumors from EGFRL858R/Rhob−/− or EGFRL858R/Rhob+/+ mice treated or not with erlotinib (125 mg/kg/day) for 4 days. The remaining hyperplastic areas were selected in erlotinib-treated mice to efficiently characterize the effect of RHOB on ERK and AKT pathways in both Rhob genotypes. Scale bars: 100 μm.

C HCC4006 cells were transduced with a plasmid coding for a constitutively active AKT mutant (AKTmyr, myristoylated) or an empty vector (ø) and treated for 72 h with increasing concentrations of erlotinib. The surviving cell fraction was determined by an MTS assay, and AKT overexpression and phosphorylation at Ser473 were assessed by Western blotting. Data are representative of at least three independent experiments. Data are expressed as mean ± SEM from three independent experiments.

Source data are available online for this figure.

Figure 4. RHOB induces resistance to erlotinib through the AKT pathway.

A HCC4006, HCC827, HCC2935, and H3255 cells were transduced with control (AdCont) or RHOB-overexpressing (AdRHOB) adenoviruses and treated for 4 h with erlotinib at concentrations corresponding to the respective IC50 values determined for each control cell line. The phosphorylation status of AKT, ERK1/2, and EGFR was assessed by Western blotting and normalized according to total protein levels. RHOB overexpression was also monitored by Western blotting.

B Representatie immunostaining of phospho-AKT (Ser473) and phospho-ERK1/2 and their total protein amounts in lung tumors from EGFRL858R/Rhob−/− or EGFRL858R/Rhob+/+ mice treated or not with erlotinib (125 mg/kg/day) for 4 days. The remaining hyperplastic areas were selected in erlotinib-treated mice to efficiently characterize the effect of RHOB on ERK and AKT pathways in both Rhob genotypes. Scale bars: 100 μm.

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contrast, when RHOB was overexpressed in the four EGFR-mutated cell lines, EGFR and ERK phosphorylation was still downregulated by erlotinib whereas AKT remained fully phosphorylated (Fig 4A), and no effect was observed on EGFR WT cells (Fig EV3). Consistent with this, erlotinib more potently inhibited AKT phosphorylation in Rhob−/− lung tumor mice compared to Rhob+/+ mice, while erlotinib inhibited ERK phosphorylation in both mouse models (Fig 4B).

These results demonstrate that RHOB prevents erlotinib-induced AKT dephosphorylation, suggesting that the RHOB/AKT axis might account for the sensitivity of EGFR-mutated tumor cells to EGFR-TKI treatment. In agreement with this hypothesis, we found that the constitutive expression of AKTmyr, an active AKT mutant, phenocopied the effect of RHOB overexpression onto HCC4006 (Fig 4C) and HCC827 cells (Appendix Fig S3) in terms of increasing their erlotinib IC50 values.

**AKT inhibition reverses RHOB-induced resistance to erlotinib-treated cell lines**

We next investigated whether AKT inhibition could reverse RHOB-induced resistance to erlotinib, using the novel selective AKT inhibitor G594 (a primary compound of GDC-0068, ipatasertib) (Lin
et al., 2013). Firstly, we confirmed that G594 induced AKT inhibition by monitoring the phosphorylation of its substrate GSK3β. Indeed, G594 induced a previously described AKT phosphorylation at both Thr 308 and Ser 473 residues (Blake et al., 2012; Lin et al., 2013) while inhibiting its activity. As expected, we evidenced that G594 prevented GSK3β phosphorylation in RHOB-overexpressing HCC4006 cells treated with erlotinib (Fig 5A). We then tested the effects of G594 on cell survival in control or RHOB-overexpressing

![Figure 5](http://example.com/figure5)

**Figure 5.** AKT inhibition sensitizes RHOB-expressing cells to erlotinib.

(A) HCC4006 cells were transduced with control (AdCont) or RHOB-overexpressing (AdRHOB) adenoviruses and treated for 4 h with erlotinib (100 nM), G594 (100 nM), or a combination of both drugs. The phosphorylation status of GSK3β (Ser9), ERK1/2, and EGFR (Tyr1173) was assessed by Western blotting and normalized according to the total protein levels. RHOB overexpression was also monitored by Western blotting.

(B) HCC4006 cells were transduced with control (AdCont) or RHOB-overexpressing (AdRHOB) adenoviruses and treated for 72 h with erlotinib alone (black and red curves) or in combination with the AKT inhibitor G594 at 100 nM (green and blue curves). The surviving cell fraction was determined by an MTS assay. Data are expressed as mean ± SEM from three independent experiments.

