The Propeptide of Preprosomatostatin Mediates Intracellular Transport and Secretion of α-Globin from Mammalian Cells

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Abstract. We have investigated the role of the somatostatin propeptide in mediating intracellular transport and sorting to the regulated secretory pathway. Using a retroviral expression vector, two fusion proteins were expressed in rat pituitary (GH3) cells: a control protein consisting of the β-lactamase signal peptide fused to chimpanzee α-globin (142 amino acids); and a chimera of the somatostatin signal peptide and proregion (82 amino acids) fused to α-globin. Control globin was translocated into the endoplasmic reticulum as determined by accurate cleavage of its signal peptide; however, α-globin was not secreted but was rapidly and quantitatively degraded intracellularly with a t1/2 of 4-5 min. Globin degradation was insensitive to chloroquine, a drug which inhibits lysosomal proteases, but was inhibited at 16°C suggesting proteolysis occurred during transport to the cis-Golgi apparatus. In contrast to the control globin, ~30% of the somatostatin propeptide-globin fusion protein was transported to the distal elements of the Golgi apparatus where it was endoproteolytically processed. Processing of the chimera occurred in an acidic intracellular compartment since cleavage was inhibited by 25 μM chloroquine. 60% of the transported chimera was cleaved at the Arg-Lys processing site in native prosomatostatin yielding "mature" α-globin. Most significantly, ~50% of processed α-globin was sorted to the regulated pathway and secreted in response to 8-Br-cAMP. We conclude that the somatostatin propeptide mediated transport of α-globin from the endoplasmic reticulum to the trans-Golgi network by protecting molecules from degradation and in addition, facilitated packaging of α-globin into vesicles whose secretion was stimulated by cAMP.

Most neuropeptides and small peptide hormones are synthesized as part of larger inactive polypeptide precursors in which the hormone sequence is flanked by pairs of basic amino acids (9). To generate a bioactive molecule, the precursors undergo one or several posttranslational modifications including glycosylation, proteolysis, phosphorylation, amidation, and acetylation (9). These processing events occur in different organelles during intracellular transport and therefore peptide hormone precursors are useful models to study movement through the secretory pathway. Recent observations demonstrate that several sorting and processing events occur in the distal elements of the Golgi apparatus/trans-Golgi network (TGN) and in maturing secretory granules (12, 29, 30, 44). In particular, endoproteolytic cleavage at paired basic residues is initiated in acidic, clathrin-coated vesicles which bud from the TGN and the resulting mature hormone is stored in secretory granules (30, 31, 44).

Peptide hormone–producing cells characteristically concentrate and store their secretory product in electron-dense secretory granules (32). Upon stimulation by an extracellular signal, these granules fuse, through a calcium-dependent process, with the plasma membrane releasing their contents into the external milieu. This type of secretion is designated "regulated" or "stimulated" (see references 4, 14, and 33 for recent reviews). Hormone-secreting cells also undergo basal or "constitutive" secretion whereby nonhormone secretory proteins and plasma membrane proteins are neither concentrated nor stored and are transported in vesicles which continuously fuse with the plasma membrane in a calcium-independent manner (4, 14). Since hormone-secreting cells undergo basal secretion, a mechanism must exist that discriminates between molecules destined for the regulated or constitutive pathways.

The molecular signals that target a polypeptide hormone to the regulated secretory pathway are poorly understood, although morphological evidence has implicated selective aggregation or precipitation, initiated in the TGN, in the sorting process (44). Current evidence suggests that in the absence of a specific topogenic signal, e.g., for retention in the ER (27, 34) or Golgi apparatus (19) or for sorting to lysosomes (16), secretion through the constitutive pathway oc-
curs by default (14, 36). Expression of heterologous precursors in different endocrine cell lines results in proteolytic cleavage to the mature hormone and, in some cases, targeting to the regulated secretory pathway; e.g., preproinsulin (26), preprolysing (5), preproenkephalin (43), preprorenin (10), preproneuropeptide Y (8), and preprosomatostatin (39, 41). Since this diverse group of proteins, which lack amino acid sequence homology, can be sorted to the regulated secretory pathway, it is likely that a common structural feature rather than a primary sequence is involved in targeting. However, the identity of putative sorting signals has been elusive.

