A two-tiered mechanism of EGFR inhibition by RALT/MIG6 via kinase suppression and receptor degradation

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Signaling by epidermal growth factor receptor (EGFR) must be controlled tightly because aberrant EGFR activity may cause cell transformation. Receptor-associated late transducer (RALT) is a feedback inhibitor of EGFR whose genetic ablation in the mouse causes phenotypes due to EGFR-driven excess cell proliferation. RALT inhibits EGFR catalytic activation by docking onto EGFR kinase domain. We report here an additional mechanism of EGFR suppression mediated by RALT, demonstrating that RALT-bound EGFR receptors undergo endocytosis and eventual degradation into lysosomes. Moreover, RALT rescues the endocytic deficit of EGFR mutants unable to undergo either endocytosis (Dc214) or degradation (Y1045F) and mediates endocytosis via a domain distinct from that responsible for EGFR catalytic suppression. Consistent with providing a scaffolding function for endocytic proteins, RALT drives EGFR endocytosis by binding to AP-2 and Intersectins. These data suggest a model in which binding of RALT to EGFR integrates suppression of EGFR kinase with receptor endocytosis and degradation, leading to durable repression of EGFR signaling.

Introduction

The EGF receptor (EGFR) is a receptor tyrosine kinase that instructs key cellular programs such as proliferation, survival, and locomotion. The implementation of these programs requires EGFR signals to be of defined strength within precise boundaries of space and time. While spurious EGFR activation is to be avoided, preventing excess EGFR activity is also crucial because the latter disrupts tissue homeostasis and may lead to cell transformation (Sibilia et al., 2007). Inadvertent activation of EGFR is prevented by self-inhibitory constraints imposed on both the extracellular ligand-binding region (Burgess et al., 2003) and the intracellular catalytic domain of the receptor (Zhang et al., 2006). Ligand binding relieves these constraints by driving dimerization of EGFR extracellular domains (Burgess et al., 2003). This is conducive to the formation of asymmetric dimers between juxtaposed kinase domains, allowing for allosteric activation of the kinase, receptor auto-phosphorylation, and initiation of downstream signaling (X. Zhang et al., 2007). EGFR signaling is in turn subject to the close control of negative regulatory circuits. Among these, a prominent role is played by (a) receptor endocytosis, which leads to fast internalization of ligand–EGFR complexes (Sorkin and Goh, 2009); and (b) a network of inducible inhibitors that target several pathway components, including the EGFR itself, in order to ensure tight control of EGFR signaling.

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Results

RALT-bound EGFR undergoes efficient endocytosis

We engineered stable NR6-EGFR cells in which ectopic RALT inhibited EGFR kinase activity by >90% and mimicked the pharmacological suppression of EGFR kinase activity observed in control NR6-EGFR cells upon treatment with the EGFR-specific inhibitor AG1478 (Fig. 1A). This cellular model is therefore suitable for quantitative biochemical studies of EGFR endocytosis under two different conditions of completely suppressed EGFR catalytic activity.

Cell imaging studies indicated that AG1478 ablated ligand-dependent EGFR internalization in NR6-EGFR cells. In contrast, a rapid relocalization of EGFR to intracellular vesicles was observed in EGF-treated NR6-EGFR/RALT cells, irrespective of AG1478 (Fig. S1A). Initial rates of \[^{125}\text{I} \]-EGF uptake were comparable in NR6-EGFR/RALT and control cells (Fig. 1B), with internalization rate constants (K\_\text{i}) being 0.184 ± 0.023 and 0.189 ± 0.029, respectively. In contrast, AG1478 led to a dramatic reduction of \[^{125}\text{I} \]-EGF uptake in NR6-EGFR cells, as reported previously (Sorkina et al., 2002; Fig. 1B). EGF-driven endocytosis caused extensive down-regulation (Fig. 1C) and eventual degradation (Fig. 1D) of EGFR in both control and NR6-EGFR/RALT cells. This was not observed in NR6-EGFR cells treated with the EGF + AG1478 combination (Fig. 1C; Fig. S1B). Finally, EGFR and RALT colocalized in vesicular structures labeled by the early (EEA1) and late (LAMP1) endosome markers (Fig. 1E), indicating that the endocytic traffic of EGFR in NR6-EGFR/RALT cells was associated to sustained EGFR–RALT physical interaction and uninterrupted suppression of EGFR catalytic function.

