

# Distinct Intracellular Fates of Membrane and Secretory Immunoglobulin Heavy Chains in a Pre-B Cell Line

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**Abstract.** The intracellular fates of membrane and secretory immunoglobulin heavy chains were examined in a pre-B cell line that has switched to the  $\gamma$  isotype. The membrane form of the heavy chain ( $\gamma_m$ ) was rapidly degraded while the secretory form ( $\gamma_s$ ) was retained intracellularly in association with BiP. The degradation of  $\gamma_m$  could not be inhibited by ammonium chloride, chloroquine, or monensin suggesting that it occurred in a nonlysosomal compartment. The inability to detect any Endo H-resistant form of  $\gamma_m$  before its degradation suggested that degradation occurs be-

fore entry into the Golgi compartment. Degradation of  $\gamma_m$  could be inhibited by incubation at 24°C. In a derivative of this cell line expressing a transfected  $\kappa$  gene,  $\gamma_s$  formed disulfide linked tetramers with  $\kappa$  and was secreted, while  $\gamma_m$ , although associated with  $\kappa$ , continued to be rapidly degraded. These observations suggest that membrane and secretory heavy chain proteins are retained by distinct intracellular mechanisms. Although masking of the CHI domain abrogates  $\gamma_s$  retention, this domain does not influence the intracellular fate of  $\gamma_m$ .

THE transport of cell surface as well as secretory proteins depends on proper folding and the complete assembly of oligomers (Kreis and Lodish, 1986; Gething et al., 1986; Hurlley and Helnius 1989). Misfolded proteins and incomplete oligomers are retained intracellularly; although retention signals have been identified for some proteins, the mechanisms involved in the process of retention remain poorly understood.

The expression of membrane and secretory immunoglobulins is regulated during B cell ontogeny not only at the levels of transcription and posttranscriptional processing but also at the level of intracellular transport. These proteins offer a unique opportunity for the analysis of the signals and mechanisms that influence the retention and transport of nonanchored secretory proteins in comparison with their membrane-anchored counterparts.

Two retention signals have been identified in incompletely assembled secretory immunoglobulins. One of these signals is the CHI domain of all immunoglobulin heavy chains, which unless masked by association with a light chain leads to retention. These retained heavy chains are associated with the immunoglobulin heavy chain binding protein (BiP; GRP 78) (Morrison and Scharff, 1976; Haas and Wabl, 1983; Munro and Pelham, 1986). BiP is an ER protein that is itself retained within the ER by virtue of a KDEL sequence at its carboxyl terminus (Pelham 1988) and presumably binds the CHI domain of immunoglobulin heavy chains (Bole et al., 1986; Hendershot et al., 1987; Hendershot, 1990). In cells that lack light chains, deletions in the CHI domain lead to secretion of the heavy chain  $\gamma$  isotype. In the case of secre-

tory  $\mu$  and  $\alpha$  heavy chains however, in addition to the CHI retention signal, a second retention signal is present in the cysteine containing tailpiece in the CH4 domain.  $\mu_s$  molecules in which the CHI domain has been deleted are still retained intracellularly and bind BiP (Sitia et al., 1990). If, in these truncated  $\mu_s$  molecules, the cysteine residue in the tailpiece is mutated, both mechanisms of retention are now lost and the truncated  $\mu_s$  no longer binds BiP and is secreted. In virgin B cells  $\mu_s$ 2L2 tetramers are retained intracellularly via the exposed cysteine containing tailpiece. Later in differentiation, the process of IgM polymerization masks the tailpiece retention region and pentameric IgM is secreted.

The signals for retention present on membrane immunoglobulins are less well defined, although in the case of membrane IgM recent studies have suggested that one such signal may reside in a polar serine and threonine rich stretch in the  $\mu_m$  transmembrane domain (Williams et al., 1990). Another possible retention signal on membrane immunoglobulin heavy chains is the CHI domain, which is the absence of being masked by a light chain may function in a manner similar to the identical region on secretory heavy chains. Indeed it is generally assumed that the CHI domain plays as important a role in the retention of membrane heavy chains as it does in the retention of their secretory counterparts.

