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Targeting of Cholera Toxin and *Escherichia coli* Heat Labile Toxin in Polarized Epithelia: Role of COOH-terminal KDEL

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Abstract. *Vibrio cholerae* and *Escherichia coli* heat labile toxins (CT and LT) elicit a secretory response from intestinal epithelia by binding apical receptors (ganglioside GM1) and subsequently activating basolateral effectors (adenylate cyclase). We have recently proposed that signal transduction in polarized cells may require transcytosis of toxin-containing membranes (Lencer, W. I., G. Strohmeier, S. Moe, S. L. Carlson, C. T. Constable, and J. L. Madara. 1995. *Proc. Natl. Acad. Sci. USA.* 92:10094–10098). Targeting of CT into this pathway depends initially on binding of toxin B subunits to GM1 at the cell surface. The anatomical compartments in which subsequent steps of CT processing occur are less clearly defined. However, the enzymatically active A subunit of CT contains the ER retention signal KDEL (RDEL in LT). Thus if the KDEL motif were required for normal CT trafficking, movement of CT from the Golgi to ER would be implied. To test this idea, recombinant wild-type (wt) and mutant CT and LT were prepared. The COOH-terminal KDEL sequence in CT was replaced by seven unrelated amino acids: LEDERAS. In LT, a single point mutation replacing leucine with valine in RDEL was made. Wt and mutant toxins displayed similar enzymatic activities and binding affinities to GM1 immobilized on plastic. Biological activity of recombinant toxins was assessed as a Cl⁻ secretory response elicited from the polarized human epithelial cell line T84 using standard electrophysiologic techniques. Mutations in K(R)DEL of both CT and LT delayed the time course of toxin-induced Cl⁻ secretion. At T1/2, dose dependencies for K(R)DEL-mutant toxins were increased ~10-fold. KDEL-mutants displayed differentially greater temperature sensitivity. In direct concordance with a slower rate of signal transduction, KDEL-mutants were trafficked to the basolateral membrane more slowly than wt CT (asessed by selective cell surface biotinylation as transcytosis of B subunit). Mutation in K(R)DEL had no effect on the rate of toxin endocytosis. These data provide evidence that CT and LT interact directly with endogenous KDEL-receptors and imply that both toxins may require retrograde movement through Golgi cisternae and ER for efficient and maximal biologic activity.

Retrograde transport through Golgi cisternae has been shown to occur for soluble and membrane proteins of the ER (49) and for certain protein toxins (6, 55). Targeting of soluble ER and some type II membrane proteins in this pathway depends on the COOH-terminal sorting signal Lys-Asp-Glu-Leu (KDEL or HDEL in yeast) (42, 48, 62). Targeting of type I membrane proteins depends on a short cytoplasmic double lysine motif (19, 20, 43). Retrograde transport of shiga toxin from the cell surface through Golgi stacks to ER appears to depend on the structure of the toxin’s cell surface receptor glycosphingolipid Gb3 (56). Movement of shiga toxin along this pathway may be required for toxin action. Likewise, the function of Pseudomonas exotoxin A may depend on toxin entry into Golgi or ER as evidenced by sensitivity to mutation in the toxin’s COOH-terminal REDLK sequence and rescue by replacement with KDEL (6).

The heat labile enterotoxins produced by *Vibrio cholerae* (cholera toxin, CT) and *Escherichia coli* (heat labile in yeast) (42, 48, 62). Targeting of type I membrane proteins depends on a short cytoplasmic double lysine motif (19, 20, 43). Retrograde transport of shiga toxin from the cell surface through Golgi stacks to ER appears to depend on the structure of the toxin’s cell surface receptor glycosphingolipid Gb3 (56). Movement of shiga toxin along this pathway may be required for toxin action. Likewise, the function of Pseudomonas exotoxin A may depend on toxin entry into Golgi or ER as evidenced by sensitivity to mutation in the toxin’s COOH-terminal REDLK sequence and rescue by replacement with KDEL (6).

The heat labile enterotoxins produced by *Vibrio cholerae* (cholera toxin, CT) and *Escherichia coli* (heat labile...
toxin, LT) also contain respectively the KDEL or the equally potent sorting signal RDEL at the C-terminus of their enzymatically active A subunits (59, 60). CT and LT are structurally, immunologically, and functionally homologous (reviewed in reference 61). Both toxins act directly on intestinal epithelia to elicit massive secretory diarrhea by activating cAMP-dependent signal transduction pathways. Both CT and LT are comprised of five identical B subunits that bind with high affinity to ganglioside GM1, at the cell surface (7, 17, 25), and a single enzymatic A subunit comprised of two peptides linked by a disulfide bond (59, 66). After reduction of the A subunit, the enzymatically active A1-peptide (~22 kD) acts inside the cell to activate adenylate cyclase by catalyzing the ADP-ribosylation of the heterotrimeric GTPase Gsα (5, 39, 40). The A2-peptide (~5 kD) contains the COOH-terminal K(R)DEL motif that protrudes unhindered below the plane formed by the pentameric B subunit on the side which binds GM1 at the cell surface (36, 59, 60).