RALT rescues the endocytic deficit of EGFR Dc214

How can RALT-bound EGFR molecules undergo efficient endocytosis and degradation despite being catalytically inert? We reasoned that RALT itself could form a platform for molecular interactions capable of organizing EGFR endocytic traffic. To test this hypothesis we focused on EGFR Dc214, a catalytically competent EGFR mutant that lacks the C-tail and is therefore unable to couple to canonical EGFR endocytic pathways (Chen et al., 1989). EGFR Dc214 retains RALT binding (Anastasi et al., 2003, 2007) and underwent ligand-dependent endocytosis in serum-starved cells expressing ectopic RALT, but not in control NR6-EGFR Dc214 fibroblasts (Fig. 2A). Colocalization studies indicated that internalized EGFR Dc214 was routed to early endosomes in complex with RALT (Fig. 2B). We next addressed whether endogenous levels of RALT protein were sufficient to signal endocytosis of EGFR Dc214. To this end, NR6-EGFR Dc214 cells were rendered quiescent by serum deprivation and subsequently stimulated with 10% serum for 3 h to induce robust expression of RALT protein (Fig. 2, C and D; see also Fiorentino et al., 2000). After serum wash-out, cells were challenged with EGF for 10 min at 37°C. Serum stimulation alone did not induce EGFR Dc214 endocytosis, which was
Figure 1. Kinase inhibition by RALT, but not by AG1478, is associated with normal rates of EGFR endocytosis and down-regulation. (A) Expression of EGFR and MYC-RALT was reconstituted in NR6 fibroblasts, which lack endogenous EGFR expression. Control and RALT-overexpressing NR6-EGFR cells were rendered quiescent and then stimulated with 100 ng/ml EGF [±3 µM AG1478] for the indicated time. Lysates were immunoblotted as indicated. (B) Control [±3 µM AG1478] and MYC-RALT–expressing NR6-EGFR cells were assayed for [125I]-EGF uptake [1 ng/ml at 37°C for the indicated time]. The graph reports the average results ± SD from four independent experiments. (C) Control [±3 µM AG1478] and MYC-RALT–expressing NR6-EGFR cells were made quiescent, incubated at 37°C with 100 ng/ml EGF for the indicated time, and processed to determine residual [125I]-EGF binding at the cell surface (percentage of binding at time 0). Results were averaged from three independent experiments ± SD. (D) EGFR degradation. Control and MYC-RALT–expressing NR6-EGFR cells were rendered quiescent and then stimulated with 100 ng/ml EGF for the indicated time [hours]. Lysates were immunoblotted with the indicated antibodies. Two different exposures of the same anti-EGFR autoradiograph are shown. (E) Quiescent MYC-RALT–expressing NR6-EGFR cells were incubated with 20 ng/ml EGF on ice for 30 min. After EGF wash-out, cells were chased at 37°C in EGF-free medium for either 10 min (for EGFR/EEA1 and EGFR/RALT colocalization) or 30 min (for EGFR/LAMP-1 colocalization). Nuclei were stained with Hoechst 33258 [blue]. Bar, 5 µm.
Figure 2. **RALT rescues the endocytic deficit of EGFR Dc214.** (A) Quiescent control and MYC-RALT–expressing NR6-EGFR Dc214 cells were either left untreated or stimulated with 20 ng/ml EGF for 10 min at 37°C. Cells were fixed and stained with anti-EGFR mAb 108 (red) and Hoechst 33258 (blue). (B) MYC-RALT–expressing NR6-EGFR Dc214 cells were rendered quiescent and then incubated with 20 ng/ml EGF on ice for 30 min. After EGF wash-out, cells were chased at 37°C in EGF-free medium for 10 min, fixed, and stained for EGFR, EEA1, and MYC-RALT immunodetection. Nuclei were stained with Hoechst 33258 (blue). (C) NR6-EGFR Dc214 cells were transfected with either control or RALT-specific siRNAs. Cells were made quiescent by serum deprivation and then challenged with 10% newborn calf serum (NCS) for 3 h to induce RALT protein expression. After serum wash-out, cells were left untreated or stimulated with 20 ng/ml EGF for 10 min at 37°C before being processed for anti-EGFR staining (red). Nuclei were stained with Hoechst 33258 (blue). Sister cultures were lysed to monitor the efficiency of RALT KD by immunoblot (top). Nontransfected NR6-EGFR Dc214 cells (±NCS stimulation) were included as additional immunoblotting controls. β-Actin was used as loading control. (D) Control and RALT siRNA-transfected NR6 Dc214 cells were made quiescent and then stimulated with NCS as in C. After serum washout, cells were incubated with 1 ng/ml [125I]-EGF for 8 min at 37°C. Nontransfected cells (±NCS stimulation) were included as additional control. Columns report the average of three independent experiments ± SD. Bars: (A and C) 20 µm; (B) 5 µm.
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namely RALT Y358A (X. Zhang et al., 2007) and RALT Δ315-361 (Anastasi et al., 2007), did not support endocytosis of EGFR Dc214 (Fig. 3, A and B; expression levels of MYC-tagged RALT proteins are shown in Fig. S2 A). These results suggest that binding to EGFR is necessary but not sufficient for RALT-mediated endocytosis. Indeed, overexpressed RALT 282–396, but not RALT Y358A, displayed dominant-negative activity toward endogenous RALT in EGFR Dc214 internalization assays (Fig. 3, C and D), most likely because it prevented recruitment of endogenous RALT to EGFR Dc214.

Based on the above results, we hypothesized that relocation of RALT onto the EGFR via the EBR enables structural determinants of RALT distinct from the EBR itself to be connected to the endocytic machinery. This model predicts that RALT should mediate endocytosis independently of its EBR when placed in cis to EGFR 1–682, namely to an EGFR lacking both the kinase domain and C-terminal tail (Fig. 4 A). The 144–411 fragment of RALT spans the evolutionarily conserved region of the protein (Anastasi et al., 2007) and was capable of driving efficient down-regulation of EGFR Dc214 (Fig. S2 B). Strikingly, a chimera spanning the RALT 144–411 fragment fused to the C-terminal end of EGFR 1–682 (ER 144–411) underwent rapid endocytosis when expressed in NR6 cells (Fig. 4 B). Instead observed in cells exposed to the EGF pulse (Fig. 2 C). Crucially, endocytosis of EGFR Dc214 was abrogated by knock-down (KD) of RALT (Fig. 2 C). [125I]-EGF uptake assayed in the same conditions confirmed that RALT-specific RNAi reduced EGFR Dc214 endocytosis to background levels (Fig. 2 D). Of note, RALT KD altered neither transferrin uptake in serum-stimulated NR6-EGFR Dc214 cells (Fig. S1 C) nor wtEGFR endocytosis in serum-stimulated NR6-EGFR cells (Fig. S1 D and E). We conclude that RALT KD does not cause a general disruption of endocytosis and that under physiological conditions RALT-bound and RALT-free EGFR molecules are internalized with comparable efficiency.

Identification of an endocytic domain in the RALT protein

To identify the structural determinants of RALT required for RALT-mediated endocytosis we focused initially on the region that contacts the EGFR kinase domain, namely the EBR module that spans positions 323–411 (X. Zhang et al., 2007). Because we could not express RALT 323–411 in NR6-Dc214 cells at suitable levels, we resorted to using RALT 282–396, which we showed was sufficient to suppress EGFR kinase activity (Anastasi et al., 2007). RALT 282–396 as well as two mutants unable to bind to EGFR, namely RALT Y358A (X. Zhang et al., 2007) and RALT Δ315-361 (Anastasi et al., 2007), did not support endocytosis of EGFR Dc214 (Fig. 3, A and B; expression levels of MYC-tagged RALT alleles were made quiescent and then assayed for [125I]-EGF uptake (1 ng/ml for 8 min at 37°C) either before or after a 3-h stimulation with 10% NCS to induce RALT expression. Results were averaged ± SD from three independent experiments. Comparison between endogenous and ectopic RALT proteins indicates that the latter are largely overexpressed (see Fig. S2 A), thus allowing the assessment of their potential dominant-negative activity over endogenous RALT.