We are studying the processing of anglerfish prosomatostatin (proSRIF) in order to identify structural domains within peptide hormone precursors which might function in targeting to the regulated secretory pathway (41, 46). Somatostatin is a 14–amino acid peptide hormone that is synthesized as part of a larger precursor, preproSRIF (13); it consists of a 25–amino acid signal peptide followed by a proregion of 82 residues. The mature hormone is located at the carboxyl terminus of the propeptide and is preceded by a single pair of basic amino acids: ArgLys. These residues are a subset of a hexapeptide domain (AlaProArgGluArgLys) which is conserved in all proSRIF species. Apart from endoproteolytic cleavage, the precursor undergoes no other posttranslational modifications.

We recently demonstrated (41) that growth hormone–producing cells (GH3) efficiently cleave proSRIF and sort the mature hormone into the regulated secretory pathway. We previously postulated that the SRIF propeptide might function in mediating intracellular transport (46). To test this hypothesis directly, we used a retroviral vector, pLJ (15), to express a fusion protein (PRO-GLO) consisting of the SRIF signal peptide and proregion and chimpanzee a-globin in pituitary GH3 cells. The a-globin polypeptide was chosen as a reporter group for these studies since (a) it is a cytoplasmic protein and is unlikely to possess intrinsic sorting information; (b) previous work demonstrated that attachment of a bacterial signal peptide to the NH2 terminus of a-globin resulted in its translocation into the ER in vitro and in vivo (17, 40); and (c) expression of an ovalbumin signal peptide–a-globin fusion protein in Xenopus oocytes led to efficient segregation of a-globin into the ER but not to its secretion (42). Here we show that a signal peptide–globin fusion protein (SIG–GLO) was translocated into the ER in vivo, but in the absence of the SRIF propeptide it was rapidly degraded with a half-life of 4–5 min. In contrast, PRO–GLO was transported from the ER to the TGN where it underwent proteolytic cleavage yielding mature a-globin which was secreted into the medium.

Materials and Methods

Materials

The following plasmids were used: pLJ, a recombinant retrovirus expression vector (15), a gift of Dr. R. Mulligan, The Whitehead Institute, Boston, MA; pSP125E encoding the b-lactamase signal peptide–a-globin (SIG–GLO), a gift of Dr. V. R. Linappa, University of California, San Francisco, CA; and pLaSI (13), containing a 462-bp cDNA encoding anglerfish preproSRIF I to which 5' and 3' Eco RI–Bam HI linkers were added (41). Rabbit anti-human hemoglobin antiserum was purchased from Cappel Laboratories (Cocranville, PA).

Construction of Recombinant Virus Encoding SIG–GLO and PRO–GLO

Standard recombinant DNA procedures (21) were followed to generate the hybrid molecules.  

pLJSIG–GLO Construction. A Bam HI fragment encoding the b-lactamase signal peptide–a-globin (SIG–GLO) was generated from pSP125E by the addition of Bam HI linkers at a blunt-ended Bgl II site; this fragment was ligated directly into the Bam HI site of pLJ to generate pLJSIG–GLO.

pLJPRO–GLO Construction. pLaSI was digested with Eco RI to generate a 462-bp fragment encoding preproSRIF (41, 46). This fragment was ligated into the Eco RI site of a pBR322 derivative in which all four Nae I sites were deleted by digestion with Nae I and Bal I generating plasmid pDWS18 (Fig. 1A). Plasmid pSP125E was digested with Nco I, filled-in using the Klenow fragment of DNA polymerase I, 12-mer Bam HI linkers were added, and following digestion with Bam HI and blunt-ending with Klenow, the DNA fragment encoding a-globin was ligated into pDWS18 which was partially digested with Nae I. This generated a hybrid gene encoding the preproSRIF signal peptide and proregion in frame with a-globin at the 3' end; four amino acids (AlaAspProArg) were introduced (double lines) by this construction. Plasmid pPRO–GLO was digested with Bam HI and the appropriate DNA fragment ligated into the unique Bam HI site of pLJ to generate pLJPRO–GLO.

Production of Recombinant Retrovirus Expressing a-Globin-related Molecules

Plasmid DNAs were amplified in Escherichia coli strain MC1000, grown in the presence of 40 #g/ml of kanamycin and plasmid DNA prepared. Infectious virus particles containing globin-related RNA transcripts were generated by transfecting Psi-2 cells (22) with plasmid DNA.

Cell Culture

Cells were grown at 37°C in an atmosphere of 7.5% CO2. GH3 cells were grown in Ham's F10 medium supplemented with 15% equine serum, 2.5% fetal bovine serum (41). Psi-2 cells were grown in DME supplemented with 10% fetal bovine serum, 2 mM glutamine, 25 U/ml penicillin, and 25 mg/ml streptomycin.

Infection of Target GH3 Cells

Medium from semiconfluent G418 resistant Psi-2 cells was filtered (41) and a dish with 106 GH3 cells was incubated for 2 h with 1 ml of the filtrate containing 10 #g/ml of polybrene. The cells were incubated with complete Ham's F10 containing 1 mg/ml G418 as previously described (41). Single G418 resistant cells were subcultured by limiting dilution in a 96-well plate and 10 clonal lines were grown to mass culture.

Biosynthetic Labeling of Cells

60-mm dishes were seeded with 2 × 105 cells, 24–72 h later the cells were washed with PBS and pulse-labeled with 1 ml of labeling medium supplemented with 2 #Ci/ml [35S]methionine exactly as previously described (41). For chase incubations, the medium also contained 10 #l/ml of actinomycin (41). After the labeling and chase periods, the medium was removed, centrifuged, and stored on ice or at -20°C until further treated. Cells were harvested (41), the suspension centrifuged, and the pellet lysed by vortexing in lysis buffer. Nuclei were removed by centrifugation (41) and the postnuclear supernatants were stored on ice or at -20°C until treated with antisera.

Immunoprecipitation

To determine the intracellular levels of globin-related polypeptides, postnuclear supernatants were adjusted to 1% SDS and incubated at room temperature for 10 min. 10 #l of buffer A (41) were added followed by addition of 10 #l of rabbit anti-human hemoglobin antiserum. Samples were incubated at 4°C for 12–24 h with constant mixing (41). To assay for secreted polypeptides, the medium was adjusted to buffer A conditions by addition of 1/3 vol of a 4x buffer A solution. Samples were centrifuged at 4°C for 12–24 h followed by incubation with protein A-Sepharose at 4°C for 3 h (41). Immune complexes were isolated by centrifugation, washed twice with buffer B containing 1 mg/ml BSA (41), twice with PBS,
Automated Microsequencing of
and used immediately or stored at -20°C until analyzed by HPLC or
Globin-related Products

Automated Edman degradation was performed using a Beckman Instru-
ments Inc. (Fullerton, CA) 890C spinning cup sequencer (41). GH3 cells
ments in the medium or cells treated
with antihemoglobin antisera as outlined above. The protein A-Sepharose
beads were incubated with 50 µl of 2 M acetic acid and 8 M urea for 30 min
at 50°C. The supernatant was removed and the pellet washed twice with 50
µl of the same solution. A SEPPAK (Waters Associates, Inc., Milford, MA)
was prepared by washing with 5 ml of 80% CH3CN in 0.1% trifluoroacetic
acid (TFA) followed by 5 ml of 0.1% TFA. To maximize binding, the com-
bined supernatants were loaded on the SEPPAK three times which was then
washed with 5 ml of 0.1% TFA. Bound material was eluted by three washes
with 1 ml of 60% CH3CN in 0.1% TFA and three washes with 1 ml of 80%
CH3CN in 0.1% TFA. 25 µl of each fraction was counted. The first two
60% CH3CN washes containing 90% of the radioactivity were combined
and loaded directly into the sequencer.

