Identification of thyroglobulin domain(s) involved in cell-surface binding and endocytosis

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Abstract

Thyroglobulin (Tg) binds to cell surfaces through various binding sites of high, moderate and low affinity. We have previously shown that binding with low to moderate affinity is pH dependent, selective, but not tissue specific. To identify the regions of Tg involved in this cell surface binding, we studied the binding of 125I-labeled cyanogen bromide peptides from human Tg to cell surfaces of thyroid cells (inside-out follicles) and of CHO cells. Electrophoretic analysis of cell homogenates after binding of native or of reduced and alkylated 125I-labeled peptides showed that three peptides, P1, P2 and P3, were always associated with the cells. Sequence analysis allowed the identification of P1 (Ser-2445 to Met-2596 or Met-2610) and P2 (Phe-2156 to Met-2306). P3 proved to be a mixture of several peptides among which two were identified: P3–1 (Cys-1306 to Met-1640) and P3–2 (Cys-2035 to Met-2413) which includes P2. P1, P2 and P3–2 are entirely (P1) or partly (P2 and P3–2) located in the C-terminal domain of Tg homologous with acetylcholinesterase. The smallest peptides, P1 and P2, were purified by preparative electrophoresis. They both displayed strong binding properties towards cell surfaces. Inhibition experiments of 125I-labeled Tg binding by P1 or P2 indicated that they were involved in Tg binding to cell surfaces. All the other peptides tested for their binding abilities were either not or only poorly involved in Tg binding to cell surfaces, which suggested that P1 and P2 are major Tg sites of binding to cell surfaces. These two peptides are not involved in the binding of Tg to the known Tg ‘receptors’ described in the literature, to which recycling, transcytosis and regulation functions have been ascribed. Thus they are potential tools to identify cell surface components involved in the process of Tg endocytosis leading to lysosomal degradation.

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Introduction

Thyroglobulin (Tg), a large glycoprotein (660 kDa) produced by thyrocytes, is the prothyroid hormone. After being synthesized and undergoing post-translational modifications, Tg is secreted into the lumen of thyroid follicles where it undergoes tyrosyl iodination and coupling of some iodotyrosyl residues: these reactions lead to the formation of tri-iodothyronine and thyroxine. Thyroid hormone secretion requires Tg to be endocytosed, transported to the lysosomes and enzymatically hydrolyzed, after which thyroid hormone release occurs (Bjorkman & Ekholm 1990).

Tg endocytosis occurs partly through fluid phase uptake and mainly through adsorptive micropinocytosis, which requires Tg binding to cell surfaces (Lemansky & Herzog 1992). Thyroglobulin interactions with thyroid membranes have been observed for several years (Consiglio et al. 1981). Several ‘receptors’ liable to mediate Tg binding to cell surfaces have been recently described: a receptor able to bind asialoagalacto Tg at acidic pH levels (Miquelis et al. 1987); the protein disulfide isomerase (PDI) (Mezghrani et al. 2000); histone H1 (Brix et al. 1998); heparin (Marino et al. 1999a); megalin (Zheng et al. 1998, Marino et al. 1999b); and rat hepatic lectin subunit of a rat asialoglycoprotein receptor (ASGPR) (Pacifico et al. 1999, Ulianich et al. 1999). Some functions have been associated with various ‘receptors’: megalin was shown to be involved in transcytosis (Marino & McCluskey 2000, Marino et al. 2000); PDI was associated with Tg recycling (Miquelis et al. 1987, Mezghrani et al. 2000); histone H1 was involved in circulating Tg uptake by macrophages (Brix et al. 1998); and a role was proposed for ASGPR in feedback regulation, ASGPR preventing thyroid-restricted gene expression under follicular Tg binding (Pacifico et al. 1999, Ulianich et al. 1999). However, none was associated with Tg binding and targeting to lysosomal degradation in thyroid cells.
One major obstacle in studying the binding of Tg to cell membrane components is the size and complexity of the molecule. The Tg gene has been cloned and mapped in several species including humans (Mercken et al. 1985, Malthiery & Lissitzky 1987, Caturegli et al. 1997, Van de Graaf et al. 1997). It is formed of several juxtaposed domains, and is thought to result from the fusion between one gene consisting of several different repeat units and possessing the main hormonogenic site, and another gene on the C-terminal side, resulting from the duplication of a primitive esterase gene, even before the divergence between vertebrates and invertebrates occurred (Takagi et al. 1991). The C-terminal part of the Tg gene has secondary hormonogenic sites and no esterase activity. Some of these domains show various degrees of homology with numerous proteins (Takagi et al. 1991, Molina et al. 1996a). This has led to various hypothetical functions (Swillens et al. 1986, Molina et al. 1996b) being attributed to Tg domains, which are thought to be mediated by Tg interactions with specific ligands. This accounts for the large number of proteins able to bind Tg.

In a previous study, we established that the thyrocyte apical membrane binding and internalization of Tg were selective, i.e. more efficient than membrane binding and internalization of various control proteins (Giraud et al. 1997). We also observed that the Tg binding and internalization were not tissue specific, which indicated that the binding selectivity displayed was an intrinsic property of the Tg molecule (Giraud et al. 1997). This prompted us to attempt to identify the domains of Tg involved in the binding of the molecule to the cell membranes. To circumvent the problems caused by the complex structure of the molecule, one possible approach is to cut the molecule into pieces and to study the binding activity of the fragments. This approach has been successfully used to identify a recycling receptor-binding peptide (Mezghrani et al. 1997), a rat asialoglycoprotein-binding domain (Montuori et al. 2000) and an immunodominant region of Tg (Duthoit et al. 2000).

In the present study, we found that two peptides located in the C-terminal part of the molecule express strong membrane binding and internalization properties and are involved in whole Tg binding. These peptides were not involved in the binding of Tg to its already known ‘receptors’ to which Tg recycling, transcytosis or regulation functions were ascribed, and are potential tools with which to characterize membrane components involved in the endocytosis of Tg molecules targeted to lysosomal degradation and hormone release.

**Materials and Methods**

**Materials**

Culture media were from Sigma Aldrich Chimie SARRL (Saint Quentin Fallavier, France) and from Gibco BRL, Life Technologies (Cergy Pontoise, France). IgG, bovine serum albumin, agaro and amphoterin B (fungizone) were from Sigma Aldrich Chimie SARL. Penicillin and streptomycin were from Life Technologies. Fetal bovine serum (FBS) was from Valbiotech (Paris, France). Protease inhibitor cocktail tablets (Complete) were from Boehringer Mannheim SA (Meylan, France). 125I-NaI was from Cis Bio International (Gif sur Yvette, France). Aquaseal (water-soluble siliconizing fluid) was from Pierce Chemical Co. (Rockford, IL, USA), Centricon YM-10 and Ultrafree-15 were from Millipore Corporation (Bedford, MA, USA). Bio-Gel A-5M column was from Bio–Rad SA (Marnes-la-Croquette, France). Sephadex G-200 column was from Amersham (Orsan, France).

**Cell cultures**

Porcine thyroid cells were isolated from fresh thyroid glands by discontinuous trypsin–EGTA treatment (Chambard et al. 1981). Inside-out follicles were obtained as described previously (Espanet et al. 1992, Giraud et al. 1997). Briefly, the cells (106 cells/ml) in Dulbecco’s modified Eagle’s medium (DMEM) containing antibiotics and fungizone and supplemented with 10% FBS were cultured in the form of unstimred suspensions in polystyrene dishes not treated for tissue culture and coated with 1% agarose. They were maintained at 36°C in a water-saturated 95% air–5% CO2 atmosphere. The cultures were used after 10–12 days (by then, most of the cells had formed inside-out follicles). Twenty-four hours before each experiment, 10–4 M dibutyryl adenosine-3’,5’-cyclic-monophosphate was added to the culture medium.

Madin–Darby canine kidney (MDCK) cells were grown in DMEM supplemented with 10% FBS and antibiotics on Petri dishes treated for tissue culture. After reaching confluence, they were suspended by applying a trypsin–EDTA treatment as described by Giraud et al. (1997) and seeded on Petri dishes not treated for tissue culture and coated with 1% agarose. They were then grown as unstirred suspensions for 24–72 h before use. They formed large aggregates and occasionally follicle-like structures.

Chinese hamster ovary (CHO) cells were handled like MDCK cells except that the growth medium was Ham’s F–12 medium supplemented with 10% FBS and antibiotics. When grown in unstirred suspensions, they form small loose aggregates.