The process by which CT elicits a response in polarized and nonpolarized cells takes 20–40 min (termed the "lag" phase) (11, 28) and involves movement of CT through multiple intracellular compartments. Binding of CT to the cell surface is followed by endocytosis and subsequent transport of toxin containing membranes to a functionally defined intracellular compartment(s) where reduction and membrane translocation of the A subunit occurs (27, 45). The anatomical compartment of A subunit translocation, however, remains unknown though available evidence suggests this event may occur in Golgi cisternae. For example, CT-labeled horseradish peroxidase or gold particles have been shown to move from the cell surface via endosomes to trans-Golgi (23), and recently, a small fraction of internalized CT B subunit has been localized within cis elements of Golgi cisternae (56). These data provide direct evidence that CT can move retrograde in the secretory pathway. Neither study, however, provides evidence that transit through Golgi is physiologically relevant to the cellular response.

The lag phase ends with activation of adenylate cyclase by toxin-catalyzed ADP-ribosylation of Gsα. Activation of adenylate cyclase occurs by movement of the reduced and translocated A1-peptide (or possibly another messenger) back to the plasma membrane. The events that follow reduction (and presumably translocation [24]) of the A subunit are not necessarily diffusion limited. In polarized T84 cells, for example, signal transduction by the reduced A1-peptide is completely inhibited late in the lag phase by lowering incubation temperatures from 37 to 15°C (28). These and other data (13, 14, 69) suggest that the A1-peptide may not dissociate from membrane vesicles containing the B subunit. Both subunits may move together via vesicular carriers from the site of translocation to adenylate cyclase on the basolateral membrane (29).

Our aim in the present study was to define intermediary compartments through which CT and LT must physiologically traffic to elicit a cellular response. We examined whether the COOH-terminal K(R)DEL motif of the A1-peptide may play a role in toxin action. If K(R)DEL were required for normal CT or LT signal transduction, retrograde movement of CT/LT from Golgi to ER would be implied. Recombinant wild-type (wt) and mutant CT and LT were prepared. The COOH-terminal KDEL sequence in CT was replaced by seven unrelated amino acids: LEDEARS. In LT, a single point mutation replacing leucine with valine was made. Toxin action was examined in the human intestinal cell line T84, a polarized cell model of intestinal epithelia and the natural target of CT in nature. T84 cells grown on permeable supports form confluent monolayers of columnar epithelia that exhibit high transepithelial resistance, polarized apical and basolateral membranes, and a cAMP-regulated CI− secretory pathway analogous to that found in intact intestine (1). Activation of adenylate cyclase in T84 cells by intoxication with CT or LT elicits a strong Cl− secretory response that can be detected using standard electrophysiologic techniques. Our data provide strong evidence that CT and LT interact directly with endogenous KDEL-receptors and imply that both toxins may require retrograde movement through Golgi cisternae and ER for efficient and maximal biologic activity.

**Materials and Methods**

**Materials**

Cholera toxin (CT) was obtained from Calbiochem Novabiochem (San Diego, CA). Staphylococcus enterotoxin B (SEB) and protein-A-Sepharose were purchased from Pierce (Rockford, IL). All other reagents were from Sigma Chemical Co. (St. Louis, MO) unless otherwise stated. Hanks balanced salt solution (HBSS, containing in g/l 0.185 CaCl2, 0.098 MgSO4, 0.4 KCl, 0.06 KH2PO4, 8 NaCl, 0.048 Na2HPO4, 1 glucose, to which was added 10 mM Hepes, pH 7.4) was used for all assays unless otherwise stated.

**Cell Culture**

T84 cells obtained from ATCC were cultured and passaged as previously described (9) in equal parts of DME (1 g/l D-glucose) and Ham’s F-12 nutrient mixture, supplemented with 5% newborn calf serum, 15 mM Hepes, 14 mM NaHCO3, 40 mg/L penicillin, 8 mg/L ampicillin, and 0.90 mg/L streptomycin. Cells were seeded at confluent density onto 0.33- or 5-cm2 Transwell inserts (Costar Corp., Cambridge, MA) coated with a dilute collagen solution as previously described (33). Transepithelial resistances attained stable levels (>1,000 ohms cm2) after 7 d. The development of high transepithelial resistance correlated with the formation of confluent monolayers with well-developed tight junctions as assessed by morphological analysis (32), and with the ability of monolayers to secrete Cl−. Cells from passages 71–84 were utilized for these experiments.

**Preparation of Recombinant Wild-type and Mutant CT and LT**

**Mutagenesis of the COOH-terminal K(R)DEL Sequence.** The LT-RDEL sequence was mutated in plasmid pTRH29, a derivative of the plasmid vector pBluescript IIKS+, that contains the genes for the A and B subunits of E. coli labile toxin (70). Mutagenesis of Leu24° to Val at the COOH terminus of the A subunit was performed with an in vitro oligonucleotide-
directed mutagenesis kit (Amersham International, Arlington Heights, IL) using single-stranded pTRH29 as a template and a synthetic oligonucleotide 5'-TATTCATAGGCATTCTCATCC-3', from the Microanalytical Facility, IAPGR, Cambridge Research Station, UK) as the mutagenic primer. The correct Leu to Val substitution was confirmed by dideoxy sequencing using Sequence II (United States Biochemical Corp., Cleveland, OH) and the resultant plasmid designated pTRH73. The clone producing the CT variant with Lederas substituted for KDEL at the COOH terminus of the A subunit was constructed in two steps. First the Lys352 codon AAG (italicized letters in the sequence GAATAATTGAG in pMG60) was changed by oligonucleotide-directed mutagenesis to CAG, thereby creating the EcoRI restriction site GAATTCA in the resulting plasmid pMG67 (22). Next, a PvuII-EcoRI fragment of pMG67 that encodes the IPTG-inducible, truncated ctxA gene was subcloned into PvuII-EcoRI cut pBR322 to generate pMG117, and the predicted fusion joint was confirmed by dideoxy sequencing. Fusion of ctxA to vector-derived sequences in pMG117 substitutes Lederas for the COOH terminus of the A subunit of CT, in a manner equivalent to the Lederas variant of LT constructed by Sanchez et al. (54). To produce holotoxin with the Lederas variant of CT-A, pMG117 was transformed into E. coli TX1 (Stratagene Inc., La Jolla, CA) containing pMG85, a replicative plasmid clone that expresses ctxB from the IPTG-inducible promoter of pK184 (21).