**Figure 3. Relocation onto EGFR is required for RALT-mediated endocytosis.** (A and B) Quiescent NR6-EGFR Dc214 cells expressing the indicated MYC-RALT alleles were assayed for [125I]-EGF uptake (1 ng/ml at 37°C for the indicated time). The graphs report average results ± SD from four (A) and three (B) independent experiments. (C and D) NR6-EGFR Dc214 cells expressing the indicated MYC-RALT alleles were made quiescent and then assayed for [125I]-EGF uptake (1 ng/ml for 8 min at 37°C) either before or after a 3-h stimulation with 10% NCS to induce RALT expression. Results were averaged ± SD from three independent experiments. Comparison between endogenous and ectopic RALT proteins indicates that the latter are largely overexpressed (see Fig. S2 A), thus allowing the assessment of their potential dominant-negative activity over endogenous RALT.
To assess whether the endocytosis of the RED-containing chimera was still EGF inducible, we used as endocytic tracer the mAb 108, which recognizes the EGFR extracellular domain independently of EGF binding (see Materials and methods).

Results presented in Fig. 4C show that mAb 108 was internalized in NR6 cells expressing the ER\textsubscript{144–323} chimera irrespective of EGF. The EBR-containing chimera (ER\textsubscript{323–411}) behaved similarly to EGFR\textsubscript{1–682} and was not internalized. The endocytic determinants of RALT were mapped to the RALT\textsubscript{144–323} fragment because the ER\textsubscript{144–323} chimera was internalized as efficiently as ER\textsubscript{144–411} (Fig. 4B).

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of EGF stimulation and was routed to the endosomal compartment (Fig. 4 D). This constitutive internalization is specific because the intracellular accumulation of mAb 108 in NR6-EGFR cells was strictly dependent on EGF stimulation.

The experiments presented in Figs. 3 and 4 indicate that kinase suppression and endocytic activity are genetically separable functions of RALT that map to two distinct modules, i.e., the EBR and RED, respectively.

**RALT signals degradation of EGFR**

Internalized EGFR can either be recycled to the cell surface or further trafficked to lysosomes for degradation. While recycling favors reiteration of EGFR signaling (Lenferink et al., 1998; Sigismund et al., 2008), sorting into MVBs terminates it and, by causing receptor degradation, also attenuates the cell’s responsiveness to further stimulation by EGFR ligands (Marmor and Yarden, 2004).

As shown before, RALT-bound EGFR molecules undergo down-regulation and degradation (Fig. 1, C and D). RALT also promoted down-regulation (Fig. 5 A and Fig. S2 C) and degradation of EGFR Dc214, as extrapolated by the observation that a sizeable amount of input [125I]-EGF underwent degradation in NR6-EGFR Dc214/RALT cells (Fig. 5 B and Fig. S2 D). Consistently, EGFR Dc214–RALT complexes trafficked to anti-LAMP1–labeled endosomes (Fig. 5 C). Thus, besides rescuing the internalization deficit of EGFR Dc214, RALT was also capable of routing internalized EGFR Dc214 to late endosomes.

Trafficking toward the MVBs and consequent lysosomal degradation depend on CBL-driven EGFR ubiquitylation. The EGFR Y1045F mutant lacks the phosphotyrosine binding site for CBL. As a consequence, EGFR Y1045F is ubiquitylated poorly and is recycled to the cell surface rather than being sorted into MVBs/late endosomes (Levkowitz et al., 1999). Strikingly, RALT overexpression rescued the degradation deficit of EGFR Y1045F. Comparable results were obtained when the expression of EGFR Y1045F and RALT was reconstituted either stably in NR6 fibroblasts (Fig. 5 D) or transiently in CHO epithelial cells (Fig. S3 A). Notably, RALT-driven degradation of EGFR Y1045F was inhibited in cells treated with chloroquine (Fig. 5 D), pointing to lysosomes as the site of RALT-dependent degradation of EGFR. Neither RALT382–396 (Fig. S3 A) nor RALT325–411 (Fig. S3 B) was capable of rescuing the degradation deficit of EGFR Y1045F. In contrast, RALT144–411 induced degradation of both wtEGFR (Fig. S2 E) and EGFR Y1045F (Fig. S3 B). Thus, the RED mediates internalization as well as degradation of EGFR.

The ubiquitylation deficit imposed on EGFR by the Y1045F mutation was not rescued by the ectopic expression of RALT (Fig. 5 E). This is consistent with the notion that binding of CBL to the EGFR requires receptor autophosphorylation (Levkowitz et al., 1998, 1999), which is abolished by RALT-mediated kinase inhibition. Indeed, also in the case of wtEGFR, RALT inhibited recruitment of CBL to the receptor as well as EGFR ubiquitylation (Fig. S3 C). The above data indicate that RALT-bound EGFR molecules undergo degradation into lysosomes in the absence of receptor ubiquitylation.

**RALT couples the EGFR to clathrin-dependent endocytosis via AP-2**

Several mechanisms of internalization were discovered for EGFR (Orth and McNiven, 2006; Accorcia et al., 2009; Sorkin and Goh, 2009). RALT colocalized with clathrin heavy chain (CHC) upon EGF stimulation (Fig. 6 A). CHC KD in NR6-EGFR Dc214 cells abolished [125I]-transferrin uptake as well as RALT-mediated uptake of [125I]-EGF (Fig. 6 B). In keeping with these results, RALT-dependent endocytosis of EGFR Dc214 required dynamin2, a GTPase implicated in the formation and fission of clathrin-coated structures at the plasma membrane (Macia et al., 2006; Loerke et al., 2009), as shown by the inhibitory activity exerted by both K44A DYN2, a dominant-negative dynamin2 mutant, and dynasore, a reversible inhibitor of dynamin GTPase activity (Macia et al., 2006; Fig. 6, C and D).

