Related Leucine-based Cytoplasmic Targeting Signals in Invariant Chain and Major Histocompatibility Complex Class II Molecules Control Endocytic Presentation of Distinct Determinants in a Single Protein

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Summary

Leucine-based signals in the cytoplasmic tail of invariant chain (Ii) control targeting of newly synthesized major histocompatibility complex class II molecules to the endocytic pathway for acquisition of antigenic peptides. Some protein determinants, however, do not require Ii for effective class II presentation, although endocytic processing is still necessary. Here we demonstrate that a dileucine-based signal in the cytoplasmic tail of the class II β chain is critical for this Ii-independent presentation. Elimination or mutation of this signal reduces the rate of re-entry of mature surface class II molecules into the endocytic pathway. Antigen presentation controlled by this signal does not require newly synthesized class II molecules and appears to involve determinants requiring only limited proteolysis for exposure, whereas the opposite is true for Ii-dependent determinants. This demonstrates that related leucine-based trafficking signals in Ii and class II control the functional presentation of protein determinants with distinct processing requirements, suggesting that the peptide binding sites of newly synthesized versus mature class II molecules are made available for antigen binding in distinct endocytic compartments under the control of these homologous cytoplasmic signals. This permits capture of protein fragments produced optimally under distinct conditions of pH and proteolytic activity.

Abbreviations used in this paper: BFA, brefeldin A; CLIP, class II–associated invariant chain peptide; HEL, hen egg lysozyme; Ii, invariant chain; MIIC, class II–rich organelles; RBL, rat basophil leukemia cell.
the class II α or β cytoplasmic tails selectively interferes with presentation of a hemagglutinin determinant whereas a matrix protein-derived determinant is instead dependent on Ii for presentation (31). These studies revealed a correlation between hemagglutinin presentation and the involvement of the class II cytoplasmic tails in entry of mature surface class II into the endocytic pathway. Similarly, Smiley et al. have demonstrated in a mouse model system that the cytoplasmic tails of class II molecules play a key role in the presentation of some antigenic determinants (32).

These various findings suggest that two distinct pathways for class II–dependent antigen presentation exist, and imply that separate protein localization signals in the cytoplasmic tails of Ii and class II play important roles in these events. The identity of the localization signal(s) in class II chains has not been established, although Smiley et al. have hypothesized that conserved dileucines in the class II β chain tail are likely to be involved (32). In addition, the role of such localization signals in class II has not been directly compared to that of Ii signals in presenting different antigenic determinants from a single protein molecule. Finally, little information is available on what predisposes presentation of different determinants within a given protein antigen to dependence on one or the other of these pathways. In the present study, we have used the well-characterized HEL antigenic model (33) to examine these issues. We demonstrate that the dileucine-containing sequence in the class II β chain noted by Smiley et al. (32) is critical for Ii-independent presentation of two HEL determinants, whereas a third determinant in the same protein requires the tail signals in Ii for its effective presentation. In combination with earlier observations, our data support a model of class II presentation involving (a) II-dependent capture of buried antigenic determinants in lysosome-related, highly proteolytic compartments by newly synthesized class II molecules and (b) β chain–tail dependent antigen capture of more superficial determinants in less proteolytic (early) endocytic organelles by mature, recycling class II. These two pathways together provide a mechanism for optimal presentation of the multiple determinants often contained in proteins entering the endocytic pathway.

**Materials and Methods**

Reagents. HEL (cat No. L6876, lot No. 89F8275), diethylamino-ethyl-dextran, chloroquine, and dimethyl sulfoxide were obtained from Sigma Chemical Co (St. Louis, MO). LPS was from DIFCO (3122-25-8; Detroit, MI), recombinant murine IFN-γ from PharMingen (San Diego, CA), brefeldin A (BFA) from Eugene Sciences (Gaithersburg, MD), leupeptin from Boehringer Mannheim (Indianapolis, IN), and G418 (Genetin) from Gibco (Gaithersburg, MD). The peptides HEL 46-61 (NTDGSTDYGILQINSR), HEL 34-45 (FESNFNTQATNR), and HEL 116-129 (KGTDVQAWIRGCRL) were synthesized and purified by HPLC before use by the National Institute of Allergy and Infectious Diseases Peptide Synthesis Facility (Rockville, MD).