**Isolation of human Tg (hTg)**

A human thyroid gland from a patient with a colloid goiter was obtained by thyroidectomy. After pathological examination, the gland was frozen and lyophilized. About 1 g lyophilized gland was fragmented and suspended in 0·1 M phosphate buffer, pH 7·2, for 15 min. After filtration on gauze, the supernatant of the thyroid homogenate was salted out (1·8 M phosphate buffer, pH 7·2). After
centrifugation, the precipitate was dissolved with water, dialyzed against 50 mM phosphate buffer, pH 7.2, and chromatographed on a Bio-Gel A-5M column (100 × 5 cm) as previously described (Marriq et al. 1977). The fractions corresponding to 19S Tg were pooled, dialyzed and lyophilized. This 19S Tg was poorly iodinated.

**Preparation of cyanogen bromide (CNBr) peptides**

CNBr peptides from iodine-poor hTg were prepared and fractionated as described by Marriq et al. (1986). In brief, hTg was treated with CNBr and the resulting CNBr peptides were filtered on a Sephadex G-200 column in 1 M propionic acid. Five fractions (I–V) were collected, dialyzed and freeze-dried.

**Preparative electrophoresis**

CNBr peptides of fraction III were further separated by performing preparative SDS-PAGE electrophoresis using a model 491 Prep Cell preparative electrophoresis apparatus (Bio-Rad SA, Marnes-la-Coquette, France). The gels (running gel: 15% acrylamide; stacking gel: 4% acrylamide) were prepared according to the manufacturer's instructions. Peptides were solubilized in the sample buffer described by Laemmli (1970) and reduced by heating them for 5 min at 100 °C in 5% 2-mercaptoethanol. They were loaded on the stacking gel and electrophoresed at 40 mA constant current for 9 h. Fractions (2 ml, elution rate 1 ml/min) were collected after elution of the bromophenol blue. The fractions containing the peptides were identified by running every fourth fraction past the ion front on analytical PAGE. Once identified, the fractions of interest were desalted and concentrated on a Centricron Y M-10 or Ultrafree-15 unit (Millipore Corporation).

**Analytical SDS-PAGE and blotting**

Analytical SDS-PAGE was performed according to Laemmli (1970). Peptide separations were performed on 15% acrylamide gels. Depending on the experiments, gels were either fixed then colored with Coomassie blue, or fixed without any coloring when labeled peptides were to be analyzed, and then dried. Gels with labeled peptides were exposed to an imaging plate radioactive energy sensor (BAS-IP.MM 2040S; Fuji Photofilm Co. Ltd, Kamagawa, Japan). The exposed plate was analyzed using a phosphorimager (Fujix BAS 1000; Fuji). In another set of experiments, peptides were electrophoretically transferred from the polyacrylamide gel to a polyvinylidene difluoride (PVDF) membrane (ProBlott membrane; Applied Biosystems, Foster City, CA, USA). The transfer buffer contained 50 mM Tris–base and 50 mM boric acid. After transfer, the PVDF membrane was washed briefly with water, and the peptides were stained with amido black (0.1% in 45% methanol, 1% acetic acid) for a few seconds, washed with water and air-dried. Ultra-pure water was used throughout the blotting steps.

**Peptide sequencing**

After the blotting procedure, the peptides colored with amido black were cut off and sent for N-terminal amino acid sequencing to the Laboratoire de Microsequençage des Protéines at the Pasteur Institute (Paris, France).

**Iodination of peptides and proteins**

hTg, IgG and peptides were iodinated with 125I using the chloramine T method as described by Giraud et al. (1997).

**Binding and endocytosis experiments**

Binding and endocytosis experiments were performed as described by Giraud et al. (1997). Briefly, they were performed at 36 °C under gentle agitation on suspended inside-out follicles (thyroid cells) or aggregates (MDCK or CHO cells). The incubations were started by adding labeled molecules: 125I-hTg, 125I-hTg peptides or 125I-IgG (1.5 × 10⁻¹³ mol/ml, with an assumed molecular weight (MW) of 330 000 for Tg, 20 000 for peptides P1 and P2 and 150 000 for IgG). They were ended 2 h later by careful cold washing in order to minimize non-specific binding evaluated as described by Giraud et al. (1997). A brief pronase treatment was carried out to separate the cell surface-associated material from the internalized material. For the competition experiments, unlabeled molecules were added to the incubation medium.

DNA was determined using the fluorimetric method described by Labarca & Paigen (1980).

**Sequence comparisons**

Sequence comparisons were obtained from the SWISSPROT database and the results obtained with the SIM Program, through the Exposy Molecular Biology Server (proteomic server of the Swiss Institute of Bioinformatics).