We wished to examine the nature of the retention signals in membrane and secretory heavy chain immunoglobulins by comparing the fate of immunoglobulins that have a similar retention motif (an exposed CHI region) in their extracellular domains and differ only in the presence or absence of membrane anchors. We studied the biosynthesis and fate of

these proteins in 18-81A2 (Burrows et al., 1983), a pre-B Abelson cell line that has switched to the  $\gamma$  isotype and which does not synthesize either the conventional  $\kappa$  or  $\lambda$  or the surrogate  $\omega$  light chain proteins. We show here that  $\gamma_m$  in this cell line is rapidly degraded, while  $\gamma_s$  (which lacks the CH4 tailpiece found in  $\mu_s$ ) is retained intracellularly bound to BiP, presumably through the CH1 domain. In a transfectant expressing a relative excess of  $\kappa$  light chain protein,  $\gamma_s 2\kappa 2$  tetramers are efficiently secreted; although  $\gamma_m$  can associate with  $\kappa$  it is nonetheless rapidly degraded. The specific degradation of  $\gamma_m$  is temperature sensitive and is not inhibited by lysosomotropic agents; this protein does not acquire resistance to Endo H before degradation, suggesting that proteolysis occurs in a pre-Golgi compartment. The rapid degradation of membrane as opposed to secretory immunoglobulins suggests that signals besides the CH1 domain may determine the fate of incomplete membrane immunoglobulin oligomers; this degradatory process may itself function as a retention mechanism. The role of putative  $\gamma$  isotype specific associated proteins, hydrophilicity of the transmembrane domain and the mechanisms involved in membrane immunoglobulin transport at the pre-B to B cell transition are discussed.

## Materials and Methods

### Reagents

Endo- $\beta$ -*N*-acetylglucosaminidase H (Endo H) was obtained from New England Nuclear (Boston, MA); PMSF, methionine, chloroquine, and monensin were obtained from Sigma Chemical Co. (St. Louis, MO); protein A-Sepharose was obtained from Pharmacia Inc. (Piscataway, NJ); anti- $\kappa$  Sepharose was from Zymed Laboratories Inc. (South San Francisco, CA); and Brefeldin A was a gift from Sandoz Ltd. (Basel, Switzerland).

### Cells

18-81A2 is a cell line that was isolated as a derivative of an AMuLV transformed pre-B cell line that underwent an isotopic switch of the heavy chain from  $\mu$  to  $\gamma_{2b}$  but has an unrearranged  $\kappa$  locus (Burrows et al., 1983). 18-81A2 $\kappa 2$  is a derivative of 18-81A2 that expresses a transfected  $\kappa$  light chain gene (Rice and Baltimore, 1983).

### Metabolic Labeling and Immunoprecipitation

Cells were metabolically pulse labeled and chased as described previously (Pillai and Baltimore, 1987b). 0.5% Triton X-100 in reticulocyte saline buffer (RSB; 10 mM Tris pH 7.5, 3 mM MgCl<sub>2</sub>, 10 mM NaCl) containing 2 mM PMSF was used as the lysis buffer. Lysates were immunoprecipitated by mixing overnight with 180  $\mu$ l of a 3% slurry of protein A-Sepharose. Samples were analyzed by electrophoresis on 9% polyacrylamide-sodium dodecyl sulfate gels.

### Metabolic Labeling in the Presence of Inhibitors

In experiments where the effects of different inhibitors were investigated, the inhibitors were added 60 min before the labeling period (during methionine starvation) and were present during the labeling and chase periods.

### Endo H Treatment

Washed protein A-Sepharose beads were boiled in 30  $\mu$ l of 100 mM sodium citrate buffer, pH 5.5, containing 0.4% SDS for 5 min, diluted twofold with water, centrifuged, and the supernatant divided into two aliquots. To one aliquot 75 ng of Endo H was added while the other aliquot served as a control. Both tubes were incubated at 37°C for 16 h.