(C) HCC4006 cells were transduced with control (AdCont) or RHOB-overexpressing adenoviruses (AdRHOB) and treated for 72 h with increasing concentrations of erlotinib in the absence or presence of increasing doses of G594. The surviving cell fraction was determined by an MTS assay, and erlotinib IC50 values were determined for each condition (***P < 0.001 versus AdCont cells; **P < 0.01 versus AdCont cells). HCC4006 cells were transduced with control (AdCont) or RHOB-overexpressing (AdRHOB) adenoviruses and treated for 48 h with erlotinib (100 nM), G594 (100 nM), or a combination of both drugs. Apoptosis was then determined by either quantification of the subG1 cell population (D) or detection of cleaved PARP and caspase-3 (E) (**P < 0.0001 versus untreated cells; ***P < 0.0001 versus G594 treated cells; †††P < 0.0001 versus erlotinib-treated AdCont cells). In vitro data are representative of at least three independent experiments. Data are expressed as mean ± SEM from three independent experiments. P-values were determined by unpaired two-tailed Student's t-test.

Source data are available online for this figure.
HCC4006 cells treated with erlotinib. G594 significantly decreased erlotinib IC_{50} values in RHOB-overexpressing cells, suggesting that AKT inhibition reversed RHOB-induced resistance to erlotinib [Fig 5B]. Interestingly, this effect was observed at concentrations of G594 as low as 1 nM in HCC4006 (Fig SC) and 10 nM in HCC827 cells (Appendix Fig S4), concentrations at which cell survival was not affected (Appendix Fig S5). We tested a panel of three other EGFR-mutated cell lines and demonstrated that G594 had similar effects on both AKT inhibition (Fig EV4A–C) and the reversal of RHOB-induced erlotinib resistance (Fig EV4D–F).

Lastly, we investigated the mechanism by which the combination of erlotinib and G594 inhibited cell survival. We tested a panel of EGFR-mutated cell lines for the induction of apoptosis, characterized by the percentage of subG1 cells, as well as cleavage of PARP and caspase-3. Erlotinib induced a significant increase in proportion of cells in subG1 phase and PARP and caspase-3 cleavage in control sensitive cells, but not in RHOB-overexpressing cells, suggesting that RHOB-overexpressing cells are resistant to erlotinib-induced apoptosis (Figs 5D and E, and EV5). These findings are consistent with the mouse model results shown in Fig 2E. Altogether, these data indicate that AKT inhibition reverses RHOB-induced resistance to erlotinib and strongly suggest that RHOB triggers resistance to erlotinib through AKT activation.

In vivo AKT inhibition reverses RHOB-induced resistance to erlotinib in EGFR^{L858R} mice

To validate the above findings, we investigated whether AKT inhibition would reverse RHOB-induced resistance to erlotinib in vivo. We tested the effect of erlotinib in combination with G594 in the mouse models described in Fig 2. We determined the tumor/total lung ratios and the proliferating index, revealed by Ki67 staining. G594 treatment alone had no effect on Rhob^{+/+} mice, but it induced a significant decrease in the tumor/total lung ratio (Fig 6A and B) and in Ki67-positive cells in Rhob^{-/−} (Fig 6C and D). We also observed a significant decrease in the tumor/total lung and the Ki67-positive cell ratios in Rhob^{+/−} mice treated with the combination of erlotinib and G594 compared to the individual treatments (Fig 6E). Interestingly, the combination of the two drugs caused the two parameters to reach the same values as the heterozygous or Rhob-invalidated mice treated with erlotinib as a single agent. In addition, we observed no difference in the tumor/total lung ratios in Rhob^{+/−} and Rhob^{-/−} mice treated with the combination of drugs. These data demonstrated that G594 is a potent agent that can re sensitize EGFR^{L858R}/Rhob^{+/−}-resistant mice to erlotinib.

Discussion

Lung cancer patients have benefited from targeted therapy in the last decade, providing new hope in the management of advanced NSCLCs. EGFR-TKI such as erlotinib (Rosell et al., 2012), gefitinib (Mok et al., 2009), and afatinib (Sequist et al., 2013) have shown clinical activity toward NSCLC, leading to their approval for the treatment of metastatic disease. However, although seventy percent of patients that harbor EGFR-mutated lung tumors respond to EGFR-TKI, almost all develop irremediable resistance mechanisms.

The major goals for increasing treatment success rates in these patients are to improve the initial response to EGFR-TKI and to postpone disease recurrence. Here, our findings demonstrate that a high level of RHOB protein expression in the primary tumor impairs the response rate through a mechanism involving AKT. In fact, AKT inhibition reverses EGFR-TKI resistance in cells with high levels of the RHOB protein. These results have led us to propose a combination of EGFR-TKI and AKT inhibitor as treatment to overcome the primary resistance to EGFR-TKI in RHOB-positive patients.