**Results**

**Identification of peptides from hTg that strongly bind cell surfaces**

hTg peptides obtained by applying CNBr treatment to hypoiodinated hTg were fractionated on a Sephadex G-200 column as described by Marriq et al. (1986). Five fractions labeled I–V were collected. SDS-PAGE analysis of these fractions showed that each of them contained several peptides and that fractions III and IV showed fairly similar patterns (Fig. 1). The five fractions were 125I-labeled and their binding capacity on the cell surfaces
was tested. They were all able to bind to the cell surfaces at both pH 7.2 and 8.2; the binding was slightly enhanced at pH 8.2, and fractions I, III and IV appeared to be the most efficiently bound (data not shown). We discarded fraction I, since it was the first fraction eluted from the G-200 column and was composed mainly of high molecular weight peptides unable to enter the gel in a 15% SDS-PAGE. To determine which peptides were bound to the cell surfaces, we incubated cells with labeled fractions II–V and studied the solubilized cell pellets by SDS-PAGE (whole cell pellets and pellets of pronase-treated cells). Three peptides present in fractions III and IV, with apparent MWs of about 18 000 (P1), 22 000 (P2) and 39 000 (P3), were regularly associated with the thyroid cells (inside-out follicles) at both pH 7.2 and 8.2 (see Fig. 2 for cell-associated peptides from fraction III). P1, P2 and P3 were only weakly recovered if at all after pronase treatment, which indicates that they were mainly located at the surface. Other peptides with lower MWs were found in the cell pellets. But since they were still recovered after pronase treatment of the cells, they were probably degradation fragments of internalized peptides. P1, P2 and P3 were the main components of fractions III and IV. Since these peptides were present in high proportions in fraction III (see Fig. 1), this fraction was used afterwards in this study. When reduction and alkylation of fraction III were performed before the labeling and binding experiments, these peptides were still able to bind to the cell surfaces (Fig. 2a and b, lanes 3 and 4).

Using MDCK cells, we observed that these peptides were also associated with cell surfaces (Fig. 3) at both pH 7.2 and 8.2: the binding of these peptides, like the binding of Tg, was not tissue specific.

**Characterization of peptides with strong binding activity**

The reduced peptides from fraction III were separated by performing analytical SDS-PAGE and transferring them onto Pro Blott membranes. After blotting and amido black staining, we cut off and sequenced the three peptides of interest (those shown on Fig. 4). With two of the peptides, P1 and P2, four amino acids at the N-terminus, SSSQ for P1 and FYAD for P2, perfectly matched single fragments of the published hTg sequence; in addition, they occurred after a methionine, which fits the peptides obtained by CNBr cleavage. P3 was a mixture of several peptides. Two N-terminus fragments were identified: CSADYAGL for P3–1 and CSEEENGGA for P3–2. Two other minor sequences recorded as being unsure did not match the published Tg sequences. The one was not identified; the other one (XSSEEENDX) is present in the human asialoglycoprotein receptor 2. Given their apparent
MW, we can assume that P1 is the Tg fragment comprised between Ser-2445 and Met-2596 or Met-2610 (Met-2596 and Met-2610 are too closely spaced to choose between them on the basis of the apparent MW of P1) and that P2 is the Tg fragment comprised between Phe-2156 and Met-2306. P3–1 is the Tg fragment comprised between Cys-1306 and Met-1640 and P3–2 is the Tg fragment comprised between Cys-2035 and Met-2413 (see Fig. 5). P3–1 holds a central position and includes the type 2 repeats. P3–2 overlaps with part of the type 3 repeat and the beginning of the homology with acetylcholinesterase (ACHE) and includes P2 (Fig. 5). The inclusion of P2 in P3–2 would explain the binding properties of this peptide III fraction.

The heavier surface-bound peptides (peptides 3) were not good candidates for determining small binding domains on the Tg molecules, whereas the smallest surface-bound peptides clearly identified, P1 and P2, could enable us to identify binding domain(s) of limited size on the Tg molecule. They were purified by preparative electrophoresis and then used for the binding and internalization experiments.