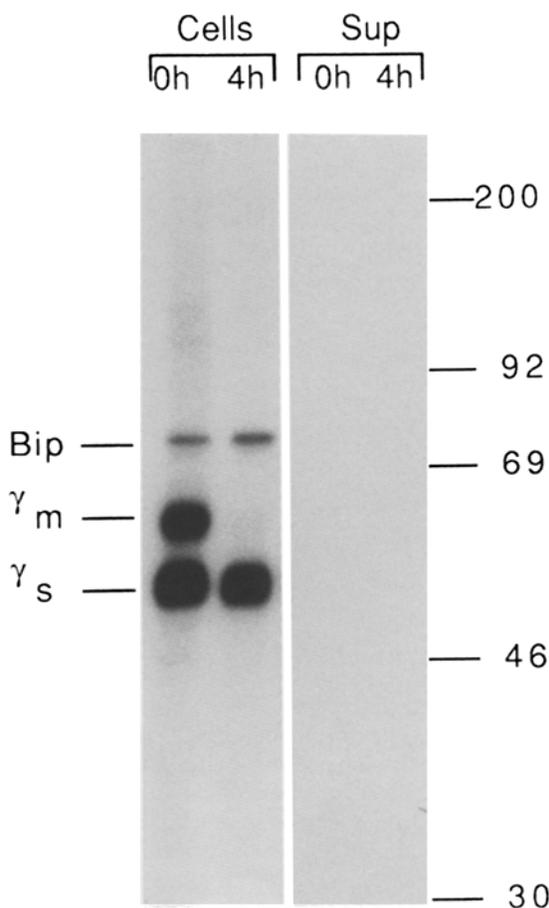
## Surface Iodination

Live cells were iodinated as described previously (Pillai and Baltimore, 1987b).

## Results

### Rapid Turnover of $\gamma_m$ , but Not $\gamma_s$ , in 18-81A2 Cells

Although  $\gamma_m$  and  $\gamma_s$  were synthesized in almost equal amounts in 18-81A2 cells,  $\gamma_m$  underwent rapid intracellular degradation and was barely detectable after 4 h of chase (Fig. 1). In contrast  $\gamma_s$  was retained intracellularly and exhibited a relatively long half-life. The coprecipitation of BiP with  $\gamma_s$  (and BiP being known to be an ER protein) suggested that  $\gamma_s$  was retained in the ER. The  $\gamma_s$  protein was not detectable in the cell supernatants, presumably due to its inability to form functional oligomers in the absence of light chain, and its consequent retention in association with BiP.



**Figure 1.** Fate of  $\gamma_m$  and  $\gamma_s$  in 18-81A2 cells. Cells were metabolically labeled, chased, and immunoprecipitated as described in the text. Samples were analyzed on a 9% polyacrylamide-sodium dodecyl sulfate gel. *Sup* refers to cell supernatants. *0h* and *4h* refer to chase times in hours after the labeling period. Position of molecular mass markers (in kilodaltons; Rainbow markers; Amersham Corp., Arlington Heights, IL) are indicated on the right.

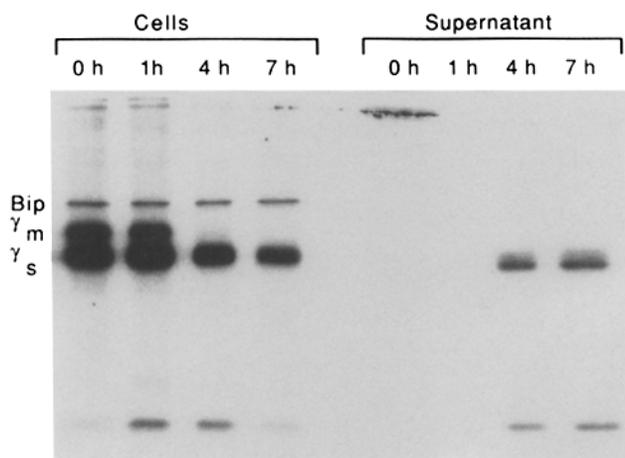


Figure 2. Fate of  $\gamma_m$  and  $\gamma_s$  in 18-81A2 $\kappa$ 2 cells. See legend to Fig. 1 and text for details.