AP-2 is the major adaptor complex involved in CME and binding to AP-2 allows cargos to be sorted into CCPs (Traub, 2009). Depletion of the μ2 chain of the AP-2 complex resulted in marked inhibition of RALT-dependent endocytosis of EGFR Dc214. This effect was proportional to the extent of μ2 depletion as determined by two different siRNAs (Fig. 6 E). Purified recombinant GST-RALT145–414 immobilized onto agarose beads was able to bind to AP-2 present in cell lysates, as assessed by immunoblotting with antibodies to β2 and μ2 chains of AP-2, whereas RALT325–414 did not (Fig. S4 A). Hence, binding of RED to AP-2 may sort EGFR–RALT complexes into CCPs.

**Role of Intersectin in RALT-dependent endocytosis**

A number of endocytic proteins, including several accessory proteins, contain one or more Src homology 3 (SH3) domains (Simpson et al., 1999; Praefcke et al., 2004). We have previously shown that RALT binds to SH3 domains, with most of the SH3-binding motifs being located in the 144–323 sequence (Fiorentino et al., 2000). We therefore sought to determine whether RALT couples to SH3-containing proteins implicated in endocytic traffic. By combining computational predictions and literature-generated hypotheses we restricted our attention to SH3 domains present in ~20 mammalian proteins. GST pull-down assays indicated that recombinant SH3 domains from GRB2, βPIX/Cool1, Intersectin1, and Intersectin2 (mammals express two ITSN isoforms encoded by distinct loci; see Pucharcos et al., 2001) bound RALT with the highest affinity (Fig. S4 B). We used RNAi to test whether the loss of GRB2, βPIX, or ITSNs impacts RALT-mediated endocytosis. Although GRB2 and βPIX are dispensable for RALT-driven endocytosis of EGFR Dc214 (Fig. S4, C and D), ITSN function appears to be necessary. In particular, the KD of ITSN2 reduced EGFR Dc214 endocytosis by ~40% (Fig. 7 A). RNAi to ITSN1 produced a minor, albeit reproducible, reduction of EGFR Dc214 internalization, which was additive to the effect of RNAi to ITSN2 in combined ITSN1 + ITSN2 KD experiments (Fig. 7 A). ITSN2 KD had no consequence on the endocytosis of wtEGFR (Fig. S4 E), which was instead compromised by GRB2 KD, as reported previously (Jiang et al., 2003; Fig. S4 C). Thus, RALT-dependent and RALT-independent endocytosis of EGFR have
Figure 5. RALT drives degradation of EGFR Dc214 and EGFR Y1045F. (A) EGFR Dc214 down-regulation. Control and MYC-RALT-expressing NR6-EGFR Dc214 cells were made quiescent and assayed for receptor down-regulation as in Fig. 1 C. Graphs indicate the average results ± SD from three independent experiments. (B) \(^{125}\text{I}\)-EGF degradation. Quiescent control and MYC-RALT–expressing NR6-EGFR Dc214 cells were allowed to bind \(^{125}\text{I}\)-EGF on ice (15 ng/ml for 45 min). After washing, cells were shifted to 37°C in EGF-free medium for the indicated time. Degraded \(^{125}\text{I}\)-EGF was measured as the fraction of TCA-soluble radioactivity (i.e., the sum of TCA-soluble cpm measured in cell lysates and extracellular medium) over bound \(^{125}\text{I}\)-EGF. Results were averaged (±SD) from three independent experiments. Note that under these conditions EGF stimulation induces significant RALT expression in control NR6-EGFR Dc214 cells by 90 min (not depicted), which likely explains why in control cells \(^{125}\text{I}\)-EGF degradation increases above background past the 1.5-h time point. (C) Quiescent MYC-RALT–expressing NR6-EGFR Dc214 cells were incubated with EGF on ice as in Fig. 2 B, washed, chased in EGF-free medium for 30 min at 37°C, and processed for EGFR, LAMP-1, and MYC-RALT immuno-imaging. Nuclei were stained by Hoechst 33258. (D) Top: control and MYC-RALT–expressing NR6-EGFR Y1045F cells were made quiescent and then stimulated with 100 ng/ml EGF for the indicated time. Where indicated, chloroquine was added to the culture medium throughout the EGF incubation time. Lysates were immunoblotted with the indicated antibodies. Two different exposures of the same anti-EGFR autoradiograph are shown. Bottom: sister plates were stimulated with 100 ng/ml EGF for 5 min at 37°C to document the extent of catalytic suppression of EGFR Y1045F by MYC-RALT. Blots were probed as indicated; AKT was used as loading control. (E) NR6 fibroblasts expressing either wtEGFR or EGFR Y1045F in the absence (Ctrl) or presence of ectopic MYC-RALT (RALT) were made quiescent and either left untreated or incubated with 20 ng/ml EGF for the indicated time (min). Anti-EGFR immunoprecipitates and total cell lysates were immunoblotted as indicated. Bar, 5 µm.
Figure 6. **RALT-mediated endocytosis is clathrin- and AP-2-dependent.** (A) MYC-RALT–expressing HeLa cells were made quiescent and then incubated with 20 ng/ml EGF for 5 min at 37°C before MYC-RALT and CHC immunostaining. (B) NR6-EGFR Dc214 RALT cells were transfected with control and CHC-specific siRNAs. Cells were rendered quiescent and assayed for [^{125}I]-EGF (1 ng/ml for 6 min at 37°C) and [^{125}I]-Tf (0.5 µg/ml for 4 min at 37°C) uptake. Results were averaged ± SD from four independent experiments. The immunoblot documents the typical efficiency of CHC KD; β-actin was used as loading control. (C) CHO cells were transfected with either GFP or dominant-negative (DN) DYN2 K44A-GFP vectors along with either pcDNA3-EGFR + pCS2MT (left) or pcDNA3-EGFR Dc214 + pCS2MT-RALT (right). 2 d after transfection, cells were made quiescent and stimulated with 20 ng/ml EGF for 10 min at 37°C before being processed for anti-EGFR staining. Nuclei were stained with Hoechst 33258 (blue). (D) Quiescent NR6-EGFR Dc214 cells were incubated for 30 min at 37°C with either vehicle or 80 µM dynasore before being assayed for [^{125}I]-EGF uptake (± dynasore) for 6 min at 37°C. Results were averaged ± SD from three independent experiments. (E) NR6-EGFR Dc214 cells were transfected with control and two different μ2-specific siRNAs. Cells were made quiescent and assayed for [^{125}I]-EGF uptake (1 ng/ml for the indicated time at 37°C). Results were averaged ± SD from three independent experiments. The immunoblot documents μ2 KD, which causes also concomitant reduction of the β2 subunit, as reported previously (Johannessen et al., 2006); CHC was used as loading control. Bars, (A) 10 µm; (inset) 5 µm; (C) 20 µm.
located coiled-coil region, and five SH3 domains (denominated A through E; O'Bryan et al., 2001). RALT bound in vitro to SH3 A, C, and E of ITSN (Fig. S5A) and coimmunoprecipitated specifically with a fragment of ITSN spanning the five differential requirements for GRB2 and ITSN2 function, at least in NR6 fibroblasts.

The prevalent isoforms of ITSN1 and ITSN2 have a modular architecture consisting of two EH domains, a centrally located coiled-coil region, and five SH3 domains (denominated A through E; O'Bryan et al., 2001). RALT bound in vitro to SH3 A, C, and E of ITSN (Fig. S5 A) and coimmunoprecipitated specifically with a fragment of ITSN spanning the five differential requirements for GRB2 and ITSN2 function, at least in NR6 fibroblasts.

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SH3 domains (Fig. S5 B). Binding of RALT to ITSN required the RED: GST-RALT_145–414, but not GST-RALT_325–414, precipitated endogenous ITSN1 and ITSN2 from cell lysates (Fig. S5 C). Moreover, endogenous ITSN1 and ITSN2 coimmunoprecipitated only with the ER$_{144-323}$ chimera in mAb 108 immunoprecipitations (Fig. 7 B); reciprocally, anti-ITSN2 antibodies brought down ER$_{144-323}$ (Fig. 7 C).

SH3 domains recognize a PXXP core sequence flanked by a positively charged amino acid (+) in either class I (+XXPXXP) or class II (PXXPXP+) orientation (Mayer, 2001). Several PXXP sequences are clustered within the RED between positions 278 and 322. Based on the probability score assigned by the Scansite program (http://scansite.mit.edu) to candidate ITSN binding motifs in RALT, we introduced Ala substitutions in the 278PEIPPR$_{284}$ and 315PKVPPPR$_{320}$ RALT sequences (underlined residues were changed to A). As shown in Fig. 7 D, RALT lost the ability to coimmunoprecipitate with a recombinant protein spanning the five SH3 domains of X/ITSN when both of the above PXXPXR sequences were mutated (RALT 4Aala). GST-5SH3 recombinant proteins from either ITSN1 or ITSN2 lost the ability to interact with RALT 4Aala (Fig. S5 D). Finally, the 4Aala mutation strongly reduced the interaction between the ER$_{144-323}$ chimera and ITSNs (Fig. 7, B and C). Strikingly, RALT 4Aala showed a significant reduction in the ability of driving EGFR endocytosis as measured by $[^{32}$S]-EGF uptake (Fig. 7 E; Fig. S5 E). We note that combined RNAi to ITSNI and ITSN2 had a stronger effect than the 4Aala mutation on EGFR Dc214 endocytosis, possibly because 4Aala mutants displayed some residual binding to ITSNs (Fig. 7, B–D).

The sum of the above results supports a model whereby the endocytic domain of RALT couples EGFR to CME via its interaction with AP-2 and Intersectins.

**Discussion**

Ligand-activated EGFR drives its own endocytic traffic by interacting with endocytic proteins. This network of protein–protein interactions is activated by post-translational modifications of the EGFR, i.e., tyrosine phosphorylation and ubiquitylation, which are induced and maintained by EGFR kinase activity. Hence, EGFR endocytic traffic is intimately connected to receptor activation (Sorkin and Goh, 2009). Deviating from this consolidated notion, we show here that RALT-bound EGFR molecules are internalized and eventually delivered to lysosomes for degradation in the absence of EGFR kinase activity.

RALT rescues the endocytic deficit of EGFR mutants unable to undergo either internalization (EGFR Dc214) or sorting from early endosomes into MVBs (EGFR Y1045F). The endocytic activities of RALT map to the 144–323 sequence, which we called RED. The isolated EBR domain phenocopies the inhibitory activity of AG1478, not supporting EGFR endocytosis. A functional EBR is nevertheless required for RALT-mediated endocytosis because it provides the docking function necessary to relocate cytosolic RALT in proximity of the endocytic machinery. We posit that RALT mediates EGFR endocytosis thanks to its ability of acting as a scaffold for components of the endocytic machinery.

Our results clearly show that RALT-dependent endocytosis of EGFR is clathrin- and AP-2–dependent. RALT binds to the AP-2 complex and we suggest that this interaction is key to sorting EGFR–RALT complexes into CCPs. Binding of RALT to AP-2 requires determinants located within the RED. Two evolutionarily conserved sequences are present in the RED, namely $284^{\text{DTDFLL}}_{288}$ (which fits well with the DE[XX]L consensus for binding to the $\alpha_2$-2 hemi-complex of AP-2) and $309^{\text{YAYE}}_{312}$ (conforming to the YXXΦ consensus for binding to the $\mu_2$ chain of AP-2; Traub, 2009). Further experiments are needed to evaluate their possible involvement in the RALT–AP-2 interaction.

RALT interacts functionally and physically with the accessory proteins ITSN1 and ITSN2, which are thought to be important for promoting maturation of cargo-loaded CCPs (Mettlen et al., 2009). ITSNs scaffold several components of the endocytic machinery, including AP-2 (Praefcke et al., 2004; Schmid et al., 2006), Epsin, EPS15 (Sengar et al., 1999), dynamin (Yamabhai et al., 1998), CIN85 (Nikolaenko et al., 2009), and CBL (Martin et al., 2006). The ITSN–RALT interaction is mediated by the SH3 domains of ITSNs and Pro-rich sequences located in the RED. As proved by RNAi experiments, ITSN1 and ITSN2 serve nonredundant functions in RALT-dependent endocytosis, with ITSN2 playing a prevalent role. Inhibiting the RALT–ITSNs interaction by the 4Aala mutation was likewise effective in reducing the rate of EGFR Dc214 endocytosis, supporting the notion that the RALT–ITSNs physical interaction is required for RALT-dependent CME.

The remarkable requirement of RALT-driven endocytosis for ITSN2 highlights mechanistic differences between the CME of kinase-active EGFR, which was insensitive to ITSN2 KD, and that of EGFR–RALT complexes. RALT-bound EGFR molecules lack ubiquitylation and are therefore unable to recruit accessory proteins containing ubiquitin-interacting motifs, i.e., EPS15, Epsin, and EPS15R (Traub, 2009). RALT may alleviate this deficit by recruiting ITSNs via SH3-directed interactions and we propose that ITSNs, as accessory protein recruited directly by RALT, could play a major role in driving the maturation of CCPs loaded with EGFR–RALT complexes (Mettlen et al., 2009). Given their ability to engage in multivalent interaction with the $\alpha_2$ and $\beta_2$ subunit of the AP-2 complex, ITSNs have been proposed to function also as accessory cargo adaptors (Schmid et al., 2006) and could therefore enhance AP-2–dependent sorting of EGFR–RALT complexes into nascent CCPs. Our results also raise the issue of why ITSN2 has a prevalent role over ITSN1 in RALT-mediated endocytosis. This may be explained by the higher affinity of ITSN2 SH3 domains for RALT (Fig. S5 D). The long isoforms (ITSN-L) of ITSNs also couple endocytosis to actin remodelling (Hussain et al., 2001; McGavin et al., 2001). Whereas ITSN1-L is restricted to neuronal cells, ITSN2-L is expressed ubiquitously (Pucharcos et al., 2001). Thus, in nonneuronal cells, ITSN2-L could contribute a signaling function crucial to RALT-dependent endocytosis.

The RED is also required for directing EGFR into late endosomes independently of EGFR ubiquitylation. Our results show that RALT rescues the degradation, but not the ubiquitylation, deficit of EGFR Y1045F. This finding underscores...
another important mechanistic difference between the endo
cytic traffic of kinase-active EGFR and that of EGFR–RALT
complexes. Cargo sorting into late endosomes in the absence
of cargo ubiquitylation has been described and may be distin-
guished from ubiquitin-dependent sorting on the basis of
differential requirements for components of the ESCRT ma-
chinery (Hislop et al., 2004). We observed that RALT-driven
degradation of EGFR was consistently slower than that of
kinase-active EGFR (Fig. 1 D), even though the rates of
EGFR down-regulation were similar in control and RALT-
expressing cells. We suppose that this may be due to delayed
sorting of RALT-bound EGFR molecules into the degradative
compartment (in the absence of significant recycling to the
cell surface; see Fig. S2 C), which in turn could reflect mech-
anistic differences between Ub-dependent and Ub-independent
sorting of EGFR into MVBs. It must be noted that such a delay
is not detrimental to RALT-dependent suppression of EGFR
signaling, given that intracellular retention of EGFR by RALT
is associated to catalytic repression of the receptor. Further
studies are required to unveil the mechanistic details of RALT-
dependent trafficking of EGFR to late endosomes.

Concluding remarks
The two-tiered mechanism of EGFR suppression enforced by
RALT has important implications to cell regulation and tumor
suppression. RALT is expressed in mid to late G1, i.e., when sus-
maintained mitogenic signals are necessary to activate the cell cycle
machinery and direct the abundant RNA and protein synthesis re-
quired for cell size increase. Within this timeframe RALT con-
curs in determining whether EGFR mitogenic signals reach the
threshold sufficient for G1 completion (Anastasi et al., 2005;
Reschke et al., 2009). The present study indicates that EGFR
kinase inactivation by RALT is associated to RALT-mediated
receptor down-modulation. The two inhibitory mechanisms act
sequentially: kinase blockade is synchronous with ligand binding,
whereas EGFR down-regulation reduces receptor expression and
therefore attenuates responsiveness to subsequent EGF stimula-
tion. We propose that this temporally dilated attenuation of EGFR
activation is key to determining that only cells receiving a robust
enough EGF signal are eventually licensed to enter S phase.

RALT endocytic activity is also predicted to protect cells
from oncogenic EGFR signaling. Oncogenic activation of
EGFR is associated to, and also dependent on, reduced rates
of receptor down-regulation. This may be caused by a variety of
mechanisms, all of which seem to converge on quelling CBL-
dependent EGFR ubiquitylation (Mosesson et al., 2008). Our
data suggest that RALT may exert a potent tumor suppressor
function not only through EGFR kinase suppression, but also by
restoring down-regulation of oncogenic EGFR molecules that
escape ubiquitylation and thus phenocopy the Y1045F mutant.

Materials and methods

Media, chemicals, and antibodies
Tissue culture media and sera were from Invitrogen and BioWhittaker. All
chemicals were obtained from Sigma-Aldrich, unless specified otherwise.
ECL, spherocyte-coupled protein A and protein G, and agaro-coupled glu-
thione were from GE Healthcare. Nitrocellulose and PVDF membranes
were from Schleicher and Schuell. EGF was from Millipore, tetramethylrhodo-
damine-EGF and tetramethylrhodamine-transferrin conjugates were from
MDS Analytical Technologies. Rabbit polyclonal anti-EGFR and anti-c-Myc
antibodies, goat polyclonal antibody to EEA1, and mAb 4D1 anti-UB and
anti-GRB2 were purchased from Santa Cruz Biotechnology, Inc. Anti-pEGFR
antibodies, anti-pERK, anti-pAKT, anti-ERK, and anti-AKT were from Cell
Signaling Technology. The anti-jpIX antibody was from Millipore. Anti-CHC
(human) (X22) was from EMG, rat antibody to mouse LAMP-1 was from
eBioscience, and mAbs to adaptin pβ2 and β2 were from BD. FITC- and
TRITC-conjugated goat anti-rabbit and anti-mouse antibodies, donkey
anti-goat, anti-mouse, anti-rabbit, and anti-rat were from Jackson Immuno-
Research Laboratories, Inc. HRP-conjugated goat anti-mouse and anti-
rabbit antibodies were from BioRad Laboratories. mAbs 108 (anti-EGFR),
12CA5 (anti-HA), and 9E10 (anti-MYC) were purified in house from hybrid-
oma supernatants. Antibodies to ITSN1 and ITSN2 were raised in rabbits
against recombinant proteins spanning positions 583–888 of hITSN1 and
618–885 of hITSN2 and purified by affinity chromatography. Anti-RALT
affinity-purified HOR3 antibody (rabbit) was described previously (Anastasi
et al., 2007). The mAb 22D/8 was generated against human RALT and
recognizes an epitope located in the 325–375 MrRALT sequence.

Cell culture and transfection procedures
NR6 fibroblasts, which lack endogenous EGFR (Pruss et al., 1978), were
obtained from American Type Culture Collection and grown in DME con-
taining 10% (vol/vol) newborn calf serum. For serum starvation, cells were
incubated in DME/Ham’s F12 (1:1 mixture) containing 0.2% serum. HEK 293
cells were the Phoenix ecotropic packaging cell line. Cells were grown in
DME containing 10% fetal calf serum. For biochemical studies, transfected HEK 293 cells
were harvested 48–72 h after transfection. Phoenix cell culture superna-
tants containing recombinant retrovirus were harvested 48–72 h after
transfection, filtered through a 45-µm disposable filter, added to 8 µg/ml
drug-free, and incubated with target cells for 3–6 h.

Immunohistochemical procedures
For most of the experiments reported here, cells were lysed on ice in HNTG
(50 mM Hepes, pH 7.5, 150 mM NaCl, 10% glycerol, 5 mM EGTA, and
1% Triton X-100) containing 0.1% sodium orthovanadate and protease
inhibitors. Lysates were cleared of nuclei and debris by centrifugation. Protein
concentration was measured with the BCA kit (Thermo Fisher Scien-
tific). For IP/WB experiments aimed at detecting ubiquitin-conjugated
proteins, cells were lysed in RIPA buffer (50 mM Tris-HCl, pH 7.5,
150 mM NaCl, 1% Triton X-100, 0.1% SDS, and 0.5% sodium deoxyco-
late) or in boiling 1% SDS. In the latter case, chromosomal DNA was
sheared by sonication and cleared lysates were diluted with nine volumes
of HNTG before being subjected to immunoprecipitation.

For immunoprecipitation experiments, antibodies were coupled to
either protein A or protein G (2–10 µg Ab/IP) and incubated with lysates at
4°C on a rocker. Immune complexes were washed with lysis buffer and eluted
with boiling Laemmli buffer. GST pull-down assays were performed as
described previously (Anastasi et al., 2007). In brief, recombinant proteins
were solubilized by sonication of bacteria, resuspended in NETN buffer
(20 mM Tris-HCl, pH 8.0, 100 mM NaCl, 1 mM EDTA, and 0.5% NP-40).
Lysates were cleared by centrifugation and GST fusion proteins purified onto
agarose-glutathione sepharose 4B beads. Cell lysates were added to beads and
binding reactions were allowed to proceed at 4°C under continuous rot-
ation. Beads were washed with HNTG, bound proteins were eluted by boiling
in Laemmli buffer and processed for immunoblot analysis.

Iodination of EGF and transferrin
[125I]-EGF binding studies
[125I]-EGF and [32P]-P1f were either purchased from PerkinElmer or gener-
cated using the IODO-GEN kit according to the supplier’s protocols (Thermo
Fisher Scientific). Specific activity of EGF was at least 1.5 × 106 cpm/ng.
For binding studies, NR6 derivatives were plated at 4 × 105 cells/well in
24-well gelatin-coated plates. For each time point we used triplicate wells,
with a fourth well being used to determine background binding in the pres-
ence of a molar excess of unlabeled EGF.

For measuring initial rates of [125I]-EGF uptake cells, we used the protocol
described by Sorkin et al. (1992). Cells were incubated with bind-
ing medium (BM; i.e., DME containing 0.2% BSA and 20 mM Hepes,
pH 7.5) for 10 min in a water bath at 37°C. Binding was initiated by adding
0.3 µl/well of 1 ng/ml [125I]-EGF in BM. At the end of binding time, plates
were put on ice, washed three times with ice-cold PBS, and incubated
for 5 min with 0.5 µl/well ice-cold elution buffer (0.5 M NaCl, 0.2 M
NaHCO3, 0.05% Tween, and 0.01% bovine serum albumin). Membranes
were processed for autoradiography.
CH₂COOH, pH 2.8). After an additional 1-min wash with elution buffer, cell monolayers were dried and lysed with 1N NaOH. Cell surface-associated cpm (eluted with elution buffer) and internal cpm (suspended in NaOH) were determined separately from triplicate wells for each time point. Background binding was determined in parallel in a fourth well containing a 300-fold molar excess of unlabelled EGF. The internalization rate constant (Ki) corresponds to the linear regression coefficient of the internal/surface ratio for each time point. Controls spanning human RALT 145–414 and 325–414 were generated by PCR amplification of human RALT cDNA fragments followed by subcloning in the pGEX-6P vector. Xenopus laevis TISN vectors were obtained from B. Kay (University of Illinois at Chicago, Chicago, IL) and have been described previously (Yamabhai et al., 1998). EGFR, GFP-, and RALT chimeras were generated by subcloning PCR-amplified fragments of RALT into pCDNA3-EGFR. pCDNA3-EGFR/RALT chimeras were also subcloned into the pBabe-puro retrovector for stable expression in NR6 cells.

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Ballarò et al., 2005). For LAMP1 labeling, cells were fixed with methanol in 20°C for 4 min. Cells were then washed with ice-cold DME and permeabilized with 0.25% Triton X-100 in PBS at 20°C, and 60x/1.40 oil objective lenses. Images were recorded on a CCD camera (SPOT; Diagnostic Instruments, Inc.) run by DeltaSystem software.

Confocal microscopy was performed with a confocal microscope (TCS-SP; Leica) equipped with PLA 40x/1.25 and 60x/1.40 oil objectives. Colocalizations were recorded using sequential recording with line average. Recorded images were processed using Adobe Photoshop software (using linear curve correction for adjusting brightness and contrast to whole images; levels were adjusted equally for all images in a set) and Image software.

**Online supplemental material**

Fig. S1 shows that RALT drives endocytosis and degradation of kinase-suppressed EGFR. Fig. S2 shows down-regulation/degradation of EGFR Dc214 by RALT as well as the endocytosis-inducing activity of the evolutionarily conserved 144–411 fragment of RALT. Fig. S3 shows that RALT rescues the degradation deficit of EGFR Y1045F independently of receptor ubiquitylation. Fig. S4 shows the analysis of SH3-containing proteins in RALT-mediated endocytosis. Fig. S5 analyzes the molecular bases of the RALT-ITSN physical interaction. Online supplemental material is available at http://www.jbc.org/cgi/content/full/jbc.201002032/D1

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**Recombinant DNA**

pcDNA3-EGFR, pcDNA3-EGFR(A50), pcDNA3-EGFR Y1045F (Haglund et al., 2003; Sigismund et al., 2008), and pcDNA3-EGFR Dc214 (Levkowitz et al., 1998) have been described previously. pCS2-MT and pBabe-puro mammalian expression vectors for MYC-tagged rat RALT have been described previously (Anastasi et al., 2007). The Y358A mutation was generated in the human RALT cDNA. Human RALT cDNAs in wt and Y358B configuration were subcloned in pBabe puro vector to express MYC-tagged proteins. GST fusion spanning human RALT 145–414 and 325–414 were generated by PCR amplification of human RALT cDNA fragments followed by subcloning in the pGEX-6P vector. Xenopus laevis TISN vectors were obtained from B. Kay (University of Illinois at Chicago, Chicago, IL) and have been described previously (Yamabhai et al., 1998). EGFR-, GFP-, and RALT chimeras were generated by subcloning PCR-amplified fragments of RALT into pCDNA3-EGFR. pCDNA3-EGFR/RALT chimeras were also subcloned into the pBabe-puro retrovector for stable expression in NR6 cells.

**Immunofluorescence analysis**

For endocytosis studies, quiescent cells were incubated for 30 min at 4°C with 20 ng/ml EGF, washed with cold DME, and then shifted to 37°C for the indicated lengths of time in EGF-free DME. Cultures were routinely rinsed with PBS (+Ca²⁺/Mg²⁺), fixed with 4% paraformaldehyde in PBS for 10 min, permeabilized with 0.25% Triton X-100 in PBS at 20°C, and processed with antibodies as described previously (Fiorentino et al., 2000; Ballarò et al., 2005). For LAP1 labeling, cells were fixed with methanol at −20°C for 5 min. Cells were incubated with primary antibodies and subsequently with a conjugated secondary antibody in 1% BSA.

Finally, coverslips were mounted with Gelvatol. A similar protocol was adopted for endocytosis of TRITC-conjugated EGF (0.5 µg/ml EGF-TRITC) and transferrin (25 µg/ml transferrin-TRITC); cultures were then fixed with 4% paraformaldehyde and mounted for visualization. For CHC detection, cells were washed with ice-cold PBS (+Ca²⁺/Mg²⁺) and fixed with 4% paraformaldehyde. The samples were routinely examined with a microscope (model AX70; Olympus) equipped with a 40x/0.75 PH2 and 60x/1.40 oil objective lenses. Images were recorded on a CCD camera (SPOT; Diagnostic Instruments, Inc.) run by DeltaSystem software.

Confocal microscopy was performed with a confocal microscope (TCS-SP; Leica) equipped with PLA 40x/1.25 and 60x/1.40 oil objectives. Colocalizations were recorded using sequential recording with line average. Recorded images were processed using Adobe Photoshop software (using linear curve correction for adjusting brightness and contrast to whole images; levels were adjusted equally for all images in a set) and Image software.

**RNA interference**

NR6 derivatives were plated at 10⁴ cells/35-mm dish and grown for 24 h. siRNAs were transfected for 6 h at a concentration of 50 nM using Lipofectamine. For CHC, ITSN1 and ITSN2 knock-down cells were transfected twice and analyzed 96 h after the first transfection cycle. Cells were transfected into 24 well plates for EGF binding studies 24 h after completing transfection procedures. A fraction of transfected cells was plated onto 35-mm dishes to monitor RNAi efficiency by WB or RT-PCR. Poor poor siRNAs directed against mouse GRB2, pBFX, and RALT were obtained from Thermo Fisher Scientific. Stealth siRNA directed against ITSN1 (5′-CAAGUUGGUUGCUACUUAGGAACUUUU-3′), ITSN2 (5′-CGAUGCUCAUGAAGCGGAAAAGGU-3′), and 5′-CCCAUUAGGUGAACUGAUCUGG-3′, denoted as A and C in the text, respectively, and CHC (5′-GAAAACCUUUGGGCGAAAUUUA-3′) were obtained from Invitrogen.

Mutant (Dc214 and Y1045F) and wtEGFR cDNA clones were subcloned in pBabe-puro to obtain vectors suitable for the generation of recombinant retrovirus stocks. Fragments encoding the 5SH3 region of human ITSN1 and ITSN2 (Pucharcos et al., 2001) were amplified by PCR and subcloned into pGEX-6P. Site-directed mutagenesis was performed using the QuikChange kit (Agilent Technologies). RNA was extracted from cultured cells using Trizol (Invitrogen).Quantitative RT-PCR was performed with the Advantage kit (Takara Bio Inc.). Primers for mouse ITSN2 were designed to amplify both short and long isoforms (primer sequences are available upon request).

**Online supplemental material**

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