ABSTRACT

We reported previously that the relative level of gene expression for sst2, a subtype of somatostatin receptors, was positively related to patient outcome in the childhood tumor neuroblastoma (NB). Because sst2 binds with high-affinity octreotide and its scintigraphic derivative, 111In-pentetreotide, we tested the hypothesis of whether NB tumor imaging with 111In-pentetreotide gives similar information to ex vivo measurement of sst2 expression. We, therefore, studied simultaneously nine NB tumors with 111In-pentetreotide single photon emission computed tomography and competitive reverse transcription-PCR for sst2, along with other prognostic markers.

To quantify the relative abundance of 111In-pentetreotide binding to NB tumors, we developed a simple semi-quantitative method, based on the mathematical analysis of 111In-pentetreotide association to cancer cell receptors at different time points (4 and 24 h). We indeed found that the ratio between the activity in a manually extracted region of interest from pathological (ROI_{t}) and background (ROI_{BT}) area was increasing between early and late acquisition only in affected tissues. The rate of this pathological increase was quite different among patients and significantly (P < 0.01) related to the abundance of sst2 gene expression, as measured by competitive reverse transcription-PCR on ex vivo tumor samples. Because we demonstrated that in 26 NB patients the density of sst2 is strongly related to survival (P < 0.0005) and apparently independent from N-myc oncogene amplification (P < 0.05), we propose that NB tumor imaging with 111In-pentetreotide may have not only a diagnostic but also a prognostic value.

INTRODUCTION

Since the late eighties it has been recognized that tumor cells of neuroendocrine origin do express SS binding sites (1). By using 123I- or 111In-labeled SS analogues, the in vivo imaging of SS binding sites was later available (2, 3) and used in several nuclear medicine centers to visualize receptor-positive tumors and their metastases. It was soon evident that SS receptor scanning offers advantages over the other scintigraphic tracers, including the possibility to obtain simultaneous information on tumor localization and tumor responsiveness to SS therapy. Early on, it was also hypothesized that the presence of SS receptor represents a favorable prognostic factor, based on a small series of breast cancer cases (4, 5). Similar results were later on reported for NB tumor (6, 7). In this childhood neuroendocrine cancer, the presence of functioning SS receptors were demonstrated by studies in vitro (7, 8) and confirmed in vivo by tumor imaging with either 123I-Tyr-octreotide or 111In-pentetreotide (3, 9). Hence, it was generally accepted, yet not demonstrated, that the presence of SS binding sites on cancer cells represents a new marker for a well-differentiated tumor (10).

The possibility to demonstrate a prognostic role of SS receptor in tumors was hampered by the heterogeneity of SS receptors. Up to now five different isoforms of SS receptors have been cloned (sst1–sst5; Refs. 11 and 12) and found to be differentially expressed in human tumors. For example, pancreatic (13) and prostate (14) cancers express sst1 but not sst2 and are, therefore, insensitive to therapy with octreotide (15), which preferentially binds to sst2 (11, 12). Accordingly, 123I-Tyr-Octreotide or 111In-DTPA-D-Phe-octreotide (111-In-pentetreotide) do not visualize these tumors (3, 14). Conversely, tumors arising from adult and embryonal adrenal medulla, such as pheochromocytoma (16, 17) and NB (18–20), express a relative abundance of sst2 mRNA and are successfully visual-
ized with octreotide scintigraphy (3, 9). Therefore, this family of neuroendocrine tumors represents an ideal target to study the relationship between sst2 gene expression and prognosis. By using RT-PCR, we found that 15 of 15 NB tumors investigated expressed sst2 (20), independently from tumor stage and amplification of the N-myc oncogene, a well-known negative prognostic factor (21). However, when we quantitated by competitive RT-PCR the level of expression of sst2 mRNA in the same NB series, we were able to demonstrate that sst2 receptor concentration is related to patient survival (20). Indeed, we found a four-log-unit difference in the level of expression of sst2 among patients. The density of sst2 was elevated in patients with favorable outcome (108_4 molecules/μg RNA) and even very low (up to 9 molecules/μg RNA) in patients with poor prognosis (20). Hence, we concluded that a quantitative more than a qualitative evaluation of sst2 gives insights on the biology of NB tumors. Studies in NB cell lines indicate there is a positive correlation between the level of expression of sst2 mRNA, binding of 125I-SS-14, and biological responsiveness to SS-14 (19, 20). Because we found a sort of biological threshold for sst2 gene expression (7 × 106 molecules/μg RNA) separating SS-responsive from unresponsive NB cells (20), we used this threshold as a cutoff to analyze patient survival. In a univariate Kaplan-Meier survival curve, we found that sst2 expression was an important prognostic indicator for NB (20). This finding was in good agreement with previous investigations based on the detection of SS-binding sites in NB tumors (6, 7).