### Intracellular Fate of $\gamma_m$ and $\gamma_s$ in 18-81A2 $\kappa$ 2 Cells

The 18-81A2 $\kappa$ 2 transfectant cell line expresses a rearranged  $\kappa$ -light chain gene which associates with the endogenous  $\gamma$  heavy chain (Rice and Baltimore, 1983). Anti- $\kappa$ -Sepharose precipitated both  $\gamma_m$  and  $\gamma_s$  in this cell line (data not shown) confirming that a functional  $\kappa$  light chain was being made.

An examination of the fate of  $\gamma_m$  and  $\gamma_s$  in 18-81A2 $\kappa$ 2 revealed that while  $\gamma_m$  was degraded at virtually the same rate as in the parent cell line,  $\gamma_s$ , in association with  $\kappa$ , formed disulfide linked tetramers that were secreted (Fig. 2). Cell surface iodination studies on 18-81A2 $\kappa$ 2 failed to reveal any  $\gamma_m$  on the surface of these cells (data not shown).

### The Effect of Inhibitors of Lysosomal Function on $\gamma_m$ Degradation

To understand the nature of the  $\gamma_m$  degradation pathway we studied the effect of different inhibitors on the degradation of  $\gamma_m$ .  $\text{NH}_4\text{Cl}$  and chloroquine are lysosomotropic agents that interfere with lysosomal activity by raising the pH of these organelles (Poole and Ohkuma, 1981). These drugs did not lead to any detectable inhibition of  $\gamma_m$  degradation (Fig. 3). Monensin is a carboxylic ionophore that is known to interfere with ER to Golgi compartment and primarily intra-Golgi transport (Tartakoff, 1983). Concentrations of monensin that significantly inhibited secretion of  $\gamma_s$  in 18-81A2 cells, did not lead to significant inhibition of degradation of  $\gamma_m$  in either 18-81A2 or 18-81A2 $\kappa$ 2 (Fig. 3). These experiments suggested that  $\gamma_m$  degradation was non-lysosomal and probably occurred before entry into the Golgi compartment either in the ER or in a post-ER, pre-Golgi compartment.

### Endo H Sensitivity of $\gamma_m$ and $\gamma_s$

To examine whether  $\gamma_m$  degradation occurred after passage through the Golgi compartment, we investigated the Endo H sensitivity of  $\gamma_m$ . Proteins in the ER which have high mannose residues are sensitive to Endo H, an enzyme that cleaves the chitobiose core (Tarentino and Maley, 1974). In proteins that have reached the Golgi compartment, peripheral mannose residues are trimmed and an *N*-acetylglucosamine moiety is added in the medial Golgi stack which renders these proteins resistant to Endo H. When we examined the sensitivity of  $\gamma_m$  and  $\gamma_s$  to Endo H in 18-81A2 cells, both of the proteins were sensitive to Endo H (Fig. 4). The  $\gamma_s$  protein continued to remain Endo H sensitive with time and the