**Structural information about P1 and P2 deduced from their sequences**

P1 and P2 are located entirely (P1) or partly (P2) in the non-repetitive C-terminal region of Tg, which is homologous with ACHE. P1 is 152 or 166 amino acids long, has a theoretical pI of 5.9, one potential glycosylation site at Asn-2582, two cysteines, Cys-2453 and Cys-2591, and a hormonogenic site, Tyr-2573. P2 is 151 amino acids long, has a theoretical pI of 8.4, two potential glycosylation sites, Asn-2250 and Asn-2295, and two cysteines, Cys-2264 and Cys-2281. The corresponding cysteines in the ACHE sequence form a disulfide bridge.

P1 and P2 sequences are well conserved between species. The identity between mouse and human sequences, which amounts to 73.8% in the case of the whole molecule, reaches 86.7% in P1 and 69% in P2. The identity between bovine and human sequences, which amounts to 77.4% in the case of the whole molecule, reaches 83.6% in P1 and 82.6% in P2, which indicates that P1 is an extremely well-conserved Tg fragment and P2 a well-conserved one.

**Functional properties of P1 and P2**

Experiments were performed with the purified peptides, to check their binding and internalization ability and their
involvement in the binding of the whole Tg molecule to the apical surfaces of thyroid cells (inside-out follicles).

Binding and internalization of 125I-labeled hTg, P1 and P2

Once purified, P1 and P2 were 125I-labeled and used in the binding and internalization experiments, along with 125I-labeled hTg (Fig. 6). These experiments were performed on thyroid cells (inside-out follicles). The hTg used was the hTg from which peptides P1 and P2 had been purified.

There was more cell surface-associated hTg than IgG at both pH 7.2 (Fig. 6a) and 8.2 (Fig. 6b), with a very clear-cut enhancement at pH 8.2; and there was more internalized Tg than IgG at both pH levels (Fig. 6a and b): the binding and internalization behavior of hTg is similar to that of porcine Tg described by Giraud et al. (1997).

The binding and internalization behavior of 125I-labeled peptides P1 and P2 were compared with that of 125I-labeled hTg. At pH 7.2, P1 and P2 bound to cell surfaces and were internalized more efficiently than Tg; indeed, many more peptides were detected inside the cells (Fig. 6a). At pH 8.2, there were slightly less surface-associated peptides than surface-associated Tg, although there were more peptides than Tg inside the cell (Fig. 6b).

Effects of unlabeled peptides on binding and internalization of 125I-labeled hTg, P1 and P2

As shown in Fig. 7, the presence of about 3.9 × 10⁻⁷M unlabeled P1 or P2 decreased the amount of 125I-labeled hTg

Figure 5 Amino acid sequence and location of P1, P2, P3–1, and P3–2 on the Tg chain. P1: Ser-2445 to Met-2596 or Met-2610 (bold, black); P2: Phe-2156 to Met-2306 (bold, black); P3–1: Cys-1306 to Met-1640 (bold, black); P3–2: Cys-2035 to Met-2413 (bold, black). The homology with ACHE is underlined.

Figure 6 Binding and internalization of 125I-labeled hTg, P1, P2 and IgG by thyroid cells (inside-out follicles). (a) pH 7.2 and (b) pH 8.2. Cell surface-associated label, hatched bars; internalized label, open bars. Results are expressed as the mean ± S.D. of the percentage of added counts recovered normalized for the amount of DNA detected in each sample (three experiments).
The binding of ¹²⁵I-labeled Tg to non-thyroid cells occurred via P1 and P2, the binding and internalization of the peptides should not be tissue specific. To test this hypothesis, binding and internalization of ¹²⁵I-labeled hTg, P1 and P2 were performed with MDCK cells (Fig. 8a and b) and CHO cells (Fig. 8c and d). As previously observed with thyroid cells, there was more cell-surface-associated Tg than IgG at both pH 7·2 and 8·2. At pH 7·2 (Fig. 8a and c), P1 and P2 bound to the cell surfaces and were internalized more efficiently than Tg. In fact, many more peptides were observed inside the cells, as was previously found to be the case with thyroid cells. At pH 8·2 (Fig. 8b and d), there were less surface-associated peptides than surface-associated Tg, as observed with thyroid cells. The amount of internalized label was greater than the amount of surface label in MDCK cells (Fig. 8b), as observed with thyroid cells, but less than the surface label in CHO cells (Fig. 8d).