The aim of this study was to extend investigation on the quantitative expression of sst2 in NB tumors and to evaluate whether the quantitative expression of sst2 is related to in vivo imaging of SS receptor, by using 111In-pentetreotide.

MATERIALS AND METHODS

Patients
Nine children affected by NB were selected at the Department of Pediatrics for the in vivo sst2 SPECT study with 111In-pentetreotide and for in vitro quantitation of sst2 gene expression by competitive RT-PCR. Both sst2 SPECT and RT-PCR were performed on the primary NB tumors, i.e., before any kind of therapy. Clinical characteristics of the children are reported in Table 1. In addition, primary NB tumors were obtained from two other children and were processed only for in vitro quantitation of sst2 gene expression by competitive RT-PCR. These two children were both males, aged 5 and 14 months with a stage I NB located in the adrenal area. They did not show progression of the disease after 22 and 14 months of follow-up, respectively. Informed consent was obtained from parents of all children.

Somatostatin Receptor Scintigraphy

Radiopharmaceutical. DTPA-d-Phe-1-octreotide (pentetreotide) and 111In-chloride were obtained from Mallinckrodt Medical BV. The radiolabeling was performed according to the instructions of the manufacturer. The chromatography of the radiopharmaceutical was performed using silica gel-impregnated glass fiber strips (ITLC SG; Gelman). The fraction of the peptide bound to 111In was more than 97%. The principal photons useful for detection and imaging studies are 171.3 and 245.4 KeV gamma rays.

Study Protocol. 111In-pentetreotide and 111I-mIBG were performed in the same patients a few days apart. For 111In-pentetreotide, they did not receive preliminary preparation and were injected with 5 MBq/kg of 111In-pentetreotide i.v. Three h after tracer injection, a planar whole-body segmentary acquisition was performed to localize the primary tumor and metastasis. The preset count modality was 300,000 cps for head and neck, 500,000 cps for thorax and abdomen, anterior and posterior views, with a 128 × 128 matrix, zoom 1.0, and medium energy collimator. Four h after the injection, a tomographic acquisition was performed on the primary tumor, with a 64 × 64 matrix, zoom 1.0, medium energy collimator, 64 frames of 60 s. Twenty-four h after the administration of labeled pentetreotide, SPECT acquisition was repeated with the same parameters on the same body region (22). A diagnostic dose of 1131I-mIBG (0.5 MBq/kg) was injected into the patients prior to imaging. The patients were given Lugol’s solution for 2 days before and 3 days after 111I-mIBG administration. A segmentary whole-body posterior and anterior scan was done at 24 and 48 h after the injection. Images were interpreted qualitatively by the observers. A tomographic reconstruction by filtered backprojection was performed, with convolution Butterworth filter (cutoff, 0.25 cycles/pixel; filter order 10) for each tomographic registration.

ROI Extraction. A ROI was manually extracted on the tumor area (ROI_T) in a transaxial slice (Fig. 1). The same ROI was also repositioned in the same slice on a different area out of the tumor and with local (vascular) and surrounding (scatter) conditions similar to ROI_T. Because liver and kidney are directly involved in the metabolic clearance of the tracer, they were not considered for ROI_N. In our series, adrenal (n = 7) and lung (n = 2) were considered for calculation of ROI_N. Both tissues contain somatostatin receptors that bind 111In-pentetreotide (23). This procedure was applied to 4- and 24-h acquisition images.

Data Processing. A ratio between the ROI_T and the ROI_N was calculated and expressed as global count activity (cpm) and average counts/pixel (cpm/pixel) for each transaxial SPECT slice. The same processing was repeated at least three times, and results are expressed as mean ± SD. Results from two independent investigators were not different. Results were evaluated as described previously (22) under three assumptions: (a) the activity in ROI_N is due to tracer binding to the sst2 in normal tissue; (b) the density of sst2 in normal tissue is a constant by time; (c) the activity retained in ROI_T and ROI_N at 4 and 24 h is due uniquely to receptor binding tracer. According to the SPECT time, ROI_T/ROI_N is defined, respectively, ROI_T/ROI_N 4 h and ROI_T/ROI_N 24 h. Under the above assumptions, if the activity in ROI_T is due to overexpression of sst2, the ratio ROI_T/ROI_N should increase between the SPECT at 4 and 24 h. Conversely, if the activity in ROI_T at 4 h is due to “nonspecific” uptake, the ratio ROI_T/ROI_N should be stable or decreased between 4 and 24 h.

The increase (INC) of the ROI_T/ROI_N ratios is expressed as mean ± SD by:

\[
INC = \frac{(ROI_T/ROI_N)^{4h} - (ROI_T/ROI_N)^{24h}}{(ROI_T/ROI_N)^{4h}}
\]
Table 1  Clinical and biological characteristics of the nine NB patients

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>Age (mo)/Sex</th>
<th>Stage</th>
<th>Serum markers</th>
<th>Site&lt;sup&gt;a&lt;/sup&gt;</th>
<th>DNA ploidy&lt;sup&gt;c&lt;/sup&gt;</th>
<th>Chrom&lt;sup&gt;c&lt;/sup&gt;</th>
<th>Degree of maturation&lt;sup&gt;d&lt;/sup&gt;</th>
<th>BM&lt;sup&gt;f&lt;/sup&gt; disease</th>
<th>Treatment&lt;sup&gt;e&lt;/sup&gt;</th>
<th>Follow-up&lt;sup&gt;b&lt;/sup&gt; (mo)</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>0.7/M</td>
<td>I</td>
<td>46/13.4/768</td>
<td>Ad</td>
<td>A</td>
<td>nl</td>
<td>Diff.</td>
<td>No</td>
<td>Total Res</td>
<td>None</td>
</tr>
<tr>
<td>2</td>
<td>3/F</td>
<td>IVS</td>
<td>40/121/1260</td>
<td>T + Ad + L</td>
<td>A</td>
<td>nl</td>
<td>Diff.</td>
<td>Yes</td>
<td>Biopsy</td>
<td>None</td>
</tr>
<tr>
<td>3</td>
<td>4/F</td>
<td>IVS</td>
<td>46/114/601</td>
<td>Ad + L</td>
<td>A</td>
<td>nl</td>
<td>Diff.</td>
<td>Yes</td>
<td>Biopsy</td>
<td>None</td>
</tr>
<tr>
<td>4</td>
<td>3/M</td>
<td>II</td>
<td>25/12.2/525</td>
<td>T</td>
<td>A</td>
<td>nl</td>
<td>Diff.</td>
<td>No</td>
<td>Total Res</td>
<td>None</td>
</tr>
<tr>
<td>5</td>
<td>42/M</td>
<td>IV</td>
<td>2537/-.1893</td>
<td>Ad + L + Bo</td>
<td>D</td>
<td>nl</td>
<td>Undiff.</td>
<td>Yes</td>
<td>Subtotal Res</td>
<td>D-CECat × 4, EX + ADR, EX + VP16, BUS-TT-LPAM + PBSC</td>
</tr>
<tr>
<td>6</td>
<td>168/M</td>
<td>IV</td>
<td>2557/62.4/2150</td>
<td>Ad + T + Bo</td>
<td>D</td>
<td>nl</td>
<td>Undiff.</td>
<td>Yes</td>
<td>Subtotal Res</td>
<td>D-CECat × 4, EX + ADR, EX + TT × 3</td>
</tr>
<tr>
<td>7</td>
<td>2/M</td>
<td>II</td>
<td>283/40/933</td>
<td>T</td>
<td>A</td>
<td>nl</td>
<td>Diff.</td>
<td>No</td>
<td>Total Res</td>
<td>D-CECat × 4, EX + ADR, EX + VP16, BUS-TT-LPAM + PBSC</td>
</tr>
<tr>
<td>8</td>
<td>42/M</td>
<td>IV</td>
<td>104/-.735</td>
<td>Ad + Bo + Br</td>
<td>D</td>
<td>nl</td>
<td>Diff.</td>
<td>Yes</td>
<td>Subtotal Res</td>
<td>None</td>
</tr>
<tr>
<td>9</td>
<td>11/M</td>
<td>IV</td>
<td>12/-.1260</td>
<td>Ad + Bo + Br</td>
<td>D</td>
<td>nl</td>
<td>Undiff.</td>
<td>Yes</td>
<td>Subtotal Res</td>
<td>None</td>
</tr>
</tbody>
</table>

<sup>a</sup>Ferr, ferritin (ng/mL); LDH, lactate dehydrogenase (U/L); NSE, neuron-specific enolase (ng/mL).

<sup>b</sup>Ad, adrenal; T, thorax; L, liver; Bo, bone; Br, brain.

<sup>c</sup>A, aneuploid; D, diploid.

<sup>d</sup>Chrom, chromosome; nl, normal.

<sup>e</sup>Diff., differentiating histology; Undiff., undifferentiated histology.

<sup>f</sup>BM, bone marrow.

<sup>s</sup>S, surgery; CT, chemotherapy; Res, resection; D-CECat, deferoxamine/cyclophosphamide/etoposide/carboplatinum; EX, cyclophosphamide; ADR, adriamycin; VP16, etoposide; TT, thiopeta; BUS, busulfan; LPAM, melphanal; PBSC, peripheral blood stomatinal cells.

<sup>z</sup>DOD, dead of disease; NED, no evident disease; AWD, alive with disease.
In Vivo using a 480 thermal cycler from Perkin-Elmer. The antisense primer (sst2-R, 5'-GCAAAGACAGATGATG-AATTG-3') was amplified at 95°C, followed by 15 min at 72°C with GeneAmp Thermostable reverse transcriptase RNA PCR kit (Perkin-Elmer, Norwalk, CT). The resulting cDNA was subsequently amplified in the presence of sst2-L primer (sst2-L, 5'-CAGTCATGAG-CATCGACC-GA-3') using a 480 thermal cycler from Perkin-Elmer programmed with an initial incubation at 95°C for 120 s, followed by 40 cycles of 60 s at 95°C and 120 s at 62°C, with a final extension step for 7 min at 62°C. Each sample was also submitted to conventional PCR with the same primers and cycling but without reverse transcription to exclude the presence of residual genomic DNA in extracted specimens. Ten μl of each reaction was run on a 12% polyacrylamide gel, stained with ethidium bromide, and quantified by CCD video camera and image analysis as reported previously (26). The ratios between the two amplification products were then plotted against the amount of competitor molecules initially added to the sample, and the equivalence (i.e., the concentration of competitor giving a 1:1 competitor:target ratio) corresponded exactly to the number of mRNA molecules present in the initial sample.

The degree of N-myc amplification was determined by a two-step competitive PCR as described previously using a DNA multiple competitor (pONC; Ref. 27). By the first competitive PCR, we determined the exact concentration of sample DNA by referring to the single-copy reference gene, β-globin, whereas in the second one, the copies of N-myc were evaluated. Each PCR cycle for both β-globin and N-myc included 1 min at 94°C, 1 min at 60°C, and 1 min at 72°C. After a 40-cycle PCR and an electrophoresis on a 12% polyacrylamide gel, the results were calculated on the basis of the densitometric ratios of competitor and genomic bands as described for mRNA evaluation.

**Statistical Analysis**

Progression-free survival was estimated from the date of diagnosis to the date of last follow-up or until disease progression was noted or death occurred. Estimates of progression-free survival of various subgroups of children with NB were calculated using the Kaplan and Meier method (28). Student's t test and linear regression were estimated after logarithmic transformation of the data to obtain a normal distribution. Results are expressed as mean ± SD.

**RESULTS**

Fig. 1 shows a typical SPECT study for the evaluation of the ROIT/ROINT ratio at different times (4 and 24 h) in the affected or unaffected adrenal of a patient with NB (patient 3). As shown in the lower part of Fig. 1, we found a positive ROIT/ROINT at both the time points investigated. However, we detected a specific increase by time in ROIT/ROINT ratio only in the affected tissue. According to a previous study (22), this finding is suggestive for the presence of octreotide binding sites in the tumor. Of the nine NB patients studied by SPECT, we found a substantial increase by time in the ROIT/ROINT ratio in five of nine (range, 1.45-0.33), a borderline value in two of nine (0.23-0.16), and a lack of increase in two of nine patients (0.09-0.01). Results from SPECT studies with 111 In-pentetreotide are shown in Table 2, along with those obtained with 111 In-pentetreotide and a classical diagnostic tool for NB. By using competitive RT-PCR on the primary tumors of the same patients, we found specific transcripts for sst2 in all of the NBs investigated with a rather different degree of expression among tumors (Table 2). Although the number of patients in this study is very limited, results obtained by competitive RT-PCR and semiquantitative SPECT are quite consistent and overall in agreement with those of a previous report (20). Indeed, they indicate that quantitation of sst2 gives significant insights into the biology of NB tumors. A low expression of sst2 was found in patients with unfavorable stage of disease [stage IV, log10 (sst2) = 7.87 ± 0.5 molecules/μg RNA, n = 4] when compared to stages with a
amplification by PCR also has a highly significant poor prog-
ductive value for NB. For sst2 gene expression, we used a
cutoff of 7 × 10^7 molecules/μg RNA, a value derived from a
previous study (20). We found that progression-free survival is
dramatically affected by sst2 expression (P = 0.00034, n = 26;
Fig. 3A). In the same study population, evaluation of N-myc
expression by PCR also has a highly significant poor prog-
nostic value (P < 0.00007, n = 25; Fig. 3B). To identify the
most powerful prognostic factor, we performed a bivariate anal-
ysis with the Cox proportional-hazards model containing sst2
and N-myc. In this model, we found that sst2 gene expression is
still a significant prognostic factor (P = 0.022), whereas N-myc
lost its predictive power (P = 0.41).

**DISCUSSION**

NB is a relatively common embryonal tumor characterized by
a remarkable biological heterogeneity (29) and, therefore, by
an enigmatic and often unpredictable clinical outcome. Hence, it
represents a therapeutic challenge. If NBs are categorized according
to clinical (tumor site, age at diagnosis) and biological features (lac-
tate dehydrogenase, histopathology, DNA ploidy, chromosome 1p
deletion, and N-myc amplification), different risk groups can be
identified (30, 31) and treated accordingly. High-risk group NB
patients are treated with intensive multiple-agent chemotherapy,
autologous bone marrow or peripheral stem cell transplantation,
immunotherapy, and radiotherapy (32). Conversely, low-risk group
NB patients, characterized by even spontaneous regression, are
treated with minimal therapy (32). Although a careful evaluation of
the known clinical and laboratory variables helps in establishing a
correct guideline for therapy, the overall cure rates for NB is not
improved much. Therefore, there is the need for new prognostic
factor(s). The ideal one would be a sensitive, repeatable, nontoxic,
and cheap indicator of the biology of the disease. We now provide
evidence that measurement of the neuroendocrine marker sst2 with
competitive RT-PCR and especially with 111In-pentetreotide
SPECT might fulfill such criteria.