The interaction of AKT with RHOB seems to be dependent on the cellular context. We and others have shown that the loss of RHOB expression is able to activate AKT (Bousquet et al., 2009, 2016) but can also sustain AKT activation in endothelial cells after angiogenic switching (Kazerounian et al., 2013). In lung cancer cells, we recently demonstrated that RHOB downregulation decreases PP2A activity, limiting AKT dephosphorylation and maintaining a high level of AKT activation. This suggests that AKT inhibition favors antitumor activity in RHOB-deficient cells. In line with this hypothesis, G594 treatment induced tumor regression in RHOB-deficient but not in wild-type mice. Together, this suggests that tumor RHOB levels could determine the response to AKT inhibitor therapy when it is administered as a single agent.

Interestingly, our in vitro and in vivo results strongly suggest that RHOB is critical for both tumor growth and the apoptotic response to erlotinib, by preventing erlotinib-induced AKT dephosphorylation and leading to the maintenance of a high level of active AKT. It has been shown that RHOB can delay the intracellular trafficking of EGFR (Gampel et al., 1999) and restrict EGFR cell surface occupancy (Kazerounian et al., 2013), thus modifying EGFR-dependent downstream signaling (Canguilhem et al., 2005; Lajoie-Mazenc et al., 2008). Our results add to this by showing that RHOB can modify AKT but not ERK signaling in response to erlotinib.

The PI3K/AKT pathway is known to control the oncogenic addiction observed in EGFR-mutated lung cancer, and its activation has been shown to be a crucial event in the resistance to targeted therapies (Obenauf et al., 2015). RHOB, through its ability to prevent AKT inhibition, appears to be a key player in the failure of targeted therapies. Importantly, our results from the analysis of RHOB expression in a series of samples from EGFR-mutated lung adenocarcinoma patients treated with EGFR-TKI showed that sensitivity to EGFR-TKI treatment is strikingly higher in patients presenting low RHOB levels, while patients with high RHOB levels had a stronger resistance to treatment. These observations clearly suggest that RHOB expression could be used as a marker in the clinic to predict the efficacy of these kinds of therapeutic strategies, which might represent a clear advantage when making decisions on alternative treatment. Moreover, RHOB predictive value is not modified by treatments given between initial assessment and EGFR-TKI treatment. RHOB high expression may thus help clinicians to anticipate frequent and rapid resistance to EGFR-TKI. The question of the variable abundance of RHOB in lung tumors is not yet fully understood. In a TCGA-based analysis using the lung adenocarcinoma database, no RHOB mutation or deletion was found (Appendix Fig S6A), which confirms previous observations in lung cancer (Sato et al., 2007) and in our laboratory (unpublished data) or in other cancers such as head and neck carcinoma (Adnane et al., 2002) or breast cancer (Fritz et al., 2002). RHOB mRNA levels were not significantly altered by copy number variations or major oncogenic mutations (Appendix Fig S6B–D), but
seemed to be rather associated with epigenetic mechanisms involving particularly miR-21 expression (Appendix Table S3), a well-known oncomir, and chromatin acetylation (Appendix Fig S7), in accordance with previous observations (Wang et al., 2003; Mazieres et al., 2007; Sato et al., 2007; Connolly et al., 2010).

Remarkably, by using mouse models we provide evidence that RHOB-induced resistance can be reversed by AKT inhibition. We clearly show that a combination of AKT inhibitors with EGFR-TKI can sustain the sensitivity of RHOB-overexpressing cells to EGFR-TKI. Interestingly, neither AKT inhibitors nor EGFR-TKI induce significant cell death by themselves, but in combination they are highly potent at inducing apoptosis, suggesting that their combined effects have lethal consequences for tumor cells. AKT inhibitors are currently under clinical development with promising results. Ipatasertib, which corresponds to the G594 parent compound GDC-0068, is in phase 1 trials for various tumors. Other AKT inhibitors such as afuresertib and MK-2206 or PI3K inhibitors such as enzastaurin and PX-866 are also being studied.

From these results, we propose that RHOB levels can predict EGFRL858 mouse tumors to erlotinib.

Figure 6. The AKT inhibitor G594 resensitizes EGFRL858 mouse tumors to erlotinib.

A Representative H&E staining of lung tumors from EGFRL858/Rhob+/+, EGFRL858/Rhob+/-, and EGFRL858/Rhob-/- mice treated or not during 4 days with erlotinib (12.5 mg/kg/day), the AKT inhibitor G594 (25 mg/kg/day), or a combination of both drugs. Scale bars: 500 μm.