Results

Expression of Globin-related Proteins in GH3 Cells

To test the hypothesis that the SRIF propeptide mediates intra-
acellular transport, we expressed two chimeric proteins in
GH3 cells: PRO-GLO, a fusion of the SRIF preproregion
and chimpanzee α-globin; and a control precursor, SIG-
GLO, consisting of the β-lactamase signal peptide fused to
α-globin (Fig. 1 B). The rationale for these experiments was
to determine if the propeptide could facilitate transport of a
normally cytoplasmic protein through the secretory pathway.
In addition, our aim was to determine if PRO-GLO would
be proteolytically processed at the proSRIF ArgLys process-
ing site and if the resulting globin polypeptide would be tar-
gested to the regulated or constitutive secretory pathway.

The starting cDNAs for these constructions were plasmids
pSP125E encoding the β-lactamase signal peptide fused
to chimpanzee α-globin (40), and pDWS18 which contained
anglerfish preproSRIF I cDNA (13) cloned into the Eco RI
site of a pBR322 derivative in which all four Nae I sites were
deleted (Fig. 1). After digestion, the appropriate DNA frag-
ments were ligated into the BamHI site of the retroviral ex-
pression vector pLJ (15) and were designated pLJSIG-GLO
and pLJPRO-GLO, respectively. Plasmid pLJSIG-GLO en-
coded the β-lactamase signal peptide (26 amino acids) fused
to α-globin (40). Plasmid pLJPRO-GLO encoded the pre-
proSRIF I signal peptide, 82 residue proregion, the first
amino acid of mature SRIF (Ala), three residues (AspPro-
Arg) resulting from the cloning and the complete chimpan-
zee α-globin chain sequence (Fig. 1, PreproSRIF-GLO).
We used the expression vector pLJ since the recombinant
virions can infect rat pituitary GH3 cells and these cells effi-
ciently cleave native proSRIF to the mature hormone (41).

Generation of Stable GH3 Cell Lines Expressing
Globin-related Proteins

Psi-2 cells were transfected with pLJSIG-GLO and pLJPRO-
GLO DNAs and grown in the presence of G418; subsequent
virus production and target cell (GH3) infection were ex-
actly as previously described (41). 10 G418 resistant clonal
lines expressing SIG-GLO (GH3SIG-GLO) and PRO-GLO
(GH3PRO-GLO) were generated and one clonal line ex-
pressing each chimera was selected for analysis. GH3SIG-
GLO.9 and GH3PRO-GLO.9 cells were pulse-labeled for
15 min with [35S]methionine and chased in complete media
for times up to 2 h. The cells and medium were treated with
anti-human hemoglobin antiserum and the immune com-
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**Figure 2.** Expression of SIG-GLO and PRO-GLO in GH3 cells. PRO-GLO expression: GH3PRO-GLO cells were pulse labeled for 15 min with [35S]methionine and chased for the indicated times. Cells and medium were treated with antihemoglobin antisera and immune complexes resolved by SDS-PAGE on 12% gels. Lanes 1-5, intracellular material; lanes 6-10, secreted products. Lanes 1 and 6, 15-min pulse; lanes 2 and 7, 15-min chase; lanes 3 and 8, 30-min chase; lanes 4 and 9, 60-min chase; lanes 5 and 10, 120-min chase. (Top arrow) Migration of in vitro synthesized proSRIF-α-globin (Mr 25,000); (middle arrow) migration position of globin endoproteolytically excised from PRO-GLO. SIG-GLO expression: GH3SIG-GLO cells were pulse labeled for 15 min with [35S]methionine and chased for 30 and 60 min. Cells and medium treated as in PRO-GLO expression. (Lanes 11-13) Intracellular material; (lanes 14-16) secreted material. (Lanes 11 and 14) 15-min pulse; (lanes 12 and 15) 30-min chase; (lanes 13 and 16) 60-min chase. (Bottom arrow) Migration of mature α-globin.

