CLINICAL STUDY

Oncogenic mutations in the thyrotropin receptor of autonomously functioning thyroid nodules in the Japanese population

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Abstract

Objective: Constitutively activating mutations of the thyrotropin receptor (TSHR) have been found in the majority of autonomously functioning thyroid nodules (AFTNs) in European patients. The reported frequency of these mutations varies among reports but amounts to 50–80%. To date, only one such mutation responsible for AFTNs has been identified in the Japanese population and the pathogenic role of such mutations in Japanese AFTNs has been questioned. In the present study, we evaluated the frequency of activating mutations in the TSHR and Gαs in 10 Japanese AFTNs.

Design: Genomic DNA was extracted from fresh frozen tissue. The TSHR and the almost entire sequence of the gene coding for the α subunit of Gα have been amplified and sequenced.

Results: In sequence analysis, four mutations in the TSHR (T632A, I486M, M453T and L512R) were found. To complete our analysis, we searched mutations in the gene coding for the α subunit of Gα, in the samples negative for TSHR mutations. In one case a mutation (R201H) affecting GTPase activity was found.

Conclusions: If we focus on the solitary nodules, we obtain the same mutation proportion as in European patients (70%). The absence of TSHR and Gα mutations in a significant proportion of autonomous adenomas in multinodular goiters suggests that other causes may also play a role in the genesis of these lesions.

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Introduction

Under physiological circumstances, thyroid stimulating hormone (TSH) is the main factor that controls thyroid function and growth (1–3). TSH acts by binding to its receptor which is a member of the large family of G protein-coupled receptors. In human thyroid, the TSH receptor activates adenyl cyclase via a Gα protein and at higher concentrations phospholipase C via Gqα. The main second messenger of TSH action, in the human thyroid is cyclic AMP (cAMP) (2). Intracellular concentrations of cAMP control the maintenance of the differentiated phenotype of thyocytes, the level of functional activity of the gland (trapping of iodide, secretion of thyroid hormones) and growth (3, 4). A chronic increase in this concentration is thus expected to cause toxic hyperplasia if all the thyocytes of a gland are involved (4), or clonal expansion of the cell and an autonomous adenoma as a result of a somatic mutation. Clinically, autonomous functioning thyroid nodules (AFTNs) are well documented. They are well defined encapsulated benign tumors which grow, metabolize iodide and secrete thyroid hormones independently of TSH. They are diagnosed at scintigraphy by a high localized uptake of radioiodide or Tc-99m pertechnetate, surrounded by barely or non-visible quiescent tissue. The low uptake of normal tissue results from low TSH serum levels, themselves a consequence of autonomous secretion of thyroid hormones by the nodule. AFTNs can be solitary or part of a multinodular goiter. In European patients, the main cause of this disease is mutations in the TSH receptor, increasing the constitutive activity of this receptor on adenylate cyclase (5–8). The reported frequency of these mutations varies in different articles from 50–80% in Belgium and Germany (6, 9). These include studies in which only part of the TSH receptor (exon 10) has been sequenced. In Japan, a study including
45 cases reported only one TSH receptor mutation, but no increase in the basal cAMP level could be demonstrated in cells transfected with this mutated receptor (10). Since then, one TSH receptor activating mutation has been found in a Japanese patient (11).

Any other player of the cAMP cascade, if activated, would lead to the same result as an activated TSH receptor. To date, two mutations of Gαs have been identified: Q227L and R201H (in exons 8 and 9), which activate the protein, ‘locking’ it in its GTP-bound signaling conformation leading to adenyl cyclase activation in a receptor independent way (gsp mutations). gsp Mutations have been found in 3–6% of AFTNs in Europe (6, 9). A Japanese study, Tanaka et al. (12), found only one case out of 38 studied. Although the discrepancies between the Japanese and the European studies may perhaps be explained by methodological differences (13), they raise the question whether the frequency of activating mutations in the TSH receptor and Gαs in AFTNs is actually much lower in Japan than in Europe.

Subjects and methods

Patients

Ten adenomas and their juxtanodular tissue were obtained from Japanese patients. Some characteristics of the patients and their adenomas are summarized in Table 1. The diagnosis was established by scintigraphy. As shown in Table 1, four proven solitary adenomas were studied, three with total suppression of contralateral uptake, hyperthyroidism and decreased TSH levels and one with partial suppression of contralateral uptake and TSH levels. Two with euthyroidism, partial hyperthyroidism and total suppression of contralateral uptake were studied, three with total suppression of contralateral uptake, hyperthyroidism and decreased TSH levels. Six cases of multinodular goiters were studied: three with total suppression of contralateral uptake in the contralateral lobe; two with euthyroidism, partial suppression of contralateral uptake, hyperthyroidism and decreased TSH levels and one with partial suppression of contralateral uptake. The study was approved by the local ethical committee, and informed consent was obtained from all the participants before testing.