In a previous study, we found that measuring sst2 gene
expression in NB primary tumors gives insights on patient
outcome (20). We now confirm in a larger study population that
an elevated concentration of sst2 correlates with a good prog-
nosis, indicating that expression of this neuroendocrine marker
is related to a more favorable biology of the tumor. In addition,
we found that the prognostic value of sst2 is independent from
and more powerful than amplification of the N-myc oncogene, a
well-recognized, strongly unfavorable outcome predictor (21,
30, 31). Hence, it is worthwhile to test the clinical value of sst2
expression in even larger series to verify whether sst2 expres-

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>sst2 (mol/μg RNA)</th>
<th>111-In-pent. ROI1/ROI_{NT} 4 h</th>
<th>Mean ± SD</th>
<th>111-In-pent. ROI1/ROI_{NT} 24 h</th>
<th>Mean ± SD</th>
<th>111-In-pent. ROI1/ROI_{NT} INC</th>
<th>Mean ± SD</th>
<th>131-I-mIBG copies</th>
<th>N-myc</th>
<th>Follow-up (mo)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5 × 10^5</td>
<td>8.15 ± 0.06</td>
<td>20.05 ± 0.04</td>
<td>1.45 ± 0.02</td>
<td>PT</td>
<td>1</td>
<td>NED 21</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>6 × 10^5</td>
<td>1.51 ± 0.06</td>
<td>2.60 ± 0.03</td>
<td>0.71 ± 0.06</td>
<td>PT</td>
<td>M</td>
<td>NED 22</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>1 × 10^5</td>
<td>1.45 ± 0.05</td>
<td>1.94 ± 0.04</td>
<td>0.33 ± 0.07</td>
<td>PT</td>
<td>M</td>
<td>NED 22</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>1 × 10^5</td>
<td>2.14 ± 0.05</td>
<td>3.20 ± 0.03</td>
<td>0.49 ± 0.05</td>
<td>PT</td>
<td>1</td>
<td>NED 33</td>
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<tr>
<td>5</td>
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<td>1.41 ± 0.02</td>
<td>1.65 ± 0.03</td>
<td>0.16 ± 0.005</td>
<td>PT</td>
<td>1</td>
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<tr>
<td>6</td>
<td>4 × 10^7</td>
<td>1.03 ± 0.02</td>
<td>1.07 ± 0.01</td>
<td>0.04 ± 0.02</td>
<td>PT</td>
<td>M</td>
<td>3</td>
<td>DOD 21</td>
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</tr>
<tr>
<td>7</td>
<td>8 × 10^7</td>
<td>2.02 ± 0.03</td>
<td>3.50 ± 0.03</td>
<td>0.72 ± 0.04</td>
<td>PT</td>
<td>3</td>
<td>NED 38</td>
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<tr>
<td>8</td>
<td>2 × 10^7</td>
<td>2.16 ± 0.05</td>
<td>2.67 ± 0.02</td>
<td>0.23 ± 0.03</td>
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<td>AWD 03</td>
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<tr>
<td>9</td>
<td>2 × 10^7</td>
<td>1.00 ± 0.01</td>
<td>1.01 ± 0.01</td>
<td>0.01 ± 0.001</td>
<td>M</td>
<td>1</td>
<td>DOD 01</td>
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</table>

*The follow-up is also reported.

INC, [TNT24h - TNT 4 h/TNT 4 h]; PT, primary tumor; M, metastasis; DOD, dead of disease; NED, no evidence of disease; AWD, alive with disease.
In Vivo and in Vitro sst2 Expression in Neuroblastoma

The relative follow-up is reported. SPECT of ROI.,/ROI mRNA molecules, as determined by competitive RT-PCR, and the log concentration of binding sites for 55 and sites concordance between the targets, this increase was not present (22). Because there was from the administration of the tracer, whereas in nontumoral reotide to tumoral binding sites was still increasing after 24 h (c) highest affinity reotide that binds the sst2 subtype of 55 receptors with the percentage of the increase of sst2 is striking indeed, taking into account that RI-PCR measures and a between an early (4 h) sst2 correlates with the two methodologies were in close agreement (P < 0.01). Ibis is noteworthy that children with a low density of sst2 mRNA by using semiquantitative 111In-pentetreotide SPECT imaging in gastroenteropancreatic tumors correlates with sst2 gene expression, as measured by semiquantitative RT-PCR (33), and tumor markers (34). In a preliminary study, we noted that the association kinetic of "In-pentetreotide "In-pentetreotide SPECI is the method for evaluation of in vivo sst2 receptors in NB patients: (a) 111In-pentetreotide is derived from the cyclic octapeptide octreotide that binds the sst2 subtype of SS receptors with the highest affinity (11, 12); (b) there is a strict correlation between the concentration of binding sites for SS and the sst2 gene expression in a wide panel of NB cell lines (19, 20); and (c) 111In-pentetreotide imaging in gastroenteropancreatic tumors correlates with sst2 gene expression, as measured by semiquantitative RT-PCR (33), and tumor markers (34). In a preliminary study, we noted that the association kinetic of 111In-pentetreotide to tumoral binding sites was still increasing after 24 h from the administration of the tracer, whereas in nontumoral targets, this increase was not present (22). Because there was concordance between the 111In-pentetreotide association study and a parallel cold-displacement study, we inferred that the percentage of the increase of 111In-pentetreotide binding between an early (4 h) and a late (24 h) time point represents an in vivo index of sst2 receptor density (22). In this study, we analyzed the value of this scintigraphic index in nine NB patients and compared results with those derived from competitive RT-PCR studies in the same subjects. Results we obtained with the two methodologies were in close agreement (P < 0.01). This is striking indeed, taking into account that RT-PCR measures sst2 gene expression in tumoral tissue obtained ex vivo, whereas 111In-pentetreotide SPECT visualizes sst2 binding sites in vivo. Although the number of patients investigated with both methods is limited, it is noteworthy that children with a low density of sst2 by RT-PCR and sst2 by scintigraphy have a poor outcome, whereas the highest concentration of receptors was found in two patients at stage IVs, characterized by a relative good prognosis (35). Assuming that further studies confirm the concordance between semiquantitative 111In-pentetreotide SPECT and competitive RT-PCR in evaluating sst2 in NB, we believe that the former method provides more information than the latter one. Indeed, NB imaging with 111In-pentetreotide not only has a potential prognostic value but also retains a definitive diagnostic value, allowing localization of primary tumors and/or metastasis (3, 9). In addition, NB imaging with 111In-pentetreotide offers the possibility of serial measurements over the course of the disease, monitoring spontaneous and therapy-induced regression or differentiation along a more mature chromaffin phenotype.

In conclusion, in this study, we provided evidence that measuring sst2 gene expression by competitive RT-PCR provides useful insights for NB patient outcome, apparently independently from amplification of N-myc. In addition, we showed, although in a limited number of patients, that similar information was acquired with competitive RT-PCR and a with a semiquantitative imaging of sst2, based on a time-related increase of 111In-pentetreotide binding to NB cells.
ACKNOWLEDGMENTS

We thank Dr. V. Giachè for his contribution to the statistical analysis of the data. We thank Professor A. Pupi for helpful comments on the manuscript.

REFERENCES


Imaging of somatostatin receptors by indium-111-pentetreotide correlates with quantitative determination of somatostatin receptor type 2 gene expression in neuroblastoma tumors.

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