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**Figure 3.** Effect of chloroquine on SIG-GLO turnover. GH3SIG-GLO cells were pulse labeled for 15 min with [35S]methionine in the absence or presence of the indicated concentrations of chloroquine and chased for 60 min in the absence and presence of chloroquine. At each time point, the cell lysates and medium were treated with antihemoglobin antisera and immune complexes resolved by SDS-PAGE. (Lanes 1 and 5) No chloroquine; (lanes 2 and 6) 50 μM chloroquine; (lanes 3 and 7) 100 μM chloroquine; (lanes 4 and 8) 150 μM chloroquine. (Fig. 3), a weak base that neutralizes the intralysosomal acidic pH, thereby inactivating lysosomal hydrolases (23, 28). At each chloroquine concentration (up to 150 μM), α-globin was degraded intracellularly and globin secretion was not observed (data not shown). This result suggested that the rapid turnover of the α-globin molecules was not dependent on or occurring in an acidic compartment. The intracellular half-life of SIG-GLO was then determined by pulse-labeling GH3SIG-GLO cells with [35S]methionine for 15 min and chasing for times up to 40 min; at each time point cells were lysed and the globin–immunoreactive products analyzed by SDS-PAGE (Fig. 4). By 5 min of chase, >60% of α-globin had disappeared and by 40 min of chase globin was undetectable in the lysate; at no time point was globin detected in the medium. However, when cells were chased for 40 min at 16°C to prevent exit from the ER, 80–90% of the pulse-labeled α-globin was still present intracellularly. Based on the rapid kinetics of the α-globin disappearance, the temperature sensitivity, and the chloroquine data, it seemed unlikely that globin was transported to lysosomes for degradation.

The preceding data confirmed that a signal peptide was sufficient to effect translocation of globin into the ER in vivo but not for globin secretion. To determine if a propeptide could mediate secretion, GH3PRO-GLO cells were pulse-labeled for 15 min with [35S]methionine and chased for up to 2 h (Fig. 2). During the 15-min pulse, a prominent globin–immunoreactive polypeptide migrating with the predicted molecular weight for PRO-GLO lacking a signal peptide (Mr 25,000) was detected intracellularly (Fig. 2, lane 1, top arrow). A second intracellular, globin-specific polypeptide (Mr 15,000) was detected between 15 and 30 min of chase (middle arrow; Fig. 2, lanes 2 and 3). The appearance of this
molecule, which had an electrophoretic mobility slightly slower than authentic α-globin (Fig. 2, bottom arrow), was consistent with PRO-GLO being proteolytically processed at the single ArgLys site in proSRIF generating "mature" α-globin: α-globin with four additional NH₂-terminal amino acids (see Fig. 1). Cleavage following the ArgLys was subsequently confirmed by partial NH₂-terminal sequencing (see below and Fig. 6). With prolonged chase times, the level of M₅₂₀₀₀ globin increased with a concomitant reduction of the PRO-GLO polypeptide (Fig. 2, lanes 2-5) suggesting a precursor product relationship. Some unprocessed M₅₂₀₀₀ PRO-GLO was rapidly secreted (Fig. 2, lanes 7-10) but most significantly, processed mature M₁₅₀₀₀ globin was also secreted into the medium (Fig. 2, lanes 8-10, and Fig. 5).