Sequencing of the TSHR and Gαs genes

Fresh tissue, obtained by surgery in Japan, was frozen and sent to Brussels. Genomic DNA was extracted from adenomatous tissue and from juxtanodular quiescent tissue. Briefly, the samples were incubated with 10 mg/ml proteinase K in 50 mM Tris–HCl pH 8.0, 100 mM EDTA, 100 mM NaCl and 1% SDS at 56°C overnight, then phenol extracted and ethanol precipitated. Genomic DNA was finally resuspended in 500 µl TE pH 7.5 (10 mM Tris–HCl, 1 mM EDTA). All coding portions of the TSH receptor gene were sequenced using a total of 14 PCR amplified fragments. Except for exon 1, the entire Gαs gene was amplified using nine couples of primers. Table 2 summarizes the pairs of primers chosen to amplify the TSHR and Gαs. Each PCR was performed in a final volume of 20 µl containing 200 ng DNA, 0.5 µl Taq DNA polymerase (BRL), 3 pmol of each primer, 10 mM Tris–HCl pH 8.3, 50 mM KCl, 1.5 mM MgCl2, 0.01% gelatin and 0.2 mM dNTPs. For the amplification of the Gαs exon 12, we used the Ampli Taq Gold (Roche). All the reactions were started with an initial denaturation at 93°C for 2 min 30 s (except for: Gαs exon 8–9, 95°C for 3 min; Gαs exon 10–11, 95°C for 2 min 30 s; Gαs exon 12, 95°C for 12 min) followed by 30 cycles (for the Gαs exon 6: 35 cycles). Annealing temperature was 54°C for TSHR 1, 4, 5, 7; 48°C for TSHR 2, 10 residues 635–stop; 52°C for TSHR 3, 6, 8, 10 residues 322–449, 10 residues 295–344, 10 residues 430–537, Gαs exon 7: 61°C for TSHR 9; 50°C for TSHR 10 residues 322–449, 10 residues 526–646. Gαs exon 3, 4–5, 10–11, 12, 13, 58°C for Gαs Exon 2.6 and 59°C for Gαs exon 8–9.

PCR products were sequenced on both strands using the DNA Sequencing Kit (PE Applied Biosystems).
Table 2: Summary of the primers used for the PCR amplification of the TSHR and Gαs.

