Intracellular expression of reactive oxygen species-generating NADPH oxidase NOX4 in normal and cancer thyroid tissues

Urbain Weyemi¹,²,³*, Bernard Caillou³*, Monique Talbot¹,³, Rabii Ameziane-El-Hassani¹,⁴, Ludovic Lacroix³, Odile Lagent-Chevallier¹,²,³, Abir Al Ghuzlan³, Dirk Roos⁵, Jean-Michel Bidart²,³, Alain Virion¹,²,³, Martin Schlumberger²,³ and Corinne Dupuy¹,²,³

¹CNRS, FRE2939, Villejuif F-94805, France
²University Paris-Sud 11, Orsay F-91400, France
³Institut Gustave Roussy, FRE2939 CNRS, 39 rue Camille Desmoulins, Villejuif F-94805, France
⁴UBRM, Centre National de l’Energie, des Sciences et des Techniques Nucléaires, Rabat M-10001, Morocco
⁵Sanquin Research, and Landsteiner Laboratory, Academic Medical Centre, University of Amsterdam, Amsterdam NL-1006, The Netherlands

(Correspondence should be addressed to C Dupuy at Institut Gustave Roussy, FRE2939 CNRS; Email: dupuy@igr.fr)

*(U Weyemi and B Caillou contributed equally to this work)

Abstract

NADPH oxidase 4 (NOX4) belongs to the NOX family that generates reactive oxygen species (ROS). Function and tissue distribution of NOX4 have not yet been entirely clarified. To date, in the thyroid gland, only DUOX1/2 NOX systems have been described. NOX4 mRNA expression, as shown by real-time PCR, was present in normal thyroid tissue, regulated by TSH and significantly increased in differentiated cancer tissues. TSH increased the protein level of NOX4 in human thyroid primary culture and NOX4-dependent ROS generation. NOX4 immunostaining was detected in normal and pathologic thyroid tissues. In normal thyroid tissue, staining was heterogeneous and mostly found in activated columnar thyrocytes but absent in quiescent flat cells. Papillary and follicular thyroid carcinomas displayed more homogeneous staining. The p22phox protein that forms a heterodimeric enzyme complex with NOX4 displayed an identical cellular expression pattern and was also positively regulated by TSH. ROS may have various biological effects, depending on the site of production. Intracellular NOX4–p22phox localization suggests a role in cytoplasmic redox signaling, in contrast to the DUOX localization at the apical membrane that corresponds to an extracellular H₂O₂ production. Increased NOX4–p22phox in cancer might be related to a higher proliferation rate and tumor progression but a role in the development of tumors has to be further studied and established in the future.

Endocrine-Related Cancer (2010) 17 27–37

Introduction

Reactive oxygen species (ROS) are highly reactive O₂ metabolites, including superoxide radical (O₂‾) and hydrogen peroxide (H₂O₂). ROS were first considered as toxic byproducts resulting in oxidative stress and damaging to biomolecules, but some early studies revealed their physiological properties (Lambeth 2007). Until 1999, the NADPH oxidase (NOX) of phagocytes was the only enzymatic system known to produce O₂‾ and H₂O₂ (Babior 1999). This enzyme, which consists of a large β-subunit termed NOX2, formerly known as gp91phox, and a 22 kDa α-subunit (p22phox), is involved in bacterial killing. To date, six homologs of NOX2 have been discovered, which are expressed in many tissues and constitute a new family of enzymes called NOX/DUOX (Bedard & Krause 2007). The different localizations of NOX/DUOX at the tissue, cellular and/or subcellular levels also appear related to their various functions (Babior 1999, Bedart & Krause 2007, Lambeth 2007).
**DUOX** genes are strongly expressed in the thyroid gland, and DUOX proteins are located at the apical membrane of the thyrocytes (Dupuy et al. 1999, De Deken et al. 2000). DUOX2 generates the H₂O₂ in the extracellular colloid space that is used by the thyroid peroxidase (TPO) to organify iodide, whereas the role of DUOX1 is still unknown. Up to now, these two DUOX proteins were the only H₂O₂ generating systems described in this tissue.