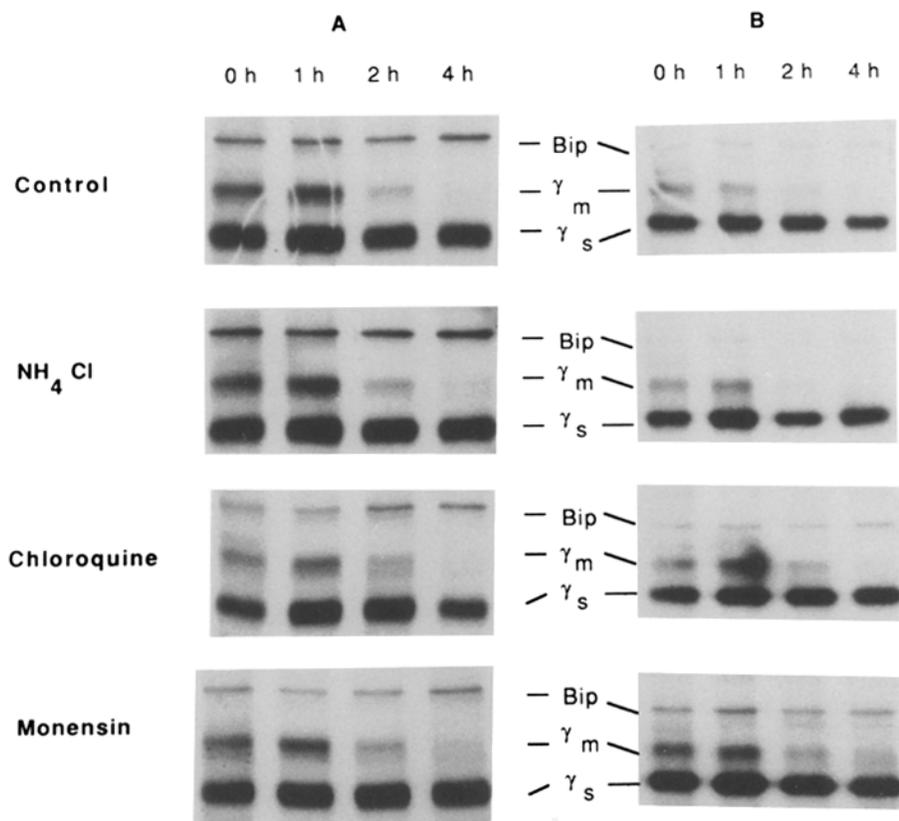
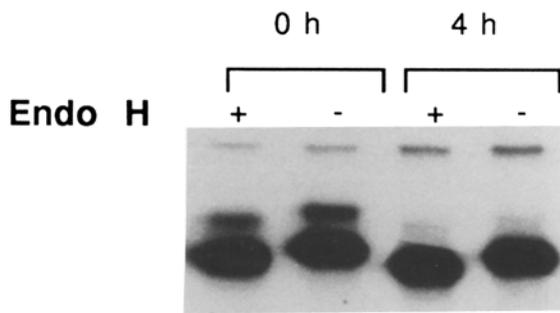


Figure 3. Effect on drugs on the degradation of  $\gamma_m$ . 18-81A2 and 18-81A2 $\kappa$ 2 cells were starved, metabolically labeled, and chased as described in the text in medium containing either  $\text{NH}_4\text{Cl}$  (50 mM), Chloroquine (100  $\mu\text{M}$ ) or monensin (7  $\mu\text{g/ml}$ ). Control cells received no drugs. Cells were processed and analyzed as described in legend to Fig. 1. (A) 18-81A2; (B) 18-81A2 $\kappa$ 2.



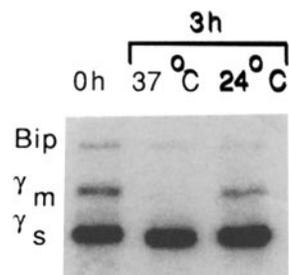
**Figure 4.** Endo H sensitivity of  $\gamma_m$  and  $\gamma_s$  in 18-81A2 cells. 18-81A2 cells were metabolically labeled and chased for 4 h in medium containing excess unlabeled methionine. Immunoprecipitates were treated (+) with Endo H as described in the text and analyzed in parallel with mock-treated (-) samples as described in the legend to Fig. 1.

residual  $\gamma_m$  that could be detected by overexposure of the autoradiograms revealed that this protein remains Endo H sensitive (Fig. 4). This suggests that the degradation of  $\gamma_m$  occurs before its entry into the Golgi.

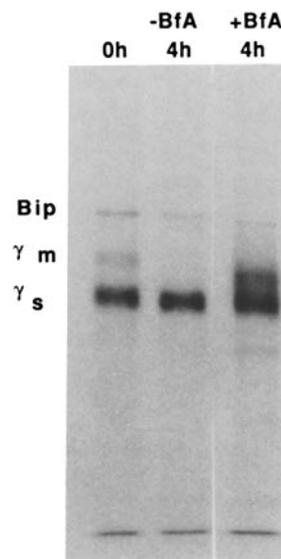
#### Effect of Temperature and Brefeldin A on $\gamma_m$ Degradation