Discussion

In a previous work (Giraud et al. 1997) we showed that Tg binding to the apical surface of thyroid inside-out follicles occurs through numerous sites considered non-specific on account of their low affinity, while at pH 8·2 specific sites of moderate affinity appeared, contributing to a strengthened binding. In addition, at both pH values, Tg binding was selective relative to the binding of other molecules. Also these binding properties were not restricted to thyroid tissue. The main role of Tg binding and endocytosis is lysosomal degradation and hormone release, although other functions, involving ‘receptors’, have been described (Ulianich et al. 1999, Marino et al. 2000, Mezghrani et al. 2000). Tg is the main component of the follicular lumen and is present at very high concentrations. This is a strong argument in favor of a massive endocytosis occurring via low affinity receptors. But the nature of these receptors is still unknown, and the size of the Tg molecule, plus the fact that it recognizes different receptors via various specialized domains, mean that it cannot be used to identify the receptors involved in lysosomal degradation.

In the present study, our aim was to identify Tg fragments involved in the low and moderate affinity binding of Tg previously described. So we looked for Tg fragments able to bind cell surfaces and to hinder Tg binding to those same cell surfaces. We identified and...
puriﬁed two hTg peptides, P1 and P2, that ﬁt these criteria. P1 and P2 are both able to bind cell surfaces and to partially and independently inhibit whole Tg binding. They are both located either entirely (P1) or partly (P2) in the non-repetitive C-terminal region of Tg which is homologous with ACHE. Experiments performed with the puriﬁed peptides showed that at both pH 7·2 and pH 8·2, P1 and P2 bind to cell surfaces of inside-out thyroid follicles and are internalized (Fig. 6). The greater level of internalization of P1 and P2 relative to Tg may be due to an enhanced endocytosis and/or to a lack of recycling once the peptides are inside the cells: P1 and P2 lack the Tg recycling receptor that binds to Tg via a peptide (N3) located in the first half of the Tg molecule (Mezghrani et al. 1997). In addition, recycling of the cell surface-binding sites could modulate the binding level and contribute to the actual ligand distribution between cell surface and internal compartments. The increase in the Tg-binding level observed previously at pH 8·0 compared with pH 7·2 (Giraud et al. 1997) may be partly due to a change in the Tg conformation, facilitating access to these peptides on the Tg molecule, and/or to some ionic modiﬁcation of the peptides themselves. The reduction and alkylation of the peptides do not prevent the binding of P1 and P2 from occurring, which indicates that the binding process does not require the disulﬁde bridge that may possibly exist in hTg between Cys-2264 and Cys-2281 in P2 (by analogy with ACHE). The cysteines present in P1 (Cys-2453 and Cys-2591) are not likely to form a disulﬁde bridge inside P1, but might be involved in the formation of disulﬁde bridges in the hTg molecule, with Cys-2442 and Cys-2712 respectively (by analogy with ACHE). These disulﬁde bridges, if present, are not necessary to the binding process. P1 and P2 inhibit Tg binding: a neat but moderate inhibition was observed at pH 7·2 and a stronger one at pH 8·2 (Fig. 7). This indicates that P1 and P2 are Tg fragments involved in the binding of the whole Tg molecule. However, the fact that inhibition of Tg binding by the peptides is limited suggests that other low-afﬁnity binding sites of Tg might be involved. And there is still the possibility that puriﬁed Tg peptide conformation is not quite what it was in the native Tg molecule. Crossed competition experiments showed that the binding of either labeled peptide is only poorly inhibited, if at all, by the presence of the unlabeled other one, which suggests that P1 and P2 bind independent sites on cell surfaces. However, the internalization process is somewhat inhibited under these conditions. Competition experiments require large quantities of puriﬁed peptides. The scarcity of these materials, when they are obtained by conventional methods, restricts the experimental possibilities. P1 and P2 will have to be produced by cloning the corresponding fragments of the Tg gene in order to perform complementary experiments. In the meantime, we have performed experiments to check the tissue speciﬁcity of P1 and P2 binding and internalization. Whole Tg binding and internalization are not tissue speciﬁc, so the Tg peptides that mediate Tg binding
should not display tissue specificity when binding to cell surfaces. We found that P1 and P2 are able to bind to non-thyroid cell surfaces and are internalized by these cells. This further suggests that Tg binding occurs through P1 and P2. However, the rather low internalized label observed in CHO cells might reflect some subtle tissue difference(s) not observed previously with whole Tg.