B Quantification of the tumor/lung ratio of mice treated or not with the individual drugs or with a combination of both.

C, D Representative Ki67 immunostaining of lung tumors from EGFRL858/Rhob+/+, EGFRL858/Rhob+/-, and EGFRL858/Rhob-/- mice treated or not with erlotinib alone (12.5 mg/kg/day) or in combination with the AKT inhibitor G594 (25 mg/kg/day) for 4 days (scale bars: 50 μm), and the corresponding quantification (D).

Data information: **P < 0.001, ***P < 0.0001. EGFRL858/Rhob+/+ (placebo: n = 6, G594: n = 5; erlotinib: n = 7, G594 + erlotinib: n = 8); EGFRL858/Rhob+/- (placebo: n = 7, G594: n = 6; erlotinib: n = 8, G594 + erlotinib: n = 7); EGFRL858/Rhob-/- (placebo: n = 6, G594: n = 6; erlotinib: n = 6, G594 + erlotinib: n = 6). Three independent zones per mouse lung were used for Ki67 quantification. Data are expressed as mean ± SEM, P-values were determined by Mann–Whitney two-tailed t-test.
studying the frontline combination of erlotinib with AKT inhibitors. It is possible that RHOB expression levels vary throughout the course of treatment in EGFR-mutated patients. Indeed, the observation that the majority of patients showed an increase in RHOB tumor expression after relapse further supports a role of RHOB in EGFR-TKI resistance.

Overall, the present study offers a new strategy to increase the initial clinical response rate in EGFR-mutated lung cancer patients by providing a molecular rationale for using EGFR-TKI in combination with AKT inhibitor in patients harboring high RHOB tumor levels.

**Materials and Methods**

**Cell culture, transfection, and adenoviral transduction and inhibitors**

The human NSCLC cell lines HCC4006 (CRL-2871, EGFR del L747-E749, A750P), HCC827 (CRL-2868, EGFR del E749-A750), HCC2935 (CRL-2869, EGFR del E746-T751, S752I), A549 (CCL-185, EGFR WT, KRAS G12S), and H1299 (CRL-5803, EGFR WT, NRAS Q61K) were obtained from the American Type Culture Collection (Manassas, VA, USA). The H3255 cell line (EGFR L858R) was a kind gift from Helene Blons (APHP, Paris, France). All cell lines were replication-defective (+E1, E3) adenoviral vectors expressing RHOB (AdRHOB) or GFP (AdCont) under the transcriptional control of the CMV promoter (tetO-EGFRL858R) crossed with Rhob null (Rhob−/−), heterozygous (Rhob+/−), and wild-type (Rhob+/*) mice and purified in the 129S2/SvPasCrL strain, as previously described (Calvayrac et al, 2014). Approval from the Claudius Regaud Institute Animal Ethics Committee (# ICR-2009-021) was obtained for the use of mice in this animal model and for the study protocols. Animals were housed under controlled temperature and lighting (12/12-h light/dark cycle) and fed with commercial animal feed and water ad libitum. All procedures involving animals and their care conformed to institutional guidelines for the use of animals in biomedical research.

Animal experiments were performed with lung-specific tetracycline-inducible human EGFRL858R bi-transgenic mice (CCSP-rtTA; tetO-EGFRL858R) crossed with Rhob null (Rhob−/−), heterozygous (Rhob+/−), and wild-type (Rhob+/*) mice and purified in the 129S2/SvPasCrl strain, as previously described (Calvayrac et al, 2014). Detailed methods for tumor grading and quantification of the tumor-to-lung area ratio have been described previously (Calvayrac et al, 2014).

**Western blot analysis**

Cell extracts were analyzed by Western blotting with primary antibodies against RHOB, ERK1/2 (Santa Cruz Biotechnology), p-ERK (T202/Y204), p-AKT (S473), AKT, pGSK3 (S9), GSK3, p-EGFR (T1173), EGFR, PARP, cleaved caspase-3, caspase-3 (Cell Signaling Technology), or actin (Chemicon). Detection was performed using peroxidase-conjugated secondary antibodies and a chemiluminescence detection kit (Clarity™ ECL; Bio-Rad) with a ChemiDoc™ MP Imaging System (Bio-Rad). Quantifications were carried out for three independent experiments with ImageLab software (Bio-Rad) and normalized to actin.