PRO-GLO processing efficiency and the kinetics of α-globin secretion were determined by excising globin-specific polypeptides from gels similar to that shown in Fig. 2 and determining the radioactivity (Fig. 5). With increasing chase times, PRO-GLO decreased with a concomitant increase in the level of intracellular mature α-globin (Fig. 5 A) which remained constant from 90 to 180 min of chase. Processing of PRO-GLO to mature globin was detected between 15-30 min of chase and some α-globin was secreted into the medium following a lag of ~30 min (Fig. 5 B). It is noteworthy that in these cells, the kinetics of PRO-GLO cleavage to α-globin were identical to those of native proSRIF processing to the mature hormone (41), suggesting that the chimera and native precursors were transported through the same intracellular compartments at similar rates. About 30% of the total pulse-labeled globin-immunoreactive material could be recovered intracellularly and in the medium at 120 min of chase. We presume that the initially synthesized PRO-GLO which was not recovered after 15 min of chase was degraded intracellularly in the same compartment as SIG-GLO. Since PRO-GLO contains three methionine residues whereas mature α-globin has two methionines, we estimate that ~60-65% of the transported PRO-GLO, i.e., that present after the 15-min chase, was processed to mature α-globin at 2 h of chase. Of this processed globin, ~45% was stored intracellularly with a half-life >4 h.

Pro-SRIF-GLO Is Processed to Mature α-Globin

Approximately 60% of the transported PRO-GLO was processed to mature α-globin. Partial NH₂-terminal sequencing was performed to determine if proteolytic cleavage had occurred at the predicted processing sites: on the carboxyl side of lysine in the hexapeptide domain in PRO-GLO and the junction of the signal peptide and α-globin in SIG-GLO (Fig. 6). Chimpanzee α-globin has methionine residues at positions 1 and 33. Consistent with correct signal peptide cleavage, methionine residues were detected at positions 1 and 33 in the α-globin polypeptide from GH₂SIG-GLO cells. PRO-GLO contains four additional NH₂-terminal amino acids (AlaAspProArg; Fig. 1). Therefore, if the prohormone processing enzyme(s) recognized the endoproteolytic processing site of PRO-GLO (ArgLys), a methionine residue should be present at position 5. The sequence data demonstrated that this was the case (Fig. 6). Thus, despite the presence of an additional methionine residue, which was not recovered after 15 min of chase was degraded intracellularly and not secreted.
chloroquine PRO-GLO processing was inhibited by ~95% of increasing concentrations of chloroquine. At 25 μM chloroquine, secretion was diminished (Fig. 7, lane 5). Under these conditions, unprocessed PRO-GLO was seen (Fig. 7, lanes 7 and 8). At higher chloroquine concentrations proteolysis was quantitatively inhibited, resulting in secretion of only unprocessed precursor (Fig. 7). In the absence of proteolytic processing at 25 μM chloroquine (lanes 7 and 8). However, in the presence of chloroquine (cf. Fig. 8, lanes 5 and 9), 90% of both mature globin and PRO-GLO were secreted and virtually no globin-related material remained intracellular (Fig. 8, lane 5). We conclude that the release of stored globin and PRO-GLO in response to 8-Br-cAMP indicated targeting to the regulated pathway.

Discussion

A characteristic morphological feature of many endocrine cells is the possession of dense core secretory granules in which the mature hormone is stored in a semicrystalline form. Upon stimulation, these granules fuse with the plasma membrane releasing their contents into the circulation. In general, there is little sequence homology among a diverse array of proteins targeted to secretory granules, thus, it is unlikely that a primary consensus sequence is involved in targeting. Recent evidence, using chimeric proteins, implies targeting to the regulated secretory pathway may be an "active" sorting process that contrasts with constitutive secretion which probably occurs by bulk flow (4, 33, 47). For example, approximately 50% of processed mature globin was stored intracellularly with a half-life >6 h. It was therefore of interest to determine if globin was targeted to the regulated secretory pathway (Fig. 8). Cells were pulse labeled for 15 min and chased for 2 h, the medium was then changed and the cells incubated for an additional 2 h in the absence (Fig. 8, lanes 4 and 8) or presence of the secretagogue, 8-Br-cAMP (Fig. 8, lanes 5 and 9). During the 120-min chase in the absence of 8-Br-cAMP, unprocessed PRO-GLO and mature globin were secreted (Fig. 8, lane 6) but a significant level of both molecules was still present intracellularly at 240 min of chase (Fig. 8, lanes 3 and 4). However, in the presence of 8-Br-cAMP (cf. Fig. 8, lanes 5 and 9), 90% of both mature globin and PRO-GLO were secreted and virtually no globin-related material remained intracellular (Fig. 8, lane 5). We conclude that the release of stored globin and PRO-GLO in response to 8-Br-cAMP indicated targeting to the regulated pathway.