<table>
<thead>
<tr>
<th>Exon</th>
<th>Forward primer</th>
<th>Reverse primer</th>
</tr>
</thead>
<tbody>
<tr>
<td>TSHR 1</td>
<td>5’ M13D GAGGATGGAAGATAGCCCGGAG 3’</td>
<td>5’ M13R CACTACCCTGGGCTTTAGG 3’</td>
</tr>
<tr>
<td>TSHR 2</td>
<td>5’ M13D TAAGGGTAATATGAGAAAAAG 3’</td>
<td>5’ M13R CTGATAGACGTTGACAGAA 3’</td>
</tr>
<tr>
<td>TSHR 3</td>
<td>5’ M13D GAGAATCTAGGACGGGTCTG 3’</td>
<td>5’ M13R AGAAACGGGCCTCCCATG 3’</td>
</tr>
<tr>
<td>TSHR 4</td>
<td>5’ SP6 ACCCTGTTGGATTAGATAT 3’</td>
<td>5’ M13R GGGCCAGGCGTATACACCT 3’</td>
</tr>
<tr>
<td>TSHR 5</td>
<td>5’ M13D AGGTGACTACAGGCTTCCCT 3’</td>
<td>5’ M13R GTTGAATGCCTTGAATAG 3’</td>
</tr>
<tr>
<td>TSHR 6</td>
<td>5’ M13D TATGCTGCTGGCTTTTATTAAGGTA 3’</td>
<td>5’ M13R GTCTCTATAGAGTTATATGATAAGG 3’</td>
</tr>
<tr>
<td>TSHR 7</td>
<td>5’ M13D TGGGATCATAAGGCTGGCCTG 3’</td>
<td>5’ M13R TGGTGGCTACACTACTCGG 3’</td>
</tr>
<tr>
<td>TSHR 8</td>
<td>5’ M13D TGGTCACTTTATTTGATATTCTG 3’</td>
<td>5’ M13R ATATTCTTTTGTATGTTATACCT 3’</td>
</tr>
<tr>
<td>TSHR 9</td>
<td>5’ M13D TCATTCCCAATTAACCTCAGG 3’</td>
<td>5’ M13R GCTTCCAATTTTCCCTTCC 3’</td>
</tr>
<tr>
<td>TSHR 10 residues 295–344</td>
<td>5’ M13D TGGGACGACCTTCTTTCTGTG 3’</td>
<td>5’ M13R TGGGATACATATGTGGGACCTG 3’</td>
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<tr>
<td>TSHR 10 residues 322–449</td>
<td>5’ M13D TGATGAACTGCTTTGATG 3’</td>
<td>5’ M13R TGGCATATCTATTGAGCT 3’</td>
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<tr>
<td>TSHR 10 residues 349–421</td>
<td>5’ M13D TGGTAAGCTCTTGATG 3’</td>
<td>5’ M13R TGGGATACATATGTGGGACCTG 3’</td>
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<tr>
<td>TSHR 10 residues 430–537</td>
<td>5’ M13D TGGGAATCTACTGCTCAGGTG 3’</td>
<td>5’ M13R CCCCAAAGGCCACCTATA 3’</td>
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<tr>
<td>TSHR 10 residues 439–537</td>
<td>5’ M13D TCAGTGTTTAGGAAGATCTG 3’</td>
<td>5’ M13R CGTTGCTGTCAGTTCTC 3’</td>
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<td>TSHR 10 residues 526–646</td>
<td>5’ M13D TGGTATGCCATCACCTTC 3’</td>
<td>5’ M13R TGGGAATCTACTGCTCAGGTG 3’</td>
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<tr>
<td>TSHR 10 residues 635stop</td>
<td>5’ M13D TGTGAATGCTTGAATAGCC 3’</td>
<td>5’ M13R TGGCATATCTATTGAGCT 3’</td>
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<tr>
<td>Gαs 2</td>
<td>5’ M13D GACCTCCTCCTGCGCAAGT 3’</td>
<td>5’ M13R CAGGTTGCACATGAGAAAGC 3’</td>
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<tr>
<td>Gαs 3</td>
<td>5’ M13D CTGATGTTGGAGGAATCTG 3’</td>
<td>5’ M13R CAGGTTGCACATGAGAAAGC 3’</td>
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<td>Gαs 4</td>
<td>5’ M13D CAGAAGTCAGGAGACACCG 3’</td>
<td>5’ M13R AGAAACCAGGCACCTCAG 3’</td>
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<tr>
<td>Gαs 6</td>
<td>5’ M13D ACTAGCTTTGGAATGACAGT 3’</td>
<td>5’ M13R AGAAACCAGGCACCTCAG 3’</td>
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<tr>
<td>Gαs 7</td>
<td>5’ M13D TCCATGCTTCTGTGCTG 3’</td>
<td>5’ M13R GGAAGCTGGGCTATTG 3’</td>
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<tr>
<td>Gαs 8-9</td>
<td>5’ M13D CTGCTCCTTCTGCTGCTG 3’</td>
<td>5’ M13R TGGCATATCTATTGAGCT 3’</td>
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<tr>
<td>Gαs 10-11</td>
<td>5’ M13D GGTGGTTCAGAAAGAGC 3’</td>
<td>5’ M13R TGGCATATCTATTGAGCT 3’</td>
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<td>Gαs 12</td>
<td>5’ M13D CATGACACCCAGCTCTGTTG 3’</td>
<td>5’ M13R CATGGAACCTGGGTAGCGAC 3’</td>
</tr>
<tr>
<td>Gαs 13</td>
<td>5’ M13D CATCAGGGATAGGGTGTTTC 3’</td>
<td>5’ M13R CGTTGATCAATATGCTTTTAC 3’</td>
</tr>
</tbody>
</table>

1 Primers defined by de Roux et al. (14); M13D, M13R and SP6 correspond to universal sequencing primers (ABI).

Samples were loaded on an Applied Biosystems 373 Stretch Sequencing Instrument and analyzed using the Factura and Sequence Navigator software (ABI).

Results

By sequencing the entire TSHR gene in 10 AFTNs from Japanese patients, four mutations were identified (Table 1). The only mutation L512A described in the Japanese population by Kosugi (11) was among the four mutations found. Three mutations detected (I486M, M453T and L512R) have already been reported in the European population and all enhance the constitutive activity of the receptor versus adenylate cyclase when expressed in eukaryotic cells (6, 9, 14, 15). The fourth T632A has been found in AFTN and cancer but its activating effect has not yet been demonstrated (9, 16), although the similar mutation T632I found in AFTN and Gαs has not previously been identified in thyroid tumors (6, 9, 17).

Discussion

In the present study, we examined the incidence of TSHR and gsp mutations in a series of 10 autonomous thyroid adenomas from Japan. In a previous study, Takeshita et al. (10) examined 45 AFTNs in Japanese patients. They had found a TSHR gene alteration (deletion of three adenines which resulted in Asp 619 deletion) in one only case. This mutant did not show constitutive activation in transfection experiments. They concluded that there was no activating mutation of the TSHR in AFTNs in the Japanese population. However, the possibility that the AFTNs examined had TSHR mutations cannot be excluded because only a 167 base pair region was analyzed. Kosugi et al. who had identified a mutation responsible for AFTNs in the Japanese population sequenced the entire exon 10 of the receptor. However amino acid substitutions conferring constitutive activity of the TSHR have also been found elsewhere in the extra-cellular amino–terminal domain (18). We therefore sequenced the entire TSHR gene and identified four activating TSHR mutations among the 10 AFTNs from Japanese patients. We also searched for mutations in the gene coding for the α subunit of Gαs. We analyzed not only the two hot spots classically described but almost the entire sequence from exon 2 to 13 of the protein Gαs. One mutation at position 201, corresponding to one of the known hot spots affecting the GTPase activity, was discovered in one of the AFTN negative for TSHR activating mutations. The sequencing of the other coding portions of the Gαs has not revealed any other mutation. Thus the incidence of
oncogenic mutations of proteins of the cAMP cascade in Japanese AFTN is not rare. Indeed, the frequency of such mutations in Europe is 50–80%. The discrepancy of the prevalence of TSHR mutations among AFTNs found in different populations was suggested to be associated with different ethnic origins of the patients (10). It may in fact mainly be related to the completeness of the sequencing. It may also be related to the correspondence of the diagnosis in the different countries. It is also interesting that among the four solitary adenomas investigated, three demonstrated activating mutations of the TSH receptor or Gαs, i.e. the same proportion as in Europe. These three adenomas are those in which all the criteria for the diagnosis were fulfilled: hyperthyroidism, low TSH levels and suppression of the uptake in the contralateral lobe. For the adenoma in which no mutation was found, the patient was not hyperthyroid, and both the contralateral uptake and the TSH levels were only partially suppressed. Only two activating mutations have been found in six hot nodules of multinodular goiters. One among the three patients with hyperthyroidism and suppression of contralateral uptake and TSH levels; one among the two who were not hyperthyroid and had only partial suppression of uptake and TSH levels; none in patient 1, who was euthyroid, had normal TSH levels and only partial suppression of contralateral uptake. The diagnosis of this latter adenoma is therefore doubtful. The Belgian and Italian statistics apply to solitary adenomas although mutations have been found in different nodules of the same toxic multinodular goiter. One among the three patients with hyperthyroidism and suppression of contralateral uptake and TSH levels; one among the two who were not hyperthyroid and had only partial suppression of uptake and TSH levels; none in patient 1, who was euthyroid, had normal TSH levels and only partial suppression of contralateral uptake. The diagnosis of this latter adenoma is therefore doubtful. The Belgian and Italian statistics apply to solitary adenomas although mutations have been found in different nodules of the same toxic multinodular goiter, but less frequently (19 – 22). It should be noted that whereas single nodules are most often monoclonal, nodules of multinodular goiters are often polyclonal (23, 24). The absence of TSHR and Gαs mutations in a significant proportion of autonomous adenomas suggests that other mutations may be found in the proteins of the cAMP cascade downstream of Gαs or even in proteins of other cascades provided that the mutation leads to proliferation with conservation of differentiation (for example, constitutive activation of the IGF1 receptor, by IGF1, in transgenic mice leads to thyroid autonomy) (25).

The real difference between Japan and Europe is the low prevalence of autonomous adenomas in Japan, low prevalence has also been shown in the United States (26). This has been related to the high level of dietary iodide which has been shown in Denmark (27) and in Switzerland (28) to be inversely related to the incidence of thyroid autonomous adenomas.

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