**Animal studies**

Animal experiments were performed with lung-specific tetracycline-inducible human EGFRL858R bi-transgenic mice (CCSP-rtTA; tetO-EGFRL858R) crossed with Rhob null (Rhob−/−), heterozygous (Rhob+/−), and wild-type (Rhob+/*) mice and purified in the 129S2/SvPasCrl strain, as previously described (Calvayrac et al, 2014). Detailed methods for tumor grading and quantification of the tumor-to-lung area ratio have been described previously (Calvayrac et al, 2014).

**Patients and ethical considerations**

We selected patients harboring EGFR-activating mutations (either exon 19 deletion or exon 21 mutation) who had been treated with EGFR-TKI in our institution. Tumor samples were reanalyzed for RHOB expression in our pathology department. All patients had signed an informed consent permitting analyses of tissues. All informed consents were collected and stored in the pathology department. This study was approved by the Ethics of Human
Lung cancer remains the leading cause of cancer-related deaths worldwide. Although impressive treatment advances have been made for patients with non-small-cell lung cancer (NSCLC) whose tumors harbor mutated genes such as EGFR, almost all of them develop resistance mechanisms. To date, no clinically approved biomarker is available to identify the subset of patients that will not benefit from EGFR-tyrosine kinase inhibitor (EGFR-TKI) therapy, and no druggable target has been identified to improve the clinical response rate in resistant patients, highlighting the need for an alternative therapeutic strategy.

Results
Our findings demonstrate that a high level of the RAS-related GTPase RHOB in the primary lung tumor predicts low progression-free survival in response to EGFR-TKI. Mechanistically, RHOB impairs response to EGFR-TKI through AKT activation. Combining erlotinib with a new-generation AKT inhibitor caused synthetic lethal interaction in EGFR-mutated NSCLC harboring high RHOB levels, suggesting a novel therapeutic strategy to overcome resistance in RHOB-positive patients.

Impact
The present study offers a new strategy to increase the initial clinical response rate in EGFR-mutated lung cancer patients by providing a molecular rationale for using EGFR-TKI in combination with AKT inhibitor in patients harboring high RHOB tumor levels.

Research Committee at the Pathology Department, Toulouse Hospital, France.

Immunohistochemistry
Formalin-fixed, paraffin-embedded tissue sections were used for immunohistochemistry (IHC) procedures, as described previously (Calvayrac et al., 2014). Briefly, after rehydration, deparaffinized sections were pretreated by microwave epitope retrieval. Endogenous peroxidase activity was quenched and non-specific binding was blocked. For IHC of patient tissues, a RHOB monoclonal antibody was used (C-5, Santa Cruz Biotechnologies, Inc., 1:75). For IHC on mouse lung sections, we used the Ki67 (SP6; Thermo Scientific), ERK1/2 (Santa Cruz Biotechnology), p-ERK (T202/Y204), p-AKT (S473), AKT, and cleaved caspase-3 (Cell Signaling Technology) antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO). Sections were lightly counterstained with hematoxylin. Tissues expressing different levels of antibodies, with an Envision kit (DAKO).

Continuous variables were presented as their means (± standard deviations [SD]) or their medians (with interquartile range [IQR]) or range [min–max]), according to their distributions. Categorical variables were summarized by frequency and percentage. The chi-square or Fisher’s exact tests were used to compare categorical variables, and Student’s t-test, variance analysis, or a nonparametric test was used for continuous variables. Paired measurements of continuous data were compared using the Wilcoxon matched-pairs signed-rank test.

All survival times were calculated from the first administration of the TKI drug and estimated by the Kaplan-Meier method with 95% confidence intervals (CIs), using the following first-event definitions: progression or death for progression-free survival (PFS). Surviving patients were censored on the date of the last follow-up. Univariate analysis was performed using the log-rank test. Pearson correlation analysis was performed to determine the correlation between RHOB levels and erlotinib IC50 values.

Tests were two-sided and P-values < 0.05 were considered significant. All analyses were conducted using either Stata® version 13.0 (for patient data) or GraphPad Prism 5 software (for in vitro and mouse data).

For in vitro experiments, data are representative of at least three independent experiments.

Expanded View for this article is available online.

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Author contributions
OC, AS, JM, AP, and GF contributed to study conception and design and manuscript preparation. OC, JMa, AP, and GF contributed to data analysis and interpretation. OC, IR-L, and EB contributed to development of methodology. OC, CM-D, IR-L, EB, MF, EC-T, IR, NG, SF, JMi, and AL contributed to acquisition of data. AL performed the statistical analysis. EC-T, IR, AL, JC, NM, and SF contributed to administrative, technical, or material support. JMa and GF supervised the study.

Conflict of interest
The authors declare that they have no conflict of interest.

References


polymerization coordinate Src activation with endosome-mediated delivery to the membrane. Deu Cell 7: 855 – 869

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