ROS production has already been demonstrated in rat thyroid cells (Pomerance et al. 2000), but for the above mentioned reasons this production cannot be explained by the activity of DUOX1 and 2, suggesting the existence of other ROS-producing systems.

p22<sub>phox</sub>, a subunit functionally associated with NOX1, NOX2, NOX3 and NOX4, was shown to co-immunoprecipitate with DUOX proteins in human thyrocytes, suggesting that it could also constitute a partner of these H₂O₂-generating systems (Wang et al. 2005). However, co-transfection experiments showed that p22<sub>phox</sub> had no effect on DUOX activity, suggesting that p22<sub>phox</sub> might not interact with DUOX but rather with another NOX that might also be expressed in the thyroid tissue (Ameziane-El-Hassani et al. 2005).

In this study, we demonstrate the expression of NOX4 in normal and cancer thyroid tissues that may be a H₂O₂ generator located inside the thyroid cell. NOX4 expression is increased by TSH stimulation, suggesting a role of ROS in TSH signaling.

**Materials and methods**

**Reverse transcription and PCR**

Total RNA from cells was extracted with Trizol reagent (Invitrogen, Inc.) according to the manufacturer’s instructions. Total RNA (1 μg) was reverse transcribed using 10 U Superscript III transcriptase (Invitrogen) in 20 μl PCR buffer according to the manufacturer’s protocol for 60 min at 55°C. cDNA was then amplified by 30 temperature cycles (95°C, 30 s; 60°C, 10 s; 72°C, 1 min) in a GeneAmp 9600 apparatus and AmpliTaq Gold’s protocol (Applied Biosystems, Foster City, CA, USA). Selected primers are listed in Table 1.

**Tissue samples and real-time RT-PCR**

Eighty-nine frozen thyroid tissue samples stored in liquid nitrogen were selected after histological analysis and classification according to World Health Organization recommendations, as previously described (Lacroix et al. 2005). Tissues were collected at Institut Gustave Roussy, and informed consent was obtained from all patients. The tissue collection included 15 follicular thyroid adenomas (FTA), 26 follicular thyroid carcinomas (FTC), 19 papillary thyroid carcinomas (PTC), 4 anaplastic thyroid carcinomas (ATC), and 25 nontumoral contralateral thyroid tissues obtained from patients with a unifocal tumor and considered as normal.

### Table 1: Forward (sense) and reverse (antisense) oligonucleotides

<table>
<thead>
<tr>
<th>NOX</th>
<th>Sense</th>
<th>Sequence 5’–3’</th>
<th>Size of PCR product (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>NOX1</td>
<td>+</td>
<td>ACAAATTCAGTGTGCAGACCAC</td>
<td>371</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>AGACTGGAATATCGTGAGACCA</td>
<td></td>
</tr>
<tr>
<td>NOX2</td>
<td>+</td>
<td>GGGCTGTGCAATGCGTTGTGGCT</td>
<td>389</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>ACATTTTTCCTCTCATCATGGTGCG</td>
<td></td>
</tr>
<tr>
<td>NOX3</td>
<td>+</td>
<td>GGATCGGAGTCACTCCCTCTGCTG</td>
<td>435</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>ATGAACACCTCTGGGGTCAGCTGA</td>
<td></td>
</tr>
<tr>
<td>NOX4</td>
<td>+</td>
<td>GGTGTATTCCTCCTAGTACAC</td>
<td>299</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>AATCTGGGCTTCTCTCATACAAA</td>
<td></td>
</tr>
<tr>
<td>NOX5</td>
<td>+</td>
<td>ATCAAGGGGGCCCCCTTTTTAC</td>
<td>215</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>CTCACTTCTGACACTCTCTGACAGC</td>
<td></td>
</tr>
<tr>
<td>PAX8</td>
<td>+</td>
<td>CCT TTG TGA ATG GCA GAC CT</td>
<td>375</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>TAG GGA GTT TGA ATG GTT GC</td>
<td></td>
</tr>
<tr>
<td>TSHR</td>
<td>+</td>
<td>CTT GCT GGA GTG GTC TCA AA</td>
<td>418</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>CTG GCC AAA ACC AAT GAT CT</td>
<td></td>
</tr>
<tr>
<td>TPO</td>
<td>+</td>
<td>CGG GTC ATC TGT GAC AAC AC</td>
<td>448</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>CGG AGT CTA CