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Interactions of Drosophila Cbl with Epidermal Growth Factor Receptors and Role of Cbl in R7 Photoreceptor Cell Development

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The human proto-oncogene product c-Cbl and a similar protein in Caenorhabditis elegans (Sli-1) contain a proline-rich COOH-terminal region that binds Src homology 3 (SH3) domains of proteins such as the adapter Grb2. Cbl-Grb2 complexes can be recruited to tyrosine-phosphorylated epidermal growth factor (EGF) receptors through the SH2 domain of Grb2. Here we identify by molecular cloning a Drosophila cDNA encoding a protein (Drosophila Cbl [D-Cbl]) that shows high sequence similarity to the N-terminal region of human c-Cbl but lacks proline-rich sequences and fails to bind Grb2. Nonetheless, in COS-1 cells, expression of hemagglutinin epitope-tagged D-Cbl results in its immunoprecipitation with EGF receptors in response to EGF. EGF also caused tyrosine phosphorylation of D-Cbl in such cells, but no association of phosphatidylinositol 3-kinase with D-Cbl was detected in assays using anti-p85 antibody. A point mutation in D-Cbl (G305E) that suppresses the negative regulation of LET-23 by the Cbl homolog Sli-1 in C. elegans prevented tyrosine phosphorylation of D-Cbl as well as binding to the liganded EGF receptor in COS-1 cells. Co-localization of EGF receptors with both endogenous c-Cbl or expressed D-Cbl in endosomes of EGF-treated COS-1 cells is also demonstrated by immunofluorescence microscopy. In lysates of adult transgenic Drosophila melanogaster, GST-D-Cbl binds to the tyrosine-phosphorylated 150-kDa torso-DER chimeric receptor. Expression of D-Cbl directed by the sevenless enhancer in intact Drosophila compromises severely the development of the R7 photoreceptor neuron. These data suggest that despite the lack of Grb2 binding sites, D-Cbl functions as a negative regulator of receptor tyrosine kinase signaling in the Drosophila eye by a mechanism that involves its association with EGF receptors or other tyrosine kinases.

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The human proto-oncogene product c-Cbl is a 908-amino-acid (aa) protein containing a ring finger domain and an extended proline-rich COOH terminus with multiple PXSP motifs that bind proteins having Src homology 3 (SH3) domains, including Grb2 and Nck (4, 9, 12, 21, 23, 25, 28). Activation of hematopoietic cells leads to rapid tyrosine phosphorylation of c-Cbl and the recruitment of p85/phosphatidylinositol 3-kinase (PT 3-kinase) and Crk to tyrosine phosphorylation sites on Cbl (6, 8, 9, 12, 14, 21, 23, 25, 26, 28). In other cell types, Cbl becomes tyrosine phosphorylated in response to a variety of extracellular signals, including epidermal growth factor (EGF), nerve growth factor, granulocyte-macrophage colony-stimulating factor, and transforming growth factor α (9, 11, 13, 19, 22, 23). Rapid association of c-Cbl with autophosphorylated EGF and colony-stimulating factor 1 (CSF-1) receptors also occurs (5, 13, 22, 32). A mechanism by which Cbl is recruited to the EGF receptor in response to EGF appears to involve binding of the SH2 domain of the adapter Grb2 to tyrosine-phosphorylated sites on the receptor (22, 32). The oncogenic form, v-Cbl, is a truncated 40-kDa protein lacking the ring finger and proline-rich COOH-terminal domain (3, 17) that mediates potent signals leading to cell transformation. A recent report has shown that v-Cbl is poorly tyrosine phosphorylated upon EGF stimulation but nonetheless is recruited to the liganded EGF receptor (5). These and other data argue that the N-terminal regions of c-Cbl (13) and v-Cbl (5) may also interact directly with the EGF receptor.

The physiological functions of c-Cbl are poorly understood. The binding of Grb2 and other proteins to c-Cbl suggests that it may serve as a docking protein for adapter molecules to enhance the formation of protein complexes on activated receptors at the cell membrane. Genetic data obtained with Sli-1, a Caenorhabditis elegans protein similar to c-Cbl, indicates a potential suppressor role in signaling by LET-23, the EGF receptor homolog (35). Thus, expression of Sli-1 in the presence of a defective LET-23 receptor prevents vulva development, which is dependent on the p21ras signaling pathway (24). These data suggest the hypothesis that c-Cbl negatively modulates EGF receptor signaling and that v-Cbl may act in a dominant inhibitory mode to block the negative influence of c-Cbl. To clarify the role(s) of Cbl proteins in cellular signaling processes, we searched for similar proteins expressed in Drosophila melanogaster. Here we report the molecular cloning of a gene encoding Drosophila Cbl (D-Cbl); we show that this protein lacks the entire C-terminal proline-rich domain of mammalian Cbl and does not bind p85 or Grb2. Despite the lack of these sites, D-Cbl is rapidly recruited to EGF receptors following EGF stimulation when heterologously expressed in...
mammalian cells and exerts a negative influence on the signaling pathway required for R7 photoreceptor neuron development in intact Drosophila.

**MATERIALS AND METHODS**

**Cloning of D-Cbl.** Degenerate primers were made based on two regions, TYVEK and YELCYM, that share 100% amino acid sequence identity among the human, mouse, and C. elegans homologs of Cbl. These primers were used to amplify a 309-bp DNA fragment from Drosophila genomic DNA. This fragment was cloned, and sequence analysis confirmed that it contained an open reading frame highly homologous to the encoding Cbl protein. Drosophila eye-specific cDNA library (gift of G. M. Rubin) was screened by using the 309-bp fragment as a probe, and nine independent clones were isolated. The longest cDNA, a 2.66-kb insert, was entirely sequenced with a model 373A DNA sequencer (Applied Biosystems Inc.), using dye-coupled terminator-based cycle sequencing.

**Generation of transformants.** The D-Cbl cDNA was subcloned as an EcoRI fragment into a modified Sev-S11 vector (gift of K. Basler and E. Hafen) containing two copies of the sevenless enhancer (Sev) and an hsp70 promoter. The resulting transformation construct was named se[D-Cbl]. To generate transformant flies, Drosophila w1118 females were crossed to males containing P(D2-3)2 [as a source of transposase. The embryos from this cross were injected with se[D-Cbl], giving rise to flies carrying a D-Cbl transgene.

**Antibodies and reagents.** The Drosophila cDNA of 2.66 kb was amplified by PCR with Taq polymerase to yield an N-terminal EcoRI-methionine-noNcoI 0.66-kb fragment, using oligonucleotides 5'-GAATTCATGCGGACGAGG CAGT-3' (sense) and 5'-GCTGCGTTTCAAGGCGGCT-3' (antisense), and a terminal NcoI-BamH I methionine site of D-Cbl cDNA encoding this autocrine transforming (1, 3, 4). Interestingly, D-Cbl function of Drosophila has been submitted to GenBank and given accession number U87925.

**RESULTS**

**Isolation of a Drosophila cDNA related to the proto-oncogene cbl.** A D-cbl DNA fragment was PCR amplified from Drosophila genomic DNA by using a set of degenerate primers. Screening of a Drosophila eye disc cDNA library with this fragment led to the isolation of a 2.66-kb cDNA containing 313 nucleotides of 5' noncoding region, a 1,344-nucleotide open reading frame preceding an in-frame TAG stop codon, and 1,317 nucleotides of 3' noncoding region. A comparison of the derived amino acid sequences of human D-Cbl, C-Dbl, and C. elegans Cbl (Sli-I) (Fig. 1A) shows no homology over the longest 40 aa or beyond residue 426 of D-Cbl. However, within the conserved region of approximately 380 aa, the three species show 63% similarity between aa 46 and 205 and 93% similarity between aa 205 and 320. Within the N-terminal conserved region, several tryrosine residues found in human Cbl are not present in D-Cbl, including the human Y14EEN sequence (F1-1EDN in D-Cbl), which is a potential Src kinase SH2 binding motif. A high degree of similarity is also observed between aa 354 and 425. This region includes a ring finger domain and a sequence of 17 aa (called 702/3) which, when deleted, renders c-Cbl transforming (1, 3, 4). Interestingly, D-Cbl is only 93 residues longer than v-Cbl (Fig. 1B), but these amino acids include the important 702/3 sequence and ring finger regions. Finally, unlike the protein found in C. elegans or mammals, D-Cbl contains no proline-rich motifs.

**D-Cbl negatively regulates R7 development.** In the developing Drosophila eye, the differentiation of photoreceptor neurons (R cells) depends on signaling through the Sevenless and EGF receptor tyrosine kinases (reviewed in reference 36). The developing eye constitutes a genetic system where the in vivo function of Drosophila Cbl could be studied. Mutations in the D-cbl locus have not yet been identified, and the region encoding this locus is not covered by deficiencies or transposable elements. We therefore generated transformant flies carrying the D-Cbl cDNA under the transcriptional control of se, which will cause the expression of the D-Cbl cDNA in all cells that express Sevenless, including the R7 photoreceptor precursor (2). To assess the role of D-Cbl in R7 development, we tested these transgenic flies in a series of genetic assays (reviewed in reference 7). In one way, signaling through Sevenless is compromised by using a disabled Sevenless kinase, sevFk. This defect is partially rescued by combining sevFk with one copy of SoxC2, an allele of the son of sevenless gene encoding an overactive protein. In the resulting sevFk/Y; SoxC2+ fly, the re-
ceptor tyrosine kinase signal is weakened so that an R7 cell develops in only 17% of the facets (ommatidia) in the eye (Fig. 2).

The above-described genetic background is extremely sensitive to the dosage of genes participating in receptor tyrosine kinase signaling, and the fraction of ommatidia developing R7 cells is a readout for the strength of the transduced signal. We have previously shown that removing a single copy of a positive regulator such as Ras or Sos abolishes the development of R7 cells in this genetic background, while removing one copy of a negative regulator, such as GAP1, will increase this number significantly (29). Removing a copy of the EGF receptor in this background also completely abrogates R7 differentiation (Fig. 2). This finding suggests that the R7 developmental readout is due to the combination of Sev and EGF receptor tyrosine kinase signals. This result is consistent with the recent observations of Freeman (10) showing that both of these receptors are essential for R7 development. We introduced a copy of the D-Cbl transgene in the sensitized background to generate a fly of the genotype sevE4/Y; SosJC2/1; seD-Cbl. In the three independently generated transgenic lines shown, the development of R7 cells was essentially eliminated when the level of

FIG. 1. (A) Comparison of the amino acid sequences of D-Cbl with those of human Cbl (H-Cbl) and C. elegans Cbl (CESl1). The most conserved region of the three proteins, from residues 205 to 330 of dCbl, is overlined. The 70Z/317-17-aa sequence is underlined, and the ring finger domain is boxed. (B) Schematic representation of human c-Cbl, D-Cbl, C. elegans Cbl (CeCbl), and v-Cbl.

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D-Cbl was raised in the R7 precursors (Fig. 2). No change in phenotype was observed when D-Cbl was added to flies with a wild-type genetic background (data not shown). This result strongly argues that in the \textit{Drosophila} eye, D-Cbl acts as a negative regulator of one or more receptor tyrosine kinase pathways that are essential for photoreceptor differentiation.

D-Cbl does not bind p85 or Grb2. Since D-Cbl does not contain any of the proline-rich domain found in the \textit{C.elegans} Sli-1 homolog or in mammalian Cbl (Fig. 1) and has only one (Y370CEM) of two possible p85 binding sites, we tested whether Grb2 or p85 was bound to D-Cbl. This was accomplished by heterologously expressing D-Cbl or human c-Cbl in COS-1 monkey kidney cells and activating with EGF. COS-1 cells were transiently transfected with HA epitope-tagged D-Cbl cDNA or human c-Cbl cDNA 48 h prior to lysis and immunoprecipitation with anti-c-Cbl or anti-HA antibody. Immunoblots of anti-HA precipitates with anti-p85 showed no detectable p85 associated with D-Cbl (Fig. 3, lanes 5 and 6), consistent with the lack of the Y371EAM motif in D-Cbl. In COS cells transfected with c-Cbl cDNA, an EGF-dependent binding of p85 to Cbl is observed, as expected (Fig. 3, lanes 3 and 4), and immobilized phosphopeptide containing the c-Cbl SH2 recognition motif (Y731EAM) for p85 binds a similar amount of p85 (Fig. 3, lane 7). These data indicate that the p85 concentration in these lysates is not rate limiting for binding to D-Cbl and that the Y731EAM motif is phosphorylated by EGF and binds p85 in these cells. The Grb2 immunoblot (Fig. 3, middle panel) of the anti-HA and anti-Cbl immunoprecipitates shows that Grb2 is bound to Cbl in c-Cbl-transfected cells (Fig. 3, lanes 3 and 4) but is not associated with D-Cbl (Fig. 3, lanes 5 and 6). Interestingly, activation of COS-1 cells with EGF causes more Grb2 to be complexed with Cbl (Fig. 3, lane 4), consistent with an increased Grb2/Cbl stoichiometry observed in activated Jurkat T cells (21), as well as EGF-activated 293 kidney (22) and human mammary epithelial cells (12).

Recruitment of D-Cbl to the EGF receptor. c-Cbl is recruited to the EGF receptor upon EGF stimulation of transiently transfected COS-1 cells. Cells containing endogenous Cbl (lanes 1, 2, 5, and 6) or transfected with c-Cbl (lanes 3, 4, 7, and 8) were activated with EGF (310 ng/ml) for 20 min. Lysates were prepared, and 500 μg of protein was immunoprecipitated with anti-Cbl (α-Cbl) and blotted with antiphosphotyrosine (α-PY, top), anti-Cbl (middle), or anti-EGF receptor (α-EGFR, bottom). Lanes 1 to 4, 10 μg of total cell lysate. Sizes are indicated in kilodaltons.

Transfection of COS-1 cells with the HA epitope-tagged D-Cbl cDNA (Fig. 5) revealed a p60 polypeptide correspond-
ing to the expected migration of D-Cbl in lysates and in anti-HA immunoprecipitates of transfected cells that was immunoreactive with anti-HA MAb. This polypeptide band was not found in anti-HA immunoprecipitates of nontransfected cells (Fig. 5, lane 3). In nonstimulated cells, D-Cbl was tyrosine phosphorylated (lanes 1 and 4), and activation with EGF led to increased phosphorylation (lanes 2 and 5), as well as the appearance of p170 in anti-HA immunoprecipitates (top, lane 5). Blotting anti-HA immunoprecipitates of COS-1 cells transfected with D-Cbl cDNA with anti-EGF receptor (bottom, lane 5) showed that D-Cbl is recruited to the 170-kDa EGF receptor in an activation-dependent manner. These results were confirmed by identifying D-Cbl in immunoprecipitates of the EGF receptor (Fig. 6). When EGF receptors were immunoprecipitated from D-Cbl-transfected cells and immunoblotted with anti-HA antibody, a small amount of D-Cbl was present. EGF addition to the COS-1 cells increased this association of D-Cbl with EGF receptors several fold (lanes 5 and 6).

A Gly\textsuperscript{315}-to-Glu point mutation in the \textit{C. elegans} homolog of Cbl, Sli-1, suppresses the ability of this protein to act as a negative regulator of LET-23 signaling (35). We therefore tested whether the association of D-Cbl and the EGF receptor was also prevented by the analogous mutation in D-Cbl. In Fig. 7, COS-1 cells were transfected with D-Cbl or the corresponding G305E D-Cbl point mutation, and after stimulation with EGF, detergent-soluble lysates were immunoprecipitated with anti-HA. The anti-HA blot shows that although the wild-type and mutant proteins were expressed to the same extent (Fig. 7, bottom, lanes 2 and 3), only D-Cbl was bound to the EGF receptor (top, lane 3). Importantly, the G305E mutation of D-Cbl totally prevented tyrosine phosphorylation of the expressed protein by EGF (middle, lanes 2 and 3). We conclude that the loss-of-function mutation in \textit{C. elegans} acts by preventing the association of Cbl with the EGF receptor.

The association of transiently expressed D-Cbl with liganded EGF receptors in COS-1 cells was confirmed in \textit{Drosophila} by in vitro binding of a D-Cbl fusion protein to extracts of flies expressing a chimeric torso-DER receptor. The chimeric receptor consists of the extracellular domain of a mutant torso receptor fused to the cytoplasmic domain of DER under the control of the \textit{hsp70} heat shock promoter (27). In Fig. 8, heat shock of adult transgenic \textit{Drosophila} for 45 min at 37°C, followed by a recovery at 22°C for 3 h, causes a pronounced tyrosine phosphorylation of many proteins (lanes 1 and 2).
Addition of GST–D-Cbl fusion protein to 0.5 mg (lanes 5 and 6) or 1.0 mg (lanes 7 and 8) of cell lysate resulted in the binding of a 150-kDa protein in extracts of flies subjected to heat shock but not to control flies. No tyrosine-phosphorylated bands appeared in lysates reacted with a GST fusion protein (lanes 3 and 4). A GST–Grb2 fusion protein also binds strongly to a 150-kDa protein in extracts of activated flies (data not shown), confirming that p150 is DER.

**Colocalization of D-Cbl and human c-Cbl with the EGF receptor.** The biochemical evidence indicating a ligand-dependent association of human c-Cbl and D-Cbl with the EGF receptor (Fig. 4 to 6) was further evaluated by examining the subcellular localization of these proteins after EGF stimulation. For this purpose, COS-1 cells were grown on coverslips and incubated with or without EGF for 20 min before washing and fixing in cold formaldehyde. COS-1 cells transfected with D-Cbl cDNA were double stained with anti-HA antibody (visualized with FITC-labeled secondary antibody) and anti-EGF receptor antibody (visualized with rhodamine-labeled secondary antibody). Endogenous c-Cbl in nontransfected cells was detected with anti-c-Cbl antibody and visualized with FITC-labeled secondary antibody. Prior to the addition of EGF, endogenous EGF receptor and c-Cbl appear diffuse (Fig. 9C and D), whereas 20 min after EGF addition, the EGF receptor becomes internalized, as evidenced by the punctate rhodamine staining (Fig. 9F). Visualization of the same cell with anti-Cbl (Fig. 9E) shows that a portion of endogenous c-Cbl becomes colocalized with the internalized EGF receptor. COS cells that overexpress Cbl show the same pattern, although the greater intensity of Cbl staining throughout the cell obscures the punctate signal to some degree (data not shown).

Immunofluorescence microscopy staining of D-Cbl-transfected COS cells reveals a similar pattern of colocalization of D-Cbl with the EGF receptor in EGF-activated cells. Thus, in serum-starved cells, D-Cbl appears to be diffuse (Fig. 9A), whereas 20 min after addition of EGF, a fraction of cellular D-Cbl becomes concentrated in EGF receptor-enriched vesicles (Fig. 9G and H). We conclude that EGF causes D-Cbl and c-Cbl to be translocated into internalized vesicles containing the EGF receptor, consistent with the physical association of the Cbl proteins with EGF receptors (Fig. 4 and 5).

**DISCUSSION**

Signaling events initiated by receptor tyrosine kinases are crucial for establishing the identity of photoreceptor neurons in the developing *Drosophila* eye. We have molecularly characterized D-Cbl, the *Drosophila* homolog of the c-Cbl onco-gene product. Genetic experiments have demonstrated that in flies expressing elevated levels of D-Cbl in the R7 precursor, the development of this cell as a photoreceptor neuron is compromised (Fig. 2). This finding strongly suggests that D-Cbl is normally involved in the negative regulation of receptor tyrosine kinase-mediated signals. These results, as well as those of Freeman (10), suggest that in addition to Sevenless signaling, EGF receptor activity is also required for R7 cell fate determination. Therefore, the negative regulatory function of D-Cbl on R7 cell differentiation reflects its participation either in EGF receptor signaling or in Sevenless signaling, or possibly in both. This genetic interaction between D-Cbl and the receptor tyrosine kinase pathway is consistent with our biochemical analysis showing that D-Cbl binds to the EGF receptor (Fig. 4 to 6).

A major finding in this work is that D-Cbl is devoid of a COOH-terminal domain containing proline-rich Grb2 binding motifs. Much of the previous work on the proto-oncogene c-Cbl protein has focused on identification of signaling proteins that associate with its proline-rich motifs through SH3 binding or its tyrosine phosphate sites through SH2 binding. These associated proteins include Src family tyrosine kinases, Grb2, Nck, Crk-C3G complexes, and PI3 kinases (8, 9, 14, 21, 23, 25, 26, 28, 30). Interestingly, the motifs thought to bind all of these associated proteins are believed to reside in the proline-rich COOH-terminal region of c-Cbl containing residues 480 to 850. The recently identified *C. elegans* Cbl homolog, Sli-1, lacks much of this COOH-terminal domain but does contain several proline-rich motifs between aa 470 and 570 that can serve as binding sites for the adapter Grb2. We confirmed that D-Cbl does not bind Grb2 or PI3 kinases upon its transient expression in COS-1 cells (Fig. 3). Thus, our data indicate that D-Cbl can function in *Drosophila* without the Grb2 homolog Drk or the many other signaling proteins that bind this region in c-Cbl.

The binding of c-Cbl to Grb2 through the adapter’s N-terminal SH3 domain appears to mediate the recruitment of c-Cbl to activated EGF receptors through binding of the Grb2 SH2 domain to receptor tyrosine phosphorylation sites. However, D-Cbl, which has high sequence similarity to the N-terminal domain of c-Cbl, does retain the ability to be recruited to EGF receptors upon EGF activation of COS-1 cells (Fig. 4 to 6). We have also demonstrated that the tyrosine-phosphorylated *Drosophila* EGF receptor DER binds to a GST–D-Cbl fusion protein in detergent-soluble lysates of adult flies. Thus, the N-terminal region of Cbl proteins appears to provide a second means of EGF receptor association, as suggested by studies with v-Cbl (5) and the N-terminal region of c-Cbl (13). That this is a direct binding is indicated by Western blotting of EGF receptors with a GST fusion protein containing the N-terminal region of c-Cbl (13). Taken together, the data now available are consistent with a key role of this EGF receptor-binding N-terminal domain in the functioning of c-Cbl.

A physiologically relevant functional domain within the N-terminal region of Cbl proteins is supported by the approximate 68% amino acid sequence identity of human Cbl to D-Cbl between residues 40 and 426 of D-Cbl. Although the exact residues in Cbl that interact with the liganded EGF receptor have not been identified, we have found that a GST fusion protein encompassing the N-terminal 160 aa of Cbl does not associate (not shown). Based on the G305E mutation in D-Cbl that ablates receptor association (Fig. 7), it seems plausible that the most highly conserved region of Cbl (aa 205 to 330) may be sufficient for EGF receptor binding. It is possible that this core region of Cbl binds directly to other tyrosine kinases as well. For example, the N terminus of c-Cbl (aa 1 to 357) binds in vitro to ZAP-70 in activated T cells, and the loss-of-function point mutant G306E largely prevents this interaction (20). In T cells activated through the CD3 receptor, c-Cbl binds directly to the Src kinase Fyn in an activation-dependent manner (33), although the region of Cbl responsible for this interaction was not identified. A tyrosine kinase receptor with similarity to the EGF receptor is the hematopoietic cell CSF-1 receptor, and in the macrophage cell line P388D1, Cbl is recruited to the activated CSF-1 receptor (32). However, it is not established whether this binding is mediated through Grb2 or through the Cbl N-terminal domain, or both.

It will be important in future studies to determine what structural motifs or motifs in these tyrosine kinases bind D-Cbl and whether such motifs appear in other proteins.

It is striking that the association of EGF receptors with D-Cbl and c-Cbl observed by biochemical techniques can be
FIG. 9. Colocalization of D-Cbl and c-Cbl with internalized EGF receptors following activation with EGF. Cells were serum starved for 1 h and stimulated for 20 min. with EGF. After fixing and permeabilizing, cells were stained with sheep anti-EGF receptor (anti-EGFR) and donkey anti-sheep–rhodamine. Human Cbl was visualized with rabbit anti-Cbl plus donkey anti-rabbit–FITC; D-Cbl was visualized with rabbit anti-HA plus donkey anti-rabbit–FITC. (C to F) Nontransfected COS-1 cells; (A, B, G, and H) HA-DChbl-transfected cells.
visualized by immunofluorescence microscopy of intact COS-1 cells (Fig. 9). Colocalization of Cbl proteins and EGF receptors can be observed as early as a few minutes after addition of EGF to these cells (not shown), and by 20 min of incubation, an intense punctate pattern of Cbl and the EGF receptor proteins is evident. It is noteworthy that these images can be visualized with endogenous EGF receptors in the COS-1 cells. Our data are consistent with the hypothesis that Cbl-EGF receptor complexes are internalized into endosomes through the coated pit pathway, as previously described for EGF receptors (31). Previously, Tanaka et al. (32) demonstrated by immunofluorescence that Cbl is translocated to a perinuclear region after Fcey receptor cross-linking or EGF stimulation. The continued association of D-Cbl and c-Cbl proteins with EGF receptors trafficking within intracellular membranes correlates with the known retention of phosphorylated tyrosine residues and active tyrosine kinase activity in the intracellular EGF receptors (15, 16, 31). It seems likely from these observations that modulation of EGF function by Cbl proteins involves the transient association with both cell surface and intracellular EGF receptors. In this context, it is intriguing that mutations in the sli-1 gene, encoding the C. elegans homolog of Cbl, have been shown to interact genetically with unc-101 in the regulation of the EGF receptor pathway leading to vulval differentiation (18). unc-101 encodes a clathrin-associated protein homologous to mouse AP47, which constitutes one of the main components of coated pits and vesicles. Although sli-1 mutations alone are silent, in combination with unc-101 mutations, they cause excessive vulval differentiation. These gene products, thus, appear to cooperate synergistically in the negative control of EGF receptor signaling. Part of the mechanism whereby Cbl proteins exert an attenuation on receptor tyrosine kinase signaling might involve the downregulation of receptor activity by directing the intracellular degradation of the receptor-Cbl complexes.

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