Peptides other than P1 and P2 could be able to bind to cell surfaces and to hinder Tg binding to these same cell surfaces. We had the opportunity to test the properties of several purified Tg peptides disposed at various places along the molecule: the N-terminal domain of Tg (Marriq et al. 1986), two type 1 repeats (a kind gift from Dr R. Miquelis), the N3 peptide (a kind gift from Dr R. Miquelis), which binds to the recycling Tg receptor (Mezghrani et al. 1997) and an immunoreactive Tg peptide P40 (of about 40 kDa) (Duthoit et al. 2000) (a kind gift from Dr J. Ruff) produced during the hTg oxidative process, located at the C-terminal end of the molecule and including P1. All these peptides but one possess only very limited binding capabilities (results not shown). Indeed, the N3 peptide binds almost as efficiently to cell surfaces as Tg does. However, it fails to inhibit the Tg binding, which suggests that this part of the Tg molecule is not involved in the binding process at non-acidic pH levels. By contrast, the peptide P40 (which includes P1) displays binding and internalization capacities that match those of P1 and P2. However, with their smaller size (about 20 kDa), P1 and P2 constitute more limited binding domains on the Tg molecule and are better potential tools for identifying cell surface Tg-binding molecules. Among all the purified Tg peptides tested, only those located entirely or partly in the non-repetitive C-terminal domain of Tg express cell surface-binding capacity. The published sequences of Tg show good homology between human, bovine and murine species, and this homology increases if we consider only P1. With P2, the homology slightly decreases between man and mouse but is very marked between man and bull. The very good sequence conservation between species in P1 might be partly related to the presence of a secondary hormonogenic site. But the good sequence conservation between species in the whole C-terminal domain suggests that it is involved in some useful function(s), one of which is probably its capacity to adhere to cell membranes.

Some Tg domains responsible for the Tg binding to some receptors were recently identified. They were either a large N-terminal Tg domain (Montuori et al. 2000) or a central Tg peptide (Mezghrani et al. 1997) and bear no resemblance to P1 or P2. However, the Tg domains responsible for megalin binding (Zheng et al. 1998, Marino et al. 1999b) have not yet been clearly identified. A heparin consensus sequence (SRRLKRP) involved in megalin binding was identified on rat Tg (Marino et al. 1999a). The corresponding sequence in hTg (ARALKRS) is part of P1. But here, a neutral amino acid, A, replaces a basic one, R, and its binding capacity towards heparin is probably weaker in hTg than in rat Tg. The corresponding sequence in bovine Tg (ARVLQRA) probably shows an even weaker binding ability to heparin, since two basic amino acids are replaced (R by V and K by Q). In our study, megalin was not involved in Tg binding to cell surfaces, since it is not detectable on CHO cells (Marino et al. 1999b), and since primary cultures of porcine thyroid cells cease to express megalin after a few days (Marino et al. 1999b). In addition, the low-affinity binding that occurs at pH 7-2 suggests that here Tg binds to still unidentified molecules other than megalin.

As previously stated (Giraud et al. 1997), Tg is a ‘multireceptor’ ligand. It is worth noting that most of the Tg ‘receptors’ described so far (megalin, PDI, heparin, H1 histones) are ubiquitous proteins, or at least molecules that are not restricted to thyroid tissue (rat hepatic lectin). Their role in Tg metabolism depends on the place where they encounter Tg, and on intrinsic Tg properties. Here we studied apical binding. Since we have previously established that the low-affinity binding of Tg is not tissue specific, and since a basolateral selective Tg binding of low affinity was demonstrated by Gire et al. (1996), it seems likely that the corresponding Tg-binding molecules will turn out to be ubiquitous molecules which occur widely on various cell surfaces. However, due to experimental constraints, the present study deals with molecules that do not need thyrotropin for their cell surface expression, and we cannot exclude the possibility that some additional low-affinity, TSH-dependent, Tg-binding molecule(s) contribute to Tg endocytosis in vivo.

In conclusion, we purified two peptides, P1 and P2, located in the C-terminal domain of Tg that are able to bind apical surfaces of thyroid cells and are internalized. The results of the inhibition experiments strongly suggested that they are involved in the Tg binding previously described (Giraud et al. 1997). They are different from the Tg peptides involved in Tg recycling (Mezghrani et al. 1997), in the feedback regulation which involves correlation between Tg binding and in the suppression of thyroid-restricted gene expression (Montuori et al. 2000) and are not involved in the transcytosis involving megalin binding (Marino et al. 2000). These findings suggest that P1 and P2 are potential tools for identifying the cell surface molecules involved in the Tg binding which occurs at low or moderate affinity sites, and will help to understand the pathways mediating lysosomal degradation and hormone release.

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