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The rapid degradation of globin might be related to its inherent instability in the absence of β-globin or heme, as in certain thalassemias. It is also possible that α-globin was incompletely translocated into the lumen of the ER and degraded via the ubiquitin system; this possibility seems unlikely given its efficient translocation in Xenopus oocytes (40, 42) and in cell-free systems (17). The aforementioned studies failed to observe α-globin secretion from Xenopus oocytes; since these experiments used the same or a similar signal peptide–globin construction as was used here, most probably the resulting globin molecules were degraded intracellularly.

Our data are similar to those reported by Lippincott-Schwartz et al. (18) and Chen et al. (6) who demonstrated degradation of incompletely assembled T cell receptor (TCR) α- and Δ-subunits; we did not observe a lag period of 20 min before degradation and the half-life of globin was 4–5 min compared to 50 min for TCR α-chains. These results suggest the presence of enzymes which recognize and rapidly degrade "aberrant" proteins. This function may be distinct from any role BiP, the heavy chain binding protein (3), may have in controlling export of proteins from the ER. Our data and those on TCR assembly (6, 18) suggest that the ER or GOLGI apparatus has multiple proofreading mechanisms which regulate the flow of proteins through the secretory apparatus.

The SRIF Proregion–mediated Transport of α-Globin to the Regulated Pathway

Our results are consistent with the suggestion that the cellular sorting machinery recognizes precursor molecules rather than mature hormones (45), in this case a domain or structure in proSRIF. In contrast to the proinsulin C-peptide (35), the presence of the SRIF propeptide was essential for targeting globin to the regulated pathway. We speculate that the propeptide may enhance folding or oligomerization of the chimera which could be necessary for efficient exit from the ER as observed for other proteins (1). Alternatively, the

In the Absence of a Propeptide α-Globin Is Rapidly Degraded

The choice of α-globin for use in these experiments was based on previous in vitro (17) and in vivo (40, 42) studies which indicate that α-globin is competent for translocation across the ER membrane when fused to a signal peptide; furthermore, no degradation of the in vitro–translocated α-globin was observed (17). The rapid disappearance of α-globin (t1/2 = 4–5 min) after cleavage of the signal peptide demonstrated that globin alone did not contain sufficient sorting information to mediate secretion. The site of α-globin degradation was not determined but its rapid turnover indicated degradation shortly after completion of protein synthesis. The lack of inhibition by chloroquine, a drug that inactivates lysosomal enzymes, suggested that degradation did not occur in a lysosomal compartment. Since globin degradation was inhibited between 16 and 20°C, a temperature which prevents exit from the ER (37), the site of degradation may be between the ER and “early” Golgi regions. However at present, we cannot exclude the possibility that the degradation process is temperature sensitive; i.e., at low temperatures the proteases are inhibited and/or the substrates are less accessible. Thus, additional experiments are therefore necessary to identify the compartment where proteolysis occurs.

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propeptide could facilitate efficient transport by preventing nonspecific interactions which might retard movement in the bulk phase (36). Once the precursor reached the TGN, sorting could result from intrinsic chemical properties of the molecules rather than a sorting signal per se. For example, during passage through the acidic environment of the post-TGN, a precursor with an acidic pi value might precipitate or aggregate as it reached its isoelectric point. Precipitation, which may require the presence of a suitable cofactor such as a metal ion (e.g., proinsulin and zinc), would result in a highly condensed nucleus of protein leading to the formation of immature secretory granules (30, 44, 45). In this context, the SRIF proregion confers an acidic pi on both the native molecule and α-globin. Mature SRIF and α-globin have predicted pIs of 9.15 and 9.78, respectively; while proSRIF and PRO-GLO have predicted pIs of 5.15 and 6.49, respectively. The propeptide of SRIF therefore may function to initiate precipitation and storage of the prohormone which is subsequently cleaved by processing enzymes activated in the acidic environment of forming secretory granules.

It might be argued that since only a fraction (~30%) of PRO-GLO was transported from the ER, that the secreted globin was transported to granules by default in these cells, or that the SRIF propeptide may have facilitated nonspecific associations with endogenous secretory proteins, thereby leading to “passive” sorting into the regulated pathway. The obvious candidate for such a protein is growth hormone which is by far the most abundant polypeptide synthesized by and secreted from GH3 cells. However, we recently demonstrated (41) that, in these cells, only 5% of newly synthesized growth hormone is stored intracellularly in a cAMP-responsive compartment, whereas 95% is secreted constitutively. Consequently, if PRO-GLO were “sticking” to growth hormone, for example, only ~5% would be expected to enter the regulated pathway. In fact our data demonstrate that ~45% of the processed PRO-GLO is stored intracellularly; i.e., significantly more efficiently than endogenous growth hormone. This figure is consistent with the observation (44) that 55% of processed native proSRIF was sorted to the regulated pathway and secreted in response to 8-Br-cAMP. Approximately 90% of the stored intracellular material was secreted in response to cAMP; equivalent to a fourfold stimulation over the basal level of secretion. This observation is consistent with storage of globin in mature secretory granules. We conclude that the propeptide-mediated targeting to the regulated pathway and facilitated packaging of globin into a cAMP-stimulatable compartment. Morphologic studies are currently in progress to determine the precise cellular localization of these molecules.

**Proteolytic Processing of PRO-GLO**

Similar to observations for several native prohormones (7, 25, 29, 31) proteolytic processing of PRO-GLO required an acidic environment; cleavage was quantitatively inhibited even at low concentrations (25 μM) of chloroquine. High concentrations of chloroquine may be toxic to some cells, however, at the concentrations used in these experiments (25–100 μM) we observed no inhibition of total protein synthesis. Thus, although chloroquine was reported to not affect processing of proopiomelanocortin in pituitary AtT-20 cells (20), we observed processing inhibition at all chloroquine concentrations and the concomitant enhanced secretion of unprocessed PRO-GLO. Similar results were observed for native proSRIF (41a). We interpret our results to suggest that PRO-GLO was transported to the distal elements of the Golgi apparatus/TGN and packaged into acid vesicles where proteolytic processing was initiated.

PRO-GLO was accurately processed indicating that the native propeptide cleavage site (Arg-Lys) was recognized by the paired basic processing enzyme(s). Thus, even though chimpanzee α-globin possesses a single pair of basic amino acids (Lys60 and Lys61), most probably these were not cleaved since no smaller forms of globin-related peptides were detected. Accurate processing demonstrated the conformational dominance of the propeptide and in particular the highly conserved hexapeptide region. This is noteworthy since α-globin is 10 times the size of mature SRIF and nearly twice the size of the proregion itself; thus, it is unlikely that the chimera and native precursor would be structurally related.

In conclusion, our results have identified two novel functions for a propeptide: partial protection of nascent precursors from degradative enzymes and targeting to the regulated secretory pathway. The SRIF proregion overcame the efficient ER/pre-Golgi “proofing” mechanisms and facilitated transport of α-globin to the distal elements of the Golgi apparatus. The proregion may have afforded protection from proteolysis by allowing the molecule to assume a conformation which (a) is not recognized as “abnormal” and therefore is not a substrate for proteolysis; and (b) mediated rapid ER to Golgi transport thus separating the substrate from the degradative enzyme; these two mechanisms probably act in concert.

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