Constructs. The cDNA constructs coding for the wild-type α or β chain of Aβ with an 18 amino acid deletion at the COOH-terminus was made by placing a stop codon after the codon encoding isoleucine 220, as described elsewhere (29). The construct was placed into the expression plasmid vector pCDL-SR (36), provided by Dr. J. Boniface (National Institute of Child Health and Development, National Institutes of Health). The β chain with this COOH-terminal 18 amino acid deletion is designated as βCT18. A construct coding for a β chain with the cytoplasmic leucines at positions 236 and 237 each changed to alanine was made by oligonucleotide-directed mutagenesis using PCR, and cloned into the pCDL-SR vector. The 5′ primer was 5′ GTG AGA GCT CTA GGA GAT GCC ATC TCA GTC AGC TGC CCC TGC TGG AGG AGG GGC ACG AGG TCC 3′; mutagenesis was performed as described (37). The resultant mutant β chain was designated as βCTAA. The sequences of all constructs were confirmed as correct using an automated DNA sequencer.

**Stable Transfectants.** Cos 7.2 cells were transiently transfected with DNA of the cDNA constructs coding for the α and β chain with the COOH-terminal 18 amino acid (3 μg each) or together with DNA for the cDNA constructs coding for murine Ii31 (10 μg), using a diethylamino-ethyl-dextran method as previously reported (38). Stable transfectants were selected by electroporation with DNA of the cDNA constructs coding for the following combinations: α/β, α/βCT18, and α/βCTAA, with or without DNA for the construct encoding mlI31, using a modified protocol from Engel et al. (36). 18 μg of DNA encoding each chain of class II and 2 μg of pfneo (39) were used for each electroporation. In the case of Ii cotransfection, an additional 5 μg of DNA encoding Ii was added. Transfected cells expressing the desired proteins were cloned by limiting dilution.

**FACS® Staining.** The Aβ expression level on transfectants was measured by staining the surface using a saturating amount of FITC-conjugated goat anti–rat IgG (Jackson Laboratory, Bar Harbor, ME) to detect the bound H116.32 antibody (40) on ice for 30 min. A FITC-conjugated rabbit anti-mouse IgG (Jackson Laboratory, Bar Harbor, ME) was used to detect the bound I116.32. Li expression by the transfectants was measured by intracellular staining with IN-1 (41) and an FITC-conjugated goat anti-rat IgG (Jackson Laboratory). The fluorescence intensity was measured on a FACScan® flow cytometer (Becton-Dickinson, Mountain View, CA). Transfectants with comparable levels of surface class II and intracellular Ii in appropriate combinations were chosen for use in functional experiments.

Antigen Presentation Using B Cells and MΦs as APCs. Single cell suspensions from the spleens of CBA mice (Jackson Laboratory; 8–10 wk old, female) were made and red blood cells were removed using ammonium chloride-potassium lysing buffer (Biofluids Inc., Rockville, MD). The splenocytes were cultured for 2 d in the presence of 10 μg/ml LPS in RPMI 1640 medium containing 10% FCS. The B cell blasts were then harvested and used as APCs. For MΦ preparation, CBA mice were injected intraperitoneally with 4 ml thioglycollate (National Institutes of Health Medical Staff, Bethesda, MD) and 4 d later, the exudate MΦs were harvested by washing the peritoneal cavity with ice-cold PBS. The exudate cells were incubated in the wells of 96-well plates for 2 d in complete RPMI 1640 medium containing 20 U/ml of murine IFN-γ. The IFN-γ activated MΦs (IFN-γ MΦs) were then used without harvesting as APCs. In the antigen presentation assay, the B cell blast or MΦ APCs were pulsed with various concentrations of intact HEL antigen for 6 h, and then fixed with 1% paraformaldehyde for 20 min followed by neutralization with 0.1 M glycine.
The fixed APCs pulsed with antigen \((5 \times 10^4 \text{ cells/well})\) were mixed with antigen-specific T cell hybridomas \((5 \times 10^4 \text{ cells/well})\) in a total volume of 200 \(\mu\)l in complete RPMI medium containing 2-ME. The cultures were incubated for 18–24 h and IL-2 production in the supernatant was measured by ELISA. The hybridoma 3A9.1 specific for HEL epitope 46-61 was from Dr. Paul Allen (Washington University, St. Louis, M.D.), and hybridomas 3B11.1 and 1B9.1 specific for HEL 34-45 and 116-129 respectively were provided by Dr. L. Adorini (Roche Milano Ricerche, Milan, Italy). For inhibition of antigen presentation, APCs were pretreated with various concentrations of BFA for 15 min, chloroquine for 30 min, or leupeptin for 2 h before HEL was added. All APCs were then pulsed with 50 \(\mu\)M of HEL for 6 h in the continued presence of inhibitor before fixation and addition to T cells. Presentation of peptide was also assessed in parallel by adding the indicated concentration of peptide to the cells for the same 6-h period before washing and fixing.