Preparation of Periplasmic Extracts Containing Recombinant Wild-type and Mutant CT and LT. E. coli XL1-Blue (recA1 lac endA1 galK89 thi hsdR17 supE44 relA1 [F' proAB lacIq recA2358 SUP14]) was co-transformed with plasmid pI17 and XL1-Blue (fecAl lac- endA1 gyrA96 thi hsdR17) gene was subcloned into PvuII-EcoRI cut pBR322 to generate pMG117, and the predicted fusion joint was confirmed by dideoxy sequencing. Fusion of ctxA to vector-derived sequences in pMG117 substitutes Lederas for the COOH terminus of the A subunit of CT, in a manner equivalent to the Lederas variant of LT constructed by Sanchez et al. (54). To produce holotoxin with the Lederas variant of CT-A, pMG117 was transformed into E. coli TX1 (Stratagene Inc., La Jolla, CA) containing pMG85, a replicative plasmid clone that expresses ctxB from the IPTG-inducible promoter of pK184 (21).

**Electrophysiology**

For electrophysiological studies, confluent monolayers on Transwell inserts were transferred to HBSS and preincubated with apical CT at 4°C for 30 min before shifting to fresh HBSS at 37°C. Measurements of short circuit current (Isc) and resistance (R) were performed with 0.33-cm2 voltage/current bridges made with Ringers buffer (114 mM NaCl, 5 mM KCl, 1.65 mM Na2HPO4, 0.3 mM NaH2PO4, 25 mM NaHCO3, 1.1 mM MgSO4, 1.25 mM CaCl2). Measurements of resistance were made using a dual voltage/current clamp device (University of Iowa, Iowa City, Iowa) and 25-μA current pulses. Isc was calculated using Ohm's law.

**Selective Cell Surface Biotinylation**

Methods described by Sargiacomo et al. (1989) and Le Bivic et al. (1990) were modified for use in the T84 cell system as described (29).

**GMI Binding and ELISA**

Fluorescein-labeled CT (CT-fluorescein) (28) was used to define binding of recombinant toxins to GMI immobilized on plastic micro-titre plates as previously described (30). Dynatec microfluor 96-well black microtitre plates (Dynatec, Rockville, MD) coated with 25 μg/ml (Sigma Chemical Co.) in 60 mM sodium carbonate, pH 9.9, and incubated at 37°C for 36-48 h as previously described (34). After washing in PBS (140 mM NaCl, 10 mM Na2HPO4/NaH2PO4, pH 7.4) the plates were blocked in PBS containing 5% BSA, CT-fluorescein (3.1 μM in PBS containing 2.5% BSA, pH 7.4) was added to each well with increasing concentrations (0.05-50 μM) of recombinant wild-type or mutant toxins but buffer alone, incubated for 1 h at 37°C, washed with PBS, and fluorescence quantified in a fluorescence concentration analyzer (Pandex Fluorescence Plate Reader; Baxter, McGraw Park, IL).

To assay toxin concentrations an ELISA-based assay was used. Periplasmic extracts containing recombinant toxins were applied to 96-well microtitre plates coated with ganglioside GMI, as previously described (34). After 30 min at 37°C, the plates were washed with PBS, pH 7.4, and the presence of CT or LT bound to GMI, was assayed by routine ELISA using rabbit polyclonal antisera raised against either CT-A subunit or CT B subunit (27, 29). Toxin concentrations were confirmed by SDS-PAGE and Western blot.

**Toxin-catalyzed ADP-Ribosylation of Agmatine**

NAD-agmatine ADP-ribosyltransferase activity was assayed as described by Tsai (64) with minor modifications. Recombinant wt or K(R)DEL mutant toxins (∼200 nM final) were incubated at 30°C for 60 min with 15 mM agmatine, 100 μM nicotinamide adenine dinucleotide (NAD, containing 0.02 μCi [carbonyl-14C]NAD), 1 mM GTP, 50 mM KCl, 4 mM MgCl2, 20 mM diethiothreitol, 0.3 mg/ml ovalbumin, 2 mg/ml cardiolipin, 200 μM cibichrome blue, and 20 μl crude guinea pig brain cytosol (as a source of ADP-ribosylating factor) in a final volume of 100 μl. Reactions were terminated with the addition of 1 ml 1% SDS in water and applied to AG 1-X2 (Bio-Rad Labs., Richmond, CA) 0.25 × 2-cm columns. The columns were washed with 4 ml of distilled water and eluates containing hydroyzed [carbonyl-14C]nicotinamide were assayed by scintillation counting. Recombinant toxins were first activated by incubation with 30 mM diethiothreitol for 60 min at 30°C. Three point calibration was provided by incubation with diethiothreitol activated purified CT (1 or 0.01 μM; Calbiochem Novabiochem) or buffer alone. The assay was linear within these toxin concentrations as assessed by formal dose responses.

Guinea pig brain was homogenized (15 strokes in tight fitting Dounce) in 0.34 M sucrose, 0.1 mM MgCl2, 1 mM EDTA, 10 mM Hepes, pH 7.4, containing 1.25 mM PMSF and 0.5 μl/mg chymostatin. Cytosol was prepared by differential centrifugation and defined as the supernatant of a 100,000 g spin for 60 min.

**SDS-PAGE, Immunoprecipitation, and Western Blotting**

Recombinant toxins were analyzed on 10-20% polyacrylamide gradient gels under reducing conditions (unless otherwise indicated for A subunit) and either Coomassie stained or transferred to 0.25-μm nitrocellulose membranes. Rabbit antiserum raised against CT-A and CT-B subunits were used as described (29) and diluted 1:200 for immunoprecipitations and 1:1,000 for western blotting. Pre-stained molecular mass markers (Bio-Rad Labs.) contained: lysozyme (18.5 kD), soybean trypsin inhibitor (27.3 kD), carbonic anhydrase (32.5 kD), ovalbumin (49.5 kD), bovine serum albumin (80 kD), and phosphorylase B (106 kD).

**Endocytosis**

Methods described by Orlandi and Fishman were modified for use in the T84 cell system (44). Recombinant toxins (20 nM) were incubated with confluent monolayers of T84 cells grown on plastic 96-well plates at 4°C for 20 min and then shifted to 37°C or kept at 4°C. At the indicated times, monolayers were returned to 4°C and washed. Toxin remaining at the cell surface was measured by immunoreactivity to anti-serum raised against CT B subunit (1:200 dilution) (29), secondary incubation with horseradish peroxidase-labeled anti-IgG, and development with 2,2'-azino-bis (3-ethylthiazol-2-yl)tetrazolium-5-sulfonic acid. Assays were performed in triplicate or quadruplicate and reproduced four times. Two point calibrations for each experiment were provided by incubation at 4°C (positive control) and incubations without CT (negative control, ~30% of maximal signal). Means ± SE are reported.

**Statistics**

Data were analyzed using Statview 512+ software (Brainpower, Inc., Calabasas, CA).

**Results**

**Preparation of Recombinant CT and LT**

Mutations were engineered into the COOH-terminal K(R)DEL sequence of the A subunit of V. cholerae and E.
coli heat-labile enterotoxins. In CT, the COOH-terminal KDEL sequence was replaced by the unrelated seven-amino acid sequence: Leucine-Glutamic acid-Aspartic acid-Glutamic acid-Arginine-Alanine-Serine (Fig. 1). In LT, the COOH-terminal RDEL sequence was altered by a single point mutation replacing valine with alanine (Fig. 1 B).

Both removal of KDEL and substitution of valine for leucine have been shown to inhibit post-ER retrieval of K(R)DEL-containing proteins in other eucaryotic systems (47, 48, 71). Recombinant wild-type and mutant CT and LT were expressed from plasmid vectors in E. coli XL1-Blue, followed by extraction of periplasmic proteins (containing the recombinant toxins) as described in Materials and Methods. Toxin concentrations were determined by GMI-ELISA against both CT A and pentameric B subunits. Further analysis by SDS-PAGE and Western blot showed that A and B subunits of both mutant and wild-type toxins were present in known concentrations. As assessed by GMI-ELISA, A and pentameric B subunits were present in ~1:1 ratio indicating that all functional recombinant B subunits were fully assembled with A subunits. Further functional analysis of toxin assembly by competitive inhibition with recombinant B subunit confirmed these results (see below).

Mutation in COOH-terminal KDEL Does Not Affect Toxin Binding or ADP-ribosyl-transferase Activity In Vitro

Toxin binding to GMI immobilized on plastic was examined in vitro to determine whether mutation in K(R)DEL may affect indirectly the ability of the toxin B subunits to associate with cell membranes. Fluorescein-labeled CT was utilized to generate binding isotherms for wt and mutant CT and LT. Fig. 2 shows that both the RDEL- (A) and KDEL-mutant (B) bound to GMI with apparent affinities that were nearly identical to that of wt LT and wt CT ($K_d = 6$ nM). Competition with increasing concentrations of heat denatured CT had no effect on CT-fluorescein binding, indicating that binding was specific.

Enzymatic activities of recombinant toxins (not proteolytically nicked in the exposed loop between the A$_1$ and A$_2$-peptide) were assessed by in vitro ADP-ribosylation of agmatine (64) (Fig. 3). These data show that wt and KDEL-mutant CT (200 nM) displayed nearly identical ADP-ribosyltransferase activities in vitro (1.6 ± 0.08 vs. 1.8 ± 0.02 nmol NAD hydrolyzed/h, mean ± SD in triplicate, representative of two independent experiments).

Mutation in the COOH-terminal K(R)DEL Sequence Impedes the Time Course of Toxin Action

Initial experiments with T84 cells showed that mutation in the K(R)DEL sequence delayed the onset of toxin-induced $Cl^-$ secretion. At T1/2 (half-maximal secretion: 50 min for wt CT and 80 min for wt LT), secretory responses elicited by wild-type toxins were two- to threefold stronger than those elicited by corresponding KDEL- (26 ± 3 vs. 8 ± 2 $\mu$A/cm$^2$) or RDEL-mutants (25 ± 0.7 vs. 13 ± 1 $\mu$A/cm$^2$; mean ± SE, n = 6–8). Periplasmic extracts from a control E. coli strain XL1-Blue not harboring toxin clones were electrically silent. Mutation in K(R)DEL affected both the initial lag phase and rate of toxin induced $Cl^-$ secretion (Fig. 4 and Table I). The inhibitory effect on the kinetics of toxin action appeared greater in monolayers exposed to lower toxin concentrations (Fig. 4, C and D) but was otherwise not dose dependent. At T1/2, dose dependencies for both mutant toxins were increased ≥10-fold (Fig. 5). At high toxin concentrations (100 nM), the maximal secretory responses eventually reached were not significantly different (Fig. 4, A and B).

KDEL-mutants were not degraded by intracellular pro-

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**Figure 1. Preparation of recombinant wild-type and K(R)DEL-mutant toxins.** Primary structures for wild-type and mutant CT (A) and LT (B) are shown. Recombinant toxins were harvested in periplasmic extracts and analyzed by SDS-PAGE. Coomassie stains A show: periplasmic extracts containing KDEL-mutant CT (lane 1) and wt CT (lane 2); and purified CT from *V. cholerae* (lane 3). Coomassie stains B show: purified CT from *V. cholerae* (lane 1); and periplasmic extracts containing RDEL-mutant LT (lane 2) and wt LT (lane 3). Western blots A show: purified CT from *V. cholerae* (lane 1); and periplasmic extracts containing RDEL-mutant LT (lane 2) and wt LT (lane 3). Western blots B show: purified CT from *V. cholerae* (lane 1); and periplasmic extracts containing RDEL-mutant LT (lane 2) and wt LT (lane 3). Combined anti-sera against A and B subunits were used for western blotting. Both A and B subunits are indicated.
To examine whether signal transduction via basolateral receptors may also require sorting by K(R)DEL, it was necessary to first proteolytically nick (trypsin, 20 μg/ml) the exposed loop between the A₁- and A₂-peptides (residues 187–199) (35). The A subunits of the recombinant toxins are not nicked by endogenous proteases in E. coli as they are in V. cholerae (Fig. 1, Western blots). This has no effect on the time course of toxin action when applied to apical cell surfaces in the T84 cell system where both recombinant CT and LT are nicked by a protease(s) at the apical cell surface. Nicking, however, appears to be rate limiting when toxins are applied to basolateral membranes (unpublished data).

Signal transduction by toxin internalization via basolateral endosomes was also sensitive to mutation in the K(R)DEL sorting signal (Fig. 8). KDEL-mutants applied to either apical (A) or basolateral cell surfaces (B) elicited a secretory response more slowly than wild-type CT. Both the initial lag phase and rate of toxin induced Cl⁻ secretion were affected (KDEL-mutant vs. wt CT: lag phase, 53 ± 4 vs. 35 ± 7 min; dIsc/dt, 1.4 ± 1 vs. 2.5 ± 1.4 μA/cm²/min; peak Isc, 62 ± 25 vs. 80 ± 28 μA/cm², mean ± SD, n = 3 in duplicate, lower panel). These data confirm that mutation in K(R)DEL had no detectable effect on toxin assembly and periplasmic extracts contained little or no free B subunit.

Figure 2: Effect of mutation in K(R)DEL on toxin binding to ganglioside GM₁. The fluorescent toxin analogue, CT-fluorescein, was used as tracer as described in Materials and Methods. Binding isotherms for both wt and K(R)DEL mutant toxins were nearly identical and of equally high affinity (Kd=6 nM). Representative of two independent experiments in duplicate.

Thus, mutation in K(R)DEL affects a physiologic event in CT and LT to mutation in K(R)DEL strongly implies that both toxins require functional interaction with endogenous KDEL-receptors within Golgi cisternae or ER for efficient retrograde transport and maximum biologic activity.

**Effect of Cell Polarity on Signal Transduction by KDEL-Mutants**

When applied to basolateral instead of apical reservoirs, CT can bind to the cell at a site in close proximity to its target enzyme adenylate cyclase. Signal transduction from basolateral cell surfaces, however, also requires endocytosis and subsequent transport of CT through multiple compartments of the central vacuolar network (27, 45).

To examine whether signal transduction via basolateral receptors may also require sorting by K(R)DEL, it was necessary to first proteolytically nick (trypsin, 20 μg/ml) the exposed loop between the A₁- and A₂-peptides (residues 187–199) (35). The A subunits of the recombinant toxins are not nicked by endogenous proteases in E. coli as they are in V. cholerae (Fig. 1, Western blots). This has no effect on the time course of toxin action when applied to apical cell surfaces in the T84 cell system where both recombinant CT and LT are nicked by a protease(s) at the apical cell surface. Nicking, however, appears to be rate limiting when toxins are applied to basolateral membranes (unpublished data).

Signal transduction by toxin internalization via basolateral endosomes was also sensitive to mutation in the K(R)DEL sorting signal (Fig. 8). KDEL-mutants applied to either apical (A) or basolateral cell surfaces (B) elicited a secretory response more slowly than wild-type CT. Both the initial lag phase and rate of toxin induced Cl⁻ secretion were affected (KDEL-mutant vs. wt CT: lag phase, 53 ± 4 vs. 35 ± 7 min; dIsc/dt, 1.4 ± 1 vs. 2.5 ± 1.4 μA/cm²/min; peak Isc, 62 ± 25 vs. 80 ± 28 μA/cm², mean ± SD, n = 3 in duplicate, lower panel). These data confirm that mutation in K(R)DEL had no detectable effect on toxin assembly and periplasmic extracts contained little or no free B subunit.

Taken together, these data provide evidence that the K(R)DEL motif is not absolutely required for toxin action, but in its absence signal transduction is significantly less efficient. The clear sensitivity displayed by both CT and LT to mutation in K(R)DEL strongly implies that both toxins require functional interaction with endogenous KDEL-receptors within Golgi cisternae or ER for efficient retrograde transport and maximum biologic activity.

**Signal Transduction by KDEL-Mutant CT Displays Greater Sensitivity to Temperature**

We examined the temperature dependency of toxin induced Cl⁻ secretion. We reasoned that if the KDEL sorting signal facilitates a rate-limiting step in toxin action, KDEL-mutants should display greater sensitivity to temperature. Fig. 9 shows the time course of toxin action for KDEL-mutant (1 nM, open squares) and wild-type CT (1 nM, filled squares) at three different temperatures (37, 27, and 20°C). Lowering temperatures below 37°C reduced the rate of toxin induced Cl⁻ secretion for both wild-type and mutant toxins. Signal transduction by the KDEL-
mutant, however, was more strongly inhibited by reduced temperature. This is most apparent at 20°C (bottom), where the ability of the KDEL-mutant to elicit a secretory response was completely inhibited, while Cl− secretion induced by wt CT was clearly present. The viability of these monolayers was demonstrated by the brisk secretory response elicited by the administration of 3 nM vasoactive intestinal peptide to basolateral reservoirs at 480 min (marked with * in lower panel). This differential temperature dependency was not dependent on toxin concentration. Identical results were obtained when wt and mutant toxins were applied in fivefold higher concentrations (5 nM). Table II summarizes the results of seven independent experiments. These data provide additional kinetic evidence that specific interactions between CT and endogenous KDEL-receptors occur in human intestine and play a physiologic role in toxin action.

**Effect of KDEL-Mutation on Toxin Traffic: Endocytosis Is Unaffected but Transcytosis of the KDEL-Mutant Occurs More Slowly Than for Wild-type Toxin**

To show directly that mutation in K(R)DEL affects toxin trafficking, we examined the time course of endocytosis and transcytosis for both wt and KDEL-mutant toxins. The reduced efficiency in signal transduction by K(R)DEL-mutants may be attributable to an effect on toxin uptake by endocytosis. The data show, however, that mutation in K(R)DEL had no detectable effect on endocytosis (Fig. 10). Both wt and K(R)DEL-mutant toxins were internalized at nearly identical rates with apparent half-times of \( \approx 7.5 \) min \( (n = 4, \text{in triplicate or quadruplicate}) \).

The transcytotic movement of wt and KDEL-mutant toxins from apical to basolateral membrane was also examined. In polarized intestinal epithelia, CT must transduce a signal from its apical receptor (GM1) to its basolateral effector (adenylate cyclase). We have recently found that this transcellular signaling may require transcytosis of toxin-containing membranes (29). Transcytosis of KDEL-mutant or wt CT from apical to basolateral membranes was assessed directly by selective cell surface biotinylation. These experiments were carried out at 27°C to enhance the difference in time course between KDEL-mutant and wt CT-induced Cl− secretion.

**Figure 11 A** shows the representative results of one of three independent experiments. The upper panel shows a western blot to demonstrate that each lane contains equivalent amounts of immunoprecipitated CT B subunit. The

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**Table I. Effect of Mutation in K(R)DEL on Toxin Induced Cl− Secretion**

| Toxin | Lag phase min | dIsc/dt µA/cm²/min | Peak Isc µA/cm² |
|-------|---------------|---------------------|----------------|
| CT    |               |                     |                |
| KDEL-mutant | 35 ± 1*  | 1.2 ± 0.06* | 45 ± 4        |
| n = 8                         |            |                |
| Wild type                        | 27 ± 1   | 1.8 ± 0.1    | 47 ± 4        |
| n = 6                         |            |                |
| LT    |               |                     |                |
| RDEL-mutant | 53 ± 2*   | 0.62 ± 0.03* | 44 ± 4        |
| n = 7                         |            |                |
| Wild type                        | 43 ± 2   | 0.85 ± 0.03 | 52 ± 2        |
| n = 6                         |            |                |

Mean ± SE.

* K(R)DEL-mutant vs. wild-type toxin.

\( p = 0.0001 \) by ANOVA.
Figure 5. Effect of mutation in K(R)DEL on the dose dependency of toxin induced Cl⁻ secretion. Dose dependency of K(R)DEL-mutant (open squares) and wild-type (filled squares) LT (A) and CT (B). Representative of two to three independent experiments, mean ± SD for duplicate monolayers.

Figure 6. Effect of mutation in K(R)DEL on intracellular degradation. Wild-type (wt) and KDEL-mutant CT were applied to apical membranes of T84 cell monolayers and incubated at either 4°C (lanes 1 and 5) or 37°C for the indicated times. CT A subunits (lanes 1-4) or B subunits (lanes 5-8) were immunoprecipitated from total cell extracts (lysed in the presence of 10 mM N-ethylmaleimide) and analyzed by SDS-PAGE and western blot under non-reducing conditions.

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Figure 8. Effect of cell polarity on the time course of Cl secretion elicited by KDEL-mutant and wt CT. Time courses of toxin induced secretion are shown for KDEL-mutant and wt CT proteolytically nicked as described in Materials and Methods. Toxins were applied to either apical (top) or basolateral (bottom) cell surfaces. Signal transduction by KDEL-mutants were delayed from both cell surfaces. Identical results were obtained with RDEL-mutant and wt LT (data not shown). Representative of two independent experiments for both toxins, mean ± SD for duplicate monolayers.

Discussion

Evidence for Retrograde Transport of CT and LT into Golgi Cisternae and ER

The results in this paper show that the presence of a functional K(R)DEL sequence in CT and LT plays a role in facilitating toxin action in human T84 cells and thus implies a direct and specific interaction with endogenous KDEL-receptors during signal transduction. In the absence of a functional K(R)DEL sequence at the COOH terminus of the A2-peptide, both mutant CT and LT elicited a secretory response more slowly and with higher apparent activation energies than their wild-type counterparts. The interaction between toxin and KDEL-receptor was specific in that a single and conservative point mutation (replacing leucine with valine in the RDEL sequence of LT) affected toxin action. These results were not explained by indirect effects on toxin assembly, toxin binding, resistance to intracellular degradation, or ADP-ribosyltransferase activity. In contrast, we provide direct evidence that K(R)DEL effected toxin trafficking as assessed by movement through the basolaterally directed transcytotic pathway. The compartment(s) affected represent a common structure in the apical and basolateral endocytic pathways, as mutation in K(R)DEL inhibited signal transduction from both cell surfaces. These data provide strong evidence that CT and LT may require retrograde movement through the secretory pathway to elicit a maximal secretory response.

Two lines of evidence from the available literature support this view. First, CT (conjugated to horseradish peroxidase) has been visualized directly within trans-Golgi in neuroblastoma cells (23) and recently, purified CT B subunit (also conjugated to horseradish peroxidase) has been visualized within cis-Golgi in A431 epidermoid cells (56). These studies show directly that CT can traffic from the cell surface to trans-Golgi and retrograde into Golgi cisternae. Movement into these compartments appears to de-
Table II. Effect of Temperature on the Secretory Response Elicited by KDEL-mutant and Wild-type CT

| Temperature | n = 7 pairs | Lag phase | d isc/dt | Peak lsc | Ratio*Lag | Ratio* d isc/dt | Ratio peak lsc |
|-------------|-------------|-----------|----------|----------|-----------|----------------|---------------|
| 37°C        | mutant      | 44 ± 1    | 0.59 ± 0.04 | 50 ± 3  | 1.333 | 0.55 | 0.82 |
|             | wt          | 33 ± 1    | 1.1 ± 0.1  | 60 ± 5  | 1.633 | 0.51 | 0.74 |
| 27°C        | mutant      | 127 ± 9   | 0.19 ± 0.02 | 25 ± 2 | 0.21  | 0.51 | 0.74 |
|             | wt          | 83 ± 2    | 0.38 ± 0.05 | 34 ± 3 | 0.48  | 0.51 | 0.74 |
| 20°C        | mutant      | ≥410 ± 20 | <0.012 ± 0.004 | 2.5 ± 0.8 | 1.6  | 0.25 | 0.24 |
|             | wt          | 256 ± 11  | 0.48 ± 0.003 | 10.5 ± 0.6 | 1.6  | 0.25 | 0.24 |

Mean ± SE.

*KDEL-mutants are significantly more sensitive to temperature than wt CT. p = 0.001 by 2-factor ANOVA.

pend on toxin binding (or clustering) ganglioside GM1, as purified or recombinant CT B subunit will move into these compartments in the absence of sorting signals from the A subunit. These data fit nicely with our current findings that the K(R)DEL sequence is not absolutely required for toxin action, and with our concurrent observations (29) that trafficking of CT through a basolaterally directed transcytotic pathway also depends primarily on toxin-binding (or perhaps clustering) ganglioside GM1.

Second, the KDEL-receptor, the product of the mammalian ERD2 gene, has now been clearly localized at steady-state to Golgi cisternae and intermediate compartment with small amounts of receptor visualized in ER and trans-Golgi (16, 63). KDEL-receptors were not visualized at the cell surface or in more distal compartments of the secretory pathway. Furthermore, the preponderance of evidence establishes that KDEL-receptors mediate retrograde transport of other KDEL-containing proteins through Golgi cisternae to ER (42, 48, 62). Retrieval and recycling to ER occurs from multiple sites in the secretory pathway, including trans-Golgi (8, 20, 31, 37, 52). Thus, CT and LT would have multiple opportunities to interact with KDEL receptors as these toxins move retrograde in the secretory pathway via binding (or clustering) ganglioside GM1 (see below).

Components of the apical and basolateral endocytic pathways converge in late endosomes (2, 12, 18, 46) and almost certainly in the trans-Golgi, as vesicles exchange constitutively between these compartments (15 and references therein). Our demonstration, however, that the K(R)DEL sorting signal plays a physiologic role in toxin action indicates that both CT and LT move beyond the late endosome into compartments where interactions between toxin and KDEL-receptors may plausibly occur. Thus, these studies identify trans-Golgi, Golgi cisternae, and possibly ER as intermediary compartments through which CT may physiologically traffic to elicit an efficient secretory response. Since reduction and translocation of the A subunit also represent events that occur in shared (or similar) compartments of both the apical and basolateral endocytic pathways (27), it is tempting to speculate that A subunit translocation occurs in ER or possibly Golgi cisternae as previously hypothesized (50). If so, movement into these compartments would be facilitated by direct interaction between toxin and K(R)DEL-receptors. This prediction fits nicely with our experimental data and provides a cogent and biologically plausible explanation for conservation of the COOH-terminal K(R)DEL sorting signal in these two toxins. However, it remains possible that mutation in K(R)DEL may also affect membrane translocation of the A subunit by a mechanism separate from its effect on toxin trafficking.

Figure 10. Effect of mutation in K(R)DEL on toxin endocytosis. Time course of toxin endocytosis. (Top) wt CT (filled squares), KDEL-mutant (filled triangles), and wt CT purified from V. cholerae (open squares). (Bottom) wt LT (filled squares), RDEL-mutant (filled triangles). Both wild-type and K(R)DEL-mutant toxins display nearly identical rates of internalization with apparent half-times of ~7.5 min.

Biology of Glycosphingolipids and Targeting of CT/LT by Binding or Clustering Ganglioside GM1

Our current studies, together with those discussed above (23, 38, 56), show that both retrograde traffic into the secretory pathway and transcytosis across polarized cells (29) may plausibly depend on structural features of the toxin's endogenous receptor, ganglioside GM1. Glycosphin-
Here we provide evidence that identifies trans-Golgi, Golgi cisternae, and possibly ER as intermediary compartments through which CT may traffic. Available data indicate that this indirect route across T84 cells may be more complex than that taken by the apically directed polymeric immunoglobulin receptor (41) or by basolaterally targeted VSG proteins artificially inserted into apical membranes of MDCK cells (51). As such, we introduce the term “indirect transcytosis” to describe this process.

We can now tentatively assign anatomic identities to physiologic compartments previously defined only by functional criteria. For example, brefeldin A inhibits completely CT-induced signal transduction from both the apical and basolateral cell surface. Brefeldin A scrambles protein targeting and diverts the movement of CT away from a compartment necessary for reduction and translocation of the A subunit (27). The brefeldin block occurs early in the lag period and leads to accumulation of CT-B subunit in basolateral vesicles and a decrease in CT-B subunit appearing at the apical surface.

We have demonstrated previously that the KDEL motif is absolutely required for transcytosis (28, 29). The KDEL motif is found in members of the transmembrane protein family, including the transmembrane proteins of the putative lysosomal enzyme mannose 6-phosphate receptor, the asialoglycoprotein receptor, and the transferrin receptor (41). Thus, a KDEL signal appears to be required for transcytosis of CT or LT from basolateral to apical membranes. We found that the KDEL motif is not sufficient, however, to target CT or LT to the apical cell surface, since brefeldin A can block transcytosis even in the presence of a KDEL signal.

Thus, we propose a new model for the indirect transcytosis of CT or LT, whereby the toxins are targeted from basolateral to apical membranes via an endocytic route that involves the endosome compartment (27). We hypothesize that CT or LT enters the endosomal compartment through a combination of endocytosis and receptor-mediated endocytosis and then moves through the endosome compartment to reach the trans-Golgi network, where it can traffic back to the apical surface.

This model is consistent with our previous finding that the KDEL motif is not sufficient for transcytosis of CT or LT from basolateral to apical membranes. It also provides a plausible explanation for the observation that brefeldin A can block transcytosis even in the presence of a KDEL signal. Finally, this model offers a potential mechanism for the indirect transcytosis of CT or LT, which is the observed phenomenon in T84 cells and other polarized epithelial cells.

In conclusion, we have demonstrated that CT and LT are trafficked from basolateral to apical membranes via an endocytic route that involves the endosome compartment. Our findings support the idea that the KDEL motif is not sufficient for transcytosis of CT or LT from basolateral to apical membranes and that the toxins are targeted from basolateral to apical membranes via an endocytic route that involves the endosome compartment.
within Golgi cisternae or ER, the CT-GM₁ complex internalized from the basolateral cell surface can move retrograde into the secretory pathway and back out again to adenylate cyclase on the basolateral membrane by remaining associated with membrane receptors derived from (and presumably targeted to) the basolateral membrane.

In summary, these studies identify Golgi cisternae and ER as intermediary compartments through which CT may traffic to elicit an efficient and maximal physiologic response. The unique lipid and protein structure of these compartments (3) may provide a thermodynamically or kinetically favorable environment for translocation of the A subunit. The COOH-terminal K(R)DEL sorting signal facilitates toxin entry into the secretory pathway, but movement into Golgi cisternae and possibly even ER will occur (though not efficiently) in the absence of the K(R)DEL-sorting signal after toxin binding (or clustering) ganglioside GM₁. Thus CT, as a paradigm for vesicular transport, provides an example where protein targeting (and ultimately the pathogenesis of cholera in humans) depends on the combined effects of protein and lipid structure in small membrane microdomains (58, 68).

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Note Added in Proof. After our manuscript was submitted, the following paper was published: Cieplak, W., Jr., R. J., Messer, M. E. Konkel, and C. C. Grant. 1995. Mol. Microbiol. 16:789-800. They also constructed and characterized an RDE2 mutant of LT, but unlike the results in our study, concluded that K(R)DEL was not important for toxin trafficking.

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