Intracellular processes that are dependant on membrane fusion have been shown to be temperature dependent (Hough and Rechsteiner, 1984). Temperatures below 16°C block movement of proteins out of the ER, while temperatures below 20°C inhibit movement from the *trans*-Golgi to the cell surface (Saraste et al., 1986). We examined the effect of temperature on  $\gamma_m$  degradation. 18-81A2 cells were pulse-labeled at 37°C and chased at different temperatures. Degradation of  $\gamma_m$  was almost totally inhibited even at 24°C (Fig. 5), a temperature at which exit from the ER is not inhibited. This suggests that  $\gamma_m$  degradation is extremely sensitive to temperature, an observation made previously for other proteins that are rapidly degraded in the ER (Lippincott-Schwartz et al., 1988; Amara et al., 1989; Koppelman and Cresswell, 1990).

Brefeldin A, a fatty acid derivative that inhibits protein secretion, blocks ER to Golgi transport (Takatsuki and Tamura, 1985; Misumi et al., 1986), without inhibiting retrograde transport and fusion of the Golgi with the ER (Lippincott-Schwartz et al., 1989; Doms et al., 1989; Orci et al. 1991). In our experiments, Brefeldin A partially inhibited  $\gamma_m$  degradation (Fig. 6). The acquisition of Endo H resistance by both  $\gamma_m$  and  $\gamma_s$  (data not shown) suggests that the ER compartment was drastically altered in its biochemical



**Figure 5.** Effect of temperature on  $\gamma_m$  degradation. Cells were metabolically labeled for 15 min at 37°C and chased in excess cold methionine at either 37 or 24°C. Samples were analyzed as described in the legend to Fig. 1.



**Figure 6.** Effect of Brefeldin A on  $\gamma_m$  degradation. Cells were metabolically labeled for 15 min at 37°C and chased in medium containing excess unlabeled methionine with or without Brefeldin A (10  $\mu$ g/ml).

properties during the process of fusion with the Golgi. These biochemical alterations could account for the inhibition of the process of  $\gamma_m$  degradation.

#### Discussion

We have described the rapid and specific pre-Golgi degradation of  $\gamma_m$  but not  $\gamma_s$  in a pre-B cell line. The fate of  $\gamma_m$  could not be altered by association with a light chain suggesting that the presence of an exposed CH1 domain has little effect on the fate of membrane immunoglobulin heavy chains. In contrast,  $\gamma_s$ , which was intracellularly retained in association with BiP, had a dramatically different fate when allowed to associate with light chains and was secreted as  $\gamma_s 2\kappa 2$  tetramers. This also indicated that in contrast to earlier suggestions (Sitia et al., 1987) early B lineage cells are competent for immunoglobulin secretion although they might lack the capacity to polymerize IgM.

Rapid degradation in a pre-Golgi compartment has been described in some detail in the case of the T cell receptor (TCR)<sup>1</sup>- $\alpha$  chain expressed alone in transfected non lymphoid cell lines, or in T cell hybridomas which lack associated TCR proteins (Lippincott-Schwartz et al., 1988). Similar findings have been described for the TCR- $\beta$  and TCR- $\delta$  chains (Chen et al., 1988) as well as for a few other proteins (Amara et al., 1989; Koppelman and Cresswell, 1990; Klausner and Sitia, 1990). In all cases degradation occurred rapidly after a brief lag phase, and was sensitive to temperature.

Recent studies on the TCR- $\alpha$  chain have localized the targeting signal to a 9-amino acid stretch in the transmembrane domain (Bonifacino et al., 1990a). Two charged amino acids within this 9-amino acid stretch appear to be the major determinants for this process as mutating these residues to hydrophobic amino acids leads to protection from degradation (Bonifacino et al., 1990b). In the case of the asialoglycoprotein H2a subunit however, the signal for degradation was found to reside in a 5-amino acid stretch of the extracellular

1. Abbreviation used in this paper: TCR, T cell receptor.

domain just adjacent to the transmembrane domain (Lederkremer and Lodish, 1991). The  $\gamma$ m protein differs from  $\gamma$ s in having a short additional extracellular stretch, a transmembrane domain and a cytoplasmic tail. The signals for the degradation of  $\gamma$ m should therefore reside within this region which is encoded by the two membrane exons.

The signals for rapid degradation of the TCR- $\alpha$  chain colocalize with transmembrane segments that play a role in the process of assembly with the other subunits of the T cell receptor complex (Bonifacino et al., 1990). Since assembly with the other subunits protects TCR- $\alpha$  from degradation (Bonifacino et al., 1989, 1990; Wileman et al., 1990) it is possible that the transmembrane domain of membrane immunoglobulins (which contain polar amino acids but no charged residues) may serve as a signal for degradation as well as for assembly with associated proteins. It is interesting to note in this context that mutating a hydrophilic pentapeptide stretch in the  $\mu$ m transmembrane domain to a more hydrophobic segment resulted in the ability of  $\mu$ m to reach the cell surface (Williams et al., 1990) along with light chains in nonlymphoid cells (which lack B29 and mb-1). Transport of  $\mu$ m-light chain tetramers occurs only in B cells in association with the B29 and mb-1 proteins. The hydrophilic TTAST stretch in  $\mu$ m may be viewed as a retention signal which might be masked by the products of the mb-1 and B29 genes. The same sequence may act as a signal for both assembly with the associated proteins and as a signal for degradation in the absence of assembly.

Considerable progress has been made in identifying proteins associated with membrane immunoglobulins that are essential for their transport to the cell surface. These include the IgM( $\alpha$ ) protein which is the product of the mb-1 gene (Hombach et al., 1988a, b; Sakaguchi et al., 1988) and the Ig( $\beta$ ) protein which is the product of the B29 gene (Hombach et al., 1990b; Hermanson et al., 1988). A number of additional proteins have been demonstrated to be associated with  $\mu$ m in pre-B (Pillai and Baltimore, 1988; Takemori et al., 1990) and in B cells (Hombach et al., 1990; Wienands et al., 1990). One of these, the product of the mb-1 gene, is essential for the surface transport of  $\mu$ m in mature B cells. Associated proteins specific for the  $\delta$ m isotype have also been demonstrated (Wienands et al., 1990; Chen et al., 1990) and the existence of other isotype specific proteins (which may be relevant to the expression of these immunoglobulins on the cell surface) has been postulated (Wienands et al., 1990). Although the mb-1 and B29 genes are expressed from the earliest stages of B cell ontogeny, genes for other isotype specific proteins remain to be cloned and it is unclear if the expression of the proteins they encode is developmentally regulated.

A key event at the pre-B to B cell transition is the acquisition of the ability to transport  $\mu$ m to the cell surface. Transport of  $\mu$ m to the cell surface does not depend upon association with a conventional  $\kappa$  or  $\lambda$  light chain; in a subset of pre-B cell lines  $\mu$ m can be transported to the cell surface in the absence of  $\kappa$  or  $\lambda$  light chains (Paige et al., 1981; Findley et al., 1981; Gordon et al., 1983; Hendershot and Levitt, 1984; Hardy et al., 1986). In these cell lines and in transitional B cells in the bone marrow (which synthesize both surrogate and conventional light chains), the heavy surrogate light chain complex is transported to the cell surface (Pillai and Baltimore, 1987a, 1988; Kerr et al., 1989; Cherayil and

Pillai, 1991). The molecular basis for the acquisition of the ability to transport  $\mu$ m to the cell surface at the pre-B to B cell transition is unlikely to be the activation of the mb-1 or the mb-1 like B29 gene, since both these genes are expressed in all pre-B and B cells including cells in the process of rearranging their H-chain loci (Sakaguchi et al., 1987; Hermanson et al., 1988). The transport of  $\mu$ m to the cell surface at the pre-B to B cell transition has also been correlated with the posttranslational acquisition of hydrophobicity by the  $\mu$ m polypeptide (Pillai and Baltimore, 1987b). The inability of 18-81A2 $\kappa$ 2 cells to transport  $\gamma$ m to the cell surface even as they secrete  $\gamma$ s may therefore either reflect their lack of some (possibly  $\gamma$  isotype specific) associated protein or else the lack of some other posttranslational modification that would protect this membrane immunoglobulin heavy chain from degradation.

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