**Results**

The presentation of three distinct peptide determinants within HEL required endocytic processing for presentation, but only 46-61 requires newly synthesized proteins. B lymphoblasts were incubated with the indicated concentrations of HEL in standard medium for 6 h or with 50 \(\mu\)M HEL for 6 h in the presence of the indicated concentrations of drug. The B cells were then fixed and used as APCs with T hybridomas specific for each determinant. IL-2 production at 24 h is presented as OD obtained using an IL-2-specific capture ELISA. The data represent one of three independent experiments.

Figure 1. The 34-45, 46-61, and 116-129 determinants in HEL all require endocytic processing for presentation, but only 46-61 requires newly synthesized proteins. B lymphoblasts were incubated with the indicated concentrations of HEL in standard medium for 6 h or with 50 \(\mu\)M HEL for 6 h in the presence of the indicated concentrations of drug. The B cells were then fixed and used as APCs with T hybridomas specific for each determinant. IL-2 production at 24 h is presented as OD obtained using an IL-2-specific capture ELISA. The data represent one of three independent experiments.

To evaluate internalization of surface class II, a modified version of the procedure described by Roche et al. (43) was used. Cells were grown on coverslips, washed twice with cold, complete DMEM, and reacted with saturating amounts of 10-2.16 antibody for 2 h on ice to ensure monovalent binding. Cells were then washed extensively to remove unbound antibody. Washed cells were either left at 4°C or warmed to 37°C for various periods of time extending up to 150 min. After the appropriate time interval, the cells were fixed with 10% paraformaldehyde for 10 min at room temperature, permeabilized with 0.2% saponin for 30 min, and then blocked with 2% BSA at 4°C overnight. Samples were then washed with PBS and stained using rabbit anti-mouse IgG antibodies conjugated with FITC (Jackson Laboratory). To exclude the possibility that class II-independent uptake of antibody into endocytic structures, untransfected RBLs were treated in the same manner. Coverslips bearing stained cells were mounted and analyzed using a confocal microscope (MRC1024; Bio Rad Labs, Hercules, CA).
alone efficiently present 34-45 and 116-129, but not 46-61. Cotransfection with li dramatically increases the presentation of 46-61 (Fig. 2 A), but has little effect on presentation of 34-45 and 116-129 (Fig. 2, B and C). Again, these data are consistent with studies using rat-2 transfectants and the differential requirement for protein export from the secretory pathway for presentation of the three determinants.

Role of the Cytoplasmic Tails of A αk and A βk in Presentation of the Three HEL Fragments. In certain cells, leucine-based targeting signals in the li cytoplasmic tail are important for the endocytic accumulation of newly synthesized class II molecules (4–9). However, this is not true in all cells, and the localization of class II to late endocytic structures has been observed in several cell expressing class II without li (26–28). Pinet et al. have reported that presentation of a hemagglutinin determinant by DR is independent of li, but requires uncharacterized internalization signals in the cytoplasmic tails of the class II α and β chains (31). Smiley et al. (32) have also shown a role for class II cytoplasmic tails in antigen presentation and suggested that a dileucine-based motif in the β chain may be involved in this function. To assess whether signals in the cytoplasmic tails of the A αk molecule itself are involved in the presentation of 34-45 or 116-129, RBLs were stably transfected with constructs expressing various combinations of wild-type A αk or A βk tail deletion mutants with or without li, and clones with comparable levels of surface class II and intracellular li selected. As with COS and rat-2 cells, efficient presentation of 46-61, but not 34-45 and 116-129, by wild-type A αk expressed by RBLs depends on li (Fig. 3). Although cells expressing wild-type A αk alone can effectively stimulate 34-45- and 116-129-specific T cells after HEL exposure, truncation of the β chain tail prevents this presentation. Examination of presentation of the three determinants by cells with the β tail deleted A αk coexpressed with li revealed that each determinant has a distinctive combination of requirements for either li or the β chain tail. The 46-61 and 34-45 determinants are both presented well by cells expressing I-A αk with a truncated β chain tail together with li, but li expression does not rescue the ability of β tail deleted class II molecules to present 116-129. Therefore, the efficient presentation of 46-61 requires li irrespective of the presence or absence of the class II β chain tail, presentation of 34-45 requires either intact class II tail or li and the class II β tail is required for the presentation of 116-129 and this function cannot be replaced by li. Similar data were obtained using transiently transfected COS cells (data not shown).

The Dileucine Region Within the Cytoplasmic Tail of the Class II β Chain Is Required for Effective Ii-independent Antigen Presentation. In discussing their evidence that the class II β chain tail contributes to effective antigen presentation, Smiley et al. have noted the existence of a conserved dileu-
Table 1. Leucine-Based Motif in the Class II β Chain Cytoplasmic Tail

| Species/protein | Cytoplasmic tail sequence |
|-----------------|---------------------------|
| Human DR        | RNQKGSGLQPTGQLR           |
| Human DQ        | RSKGPQGPPAPAGLQ           |
| Chimpanzee      | RNQKGSGLQPTGQLR           |
| Mouse I-A       | RSKGPQGPPAPAGLQ           |
| Mouse I-E       | RNQGGSGLQPTGQLR           |
| Rat I-A         | R-KQGPQGPPAPAGLQ          |
| Rat I-E         | RSKGNSGLQPTGQLR           |
| Dog DR          | RNQGHSGLQPTGQLR           |
| Chicken         | RGQKRPVAAAPGQLR           |
| Mouse I-A       | RSQKGPRGPPAPAGLQ          |
| Mouse II        | RSCREPERPNLQ-LQEHNSLDRQDDM|

Alignment of the sequences in the cytoplasmic tails of MHC class II β chains of various species (63), and of mouse class II Aβ and mouse Ii. For Ii, the sequence is shown C→N from left to right because this is a type II membrane protein shown in its proper orientation relative to the membrane and the adjacent class II sequence. The double-headed arrow points to an invariant glycine residue that precedes the conserved leucine-containing pair of amino acids.

Cytosine in this segment of the protein, and suggested that it may be part of a targeting motif (32). We have independently compared the sequences of multiple class II β chains from various species, looking for highly conserved sequences and also for sequences resembling either the known leucine- or tyrosine-containing signals mediating endocytic protein targeting. As shown in Table 1, like Smiley et al., we identified the same conserved dileucine near the COOH terminus of the β chain, preceded by an invariant glycine, giving rise to the sequence GLL that closely resembles one of the two localization signals in Ii (GLI in the mouse). This sequence in class II is also spaced only one residue further from the end of the transmembrane domain as compared to the comparable Ii sequence; previous studies have shown that the distance of a signal from the membrane can play an important role in its traffic control function (46). To test directly whether these dileucines are a critical part of a functional targeting motif in the class II tail, a mutant cDNA was prepared that encodes a complete Aβ chain except for substitution of the two cytoplasmic leucines with alanines (βCTAA). This construct was stably transfected into RBLs along with plasmids encoding wild-type Aα chains, with or without the construct for Ii. The ability of the transfected cells to present the three HEL determinants was compared to the wild-type Aα transfectants (Fig. 4). Like deletion of the entire β chain tail, substitution of the two leucines with alanine prevents the presentation of 34-45 and 116-129 in cells lacking Ii, and Ii coexpression with class II containing βCTAA can rescue presentation of 34-45 but not 116-129.

Replacement of the β C chain cytoplasmic Leuines with Alanines Delays, but does Not Prevent, Aα Internalization into Endosomes. Based on the results of Pinet et al. showing that deletion of either the class II α or β tails precluded internalization of surface DR (31), we expected that the βCTAA-containing Aα molecules would fail to accumulate in the endocytic pathway, thus accounting for the lack of effective presentation of the 34-45 determinant in the absence of Ii. However, confocal immunofluorescence microscopy unexpectedly revealed the steady state localization of class II in a variety of endocytic structures, including lamp 1+ compartments, in cells expressing mutant molecules with either the β tail deletion or βCTAA (data not shown). This suggested that either a recycling model for presentation of these determinants was incorrect, or that the loss of presenting function due to these mutations resulted from a more subtle change in the trafficking of class II than revealed by such staining studies. We therefore examined the entry of mature surface class II molecules into endosomes using surface-bound antibody as a probe. Cells expressing wild-type Aα with or without Ii rapidly internalize a substantial fraction of antibody-bound surface class II; within 5 to 10 min of warming to 37°C, distinct staining of small vesicles is observed and accumulation of signal in larger vesicular structures is readily apparent by 15 to 30 min (Fig. 5).
In contrast, cells expressing A\textsubscript{\textkappa} containing either the tail-deleted or double alanine mutant \textbeta chain show little evidence of internalized class II at 10 min and only modest staining of very small vesicles at 30 min. Cells expressing class II molecules lacking both the \textbeta and \textalpha chain cytoplasmic regions show no detectable intracellular class II accumulation using this method at up to 150 min of incubation (data not shown), suggesting that the residual internalization seen with the \textbeta\textCTAA–wild-type \textalpha combination may depend on a separate, as yet uncharacterized, signal in the \textalpha chain tail.

Differential Presentation of 34-45 and 116-129 Versus 46-61 by Macrophages and B Cell Blasts, and Their Relationship to Proteolytic Activity. The 34-45, 46-61, and 116-129 determinants of HEL lie in very different locations in the folded structure of the intact HEL protein, with 116-129 being most superficial, 34-45 being partially buried, and 46-61 lying at the core of the protein in a structure maintained by disulfide bonds. Presentation of the 46-61 determinant of HEL requires the reducing environment found in lysosomes (44, 45) and this correlates with where newly synthesized class II–Ii complexes accumulate before Ii digestion and CLIP removal (10, 47–51). On the other hand, the inability of Ii to rescue presentation of 116-129 in cells expressing tail-mutated class II suggests that this determinant may not be available in such highly acidic, dense, endocytic organelles. In this regard, Frosch et al. have reported that IFN-\textgamma–activated macrophages fail to present a particular insulin determinant (52), although B cells from the same mouse are fully competent to do so. This difference appears to be related to the more rapid and complete digestion of insulin by the M\Phi, which prevents effective capture by class II. Given the different locations of the three HEL determinants in the native protein, one might expect that 116-129 and perhaps 34-45, but not 46-61, to be overdigested in activated macrophages, as compared to the B cell blasts used in the studies shown in Fig. 1. As shown in Fig. 6, this is the case. IFN-\textgamma–activated macrophages are quite effective in presenting the 46-61 determinant, but inefficient in presenting either the 34-45 or 116-129 determinants. If chloroquine or leupeptin is added to HEL-exposed macrophages before fixation, there is a paradoxical dose-dependent gain in presentation of the 34-45 and 116-129 determinants, but a decline in the presentation of 46-61.

Discussion

The various organelles comprising the endosomal/lysosomal pathway have distinct pHs, protease contents, and capacities to promote protein unfolding (53). These properties and the rate of luminal content transfer among these organelles also vary for cells of distinct tissue origin or state of activation. These differences all affect the function of the class II antigen presentation system by influencing the availability of specific sequences within any given protein for binding to MHC class II molecules in the same compartment. Likewise, heterogeneity in protein structure and binding site occupancy also modify the capacity of class II molecules to capture protein/peptide substrates in these organelles. In part, ensuring the presentation of diverse antigenic ligands is promoted by the simultaneous expression of multiple class II proteins in the cells of a single individual. However, because the different proteins of pathogens may vary from those that are highly sensitive to protease attack to some requiring extremely harsh conditions for digestion, it also makes sense that the immune system would evolve the means to enable these polymorphic class II proteins to sample several endocytic organelles for suitable li-
The data presented in this paper suggest that two different cohorts of MHC class II molecules sample endocytic content in an overlapping pattern that permits ligand capture from both early and late endocytic compartments. The control of protein trafficking necessary for the operation of these two presentation pathways lies in related cytoplasmic leucine-based signals, one of which is characterized in this study. However, it is the timing of binding site availability that appears to actually distinguish where class II molecules in each pathway most effectively acquire antigen.

Previous studies have shown that leucine-based motifs within the cytoplasmic tail of II are essential for effective localization of newly synthesized class II–II complexes to late endocytic/lysosomal organelles (7–9). These leucine-containing signals are similar to others found in proteins such as the TCR CD3γ and δ chains (54) and GLUT4 (55) that also promote trafficking of the respective proteins to endocytic organelles. II proteolysis and removal is minimal during passage through early endosomes, modest in late endosomes, and extensive in a lysosome-like fraction (10) that corresponds to the MIIC defined by immunoelectron microscopy (6). Class II molecules cannot bind a new ligand until II is degraded and CLIP is removed or dissociated from the class II binding site, in large part through the action of DM that is concentrated in the MIIC by a distinct tyrosine-containing motif (56). Therefore, II-associated, newly synthesized class II molecules are most likely to participate primarily in the presentation of determinants surviving until, or first exposed in, this highly proteolytic, acidic environment. In accord with this, the 46-61 determinant of HEL, which is located in the core of this globular protein and protected by disulfide bonds, shows a strong dependence on II for its presentation. This agrees with studies indicating that the best presentation of this determinant occurs when lysosome-like organelles with strong reducing capacity are accessed by HEL (44, 45) and showing that this peptide has lysosome-like organelles with strong reducing capacity are accessed by HEL (44, 45) and showing that this peptide has

In contrast, two other determinants within the same HEL molecule, at residues 34-45 and 116-129, show a very different behavior. Neither is well presented by activated macrophages, and partial inhibition of protease activity improves presentation of these determinants in such macrophages, but not in less proteolytically active B cell blasts. Inhibition of the trafficking of newly synthesized proteins had at best modest effects on the presentation of these determinants and neither required II for their presentation. Taken together, these data argue that both of these determinants are available to a cohort of class II molecules distinct from that associated with II. Because control experiments showed that endocytic processing was involved, these data suggested that exposure and capture of these regions of HEL occurs in early endocytic compartments and involves mature class II molecules. This in turn led to an attempt to understand how a surface pool of mature class II molecules could gain access to such endocytic organelles. Sequence alignment revealed a highly conserved GLL motif in the tail of class II β chains, which, when deleted or altered to GAA, resulted in class II molecules unable to present the 34-45 or 116-129 determinants in the absence of II. The variable effect of mutation at these leucines on presentation of distinct antigenic determinants is consistent with the earlier suggestion by Smiley et al. (32) that a signal containing these residues could play a role in differential antigen presentation by tailless versus wild-type class II molecules.

The steady state distribution of class II in transfectants with wild-type or signal-minus class II molecules did not differ grossly. Internalization experiments, however, revealed a clear effect of the mutations, namely a significant delay in the rate of internalization of surface class II into the endocytic pathway. Previous results have shown that class II binding sites lose their function rapidly at physiological temperature in the absence of ligand engagement (3, 58, 59). If the major pool of class II sites involved in acquisition of determinants such as HEL 116-129 become empty on the cell surface before internalization, delayed uptake would result in such molecules becoming incapable of peptide binding by the time they reached the site of antigen availability. Alternatively, the class II molecules involved in HEL 116-129 presentation may only shed their original peptide upon exposure to the mildly acidic pH of early endosomes, whereupon they would be immediately available to bind new ligand. Substantially decreasing the pool of such molecules reaching the endocytic pathway at any point in time could then markedly reduce antigen presentation. Both of these effects may in fact contribute to the functional defect observed with the mutant class II chains lacking the GLL motif. This model also can account for the recent findings of Smiley et al. (60), who demonstrated an increased density of CLIP-class II complexes on cells expressing class II molecules with a β chain whose cytoplasmic tail had been truncated. Because CLIP release is facilitated at acidic pH (61), decreased internalization due to the β mutation would allow such complexes to accumulate to a higher level on the plasma membrane, rather than dissociating upon internalization and recycling. The decrease we observed in class II internalization rate without a loss of steady-state localization in endocytic organelles following mutation of a dileucine signal is also very similar to results obtained in studies of the GLUT4 glucose transporter (55).

The timing of binding site availability appears to play a predominant role in dictating which set of determinants is presented by which cohort of class II molecules. The binding sites of II-associated class II become available mainly in the MIIC via the action of cathepsins and DM, and this biases these dimers for capture of those determinants able to survive transport through earlier endocytic compartments. These same class II molecules are ineffective in the capture of determinants present only in early endosomes because they do not have an accessible binding site in that location. Conversely, mature class II molecules, using a very homologous targeting signal to traffic to the same or a similar set of early and late endocytic organelles, primarily bind those ligands available in early endocytic compartments because the binding site is accessible there. Some determinants such as 34-45 appear to be available in more than one location, permitting capture by class II via either pathway.
The added breadth of determinants presented to CD4+ T cells through use of a recycling pathway has obvious advantages for the immune system. Viruses enter cells by fusing with or disrupting either plasma or early endosomal membranes. The relevant viral proteins often undergo structural changes and remain in these membranes when the viral genome enters the cytosol (62). Such refolded proteins may be highly susceptible to proteolysis shortly after viral entry, and the presentation of determinants derived from these proteins would help elicit a T cell response at the earliest time after viral infection. Data consistent with this suggestion come from the work of Pinet et al. (31), who showed that a determinant from influenza hemagglutinin was presented in an Ii-independent, class II tail-dependent manner. Another rationale besides sensitivity to proteolysis for such a pathway is the capture of ligands unable to bind tightly to class II at the highly acidic pH of the MII C.

The results presented here, together with the recent study of Pinet et al. (31) help rationalize a contradictory literature concerning the role of newly synthesized versus mature class II molecules and of Ii in class II presentation to T cells. They also emphasize the important differences in processing and presentation of the same protein by different cell types, as evidenced by the inability of activated macrophages to present 34-45 or 116-129 without addition of an inhibitor of lysosomal function. The demonstration that cytoplasmic signals in the class II b chain tail control the rate of class II entry into the endocytic pathway for capture of only a subset of antigenic determinants provides an explanation for earlier reports of a variable influence of class II tail deletion on antigen presentation (29, 30). Our evidence that a leucine-based motif is involved in this endocytic targeting emphasizes the importance of this motif in immunological function, especially as concerns T cell antigen recognition. On the other hand, the rather modest effect of elimination of the class II tail motif on in vivo immunity to a range of pathogens (32) raises some question as to the physiologic significance of this Ii-independent pathway. However, the organisms studied in this report were primarily those resident in the endocytic compartment itself, and not viruses, for which we argue the recycling pathway may have a special importance. It is also the case that the studies conducted here have not been performed in typical hematopoietic antigen presenting cells. This clearly leaves to future studies a fuller determination of the roles of the two class II pathways defined here in the protective functions of the immune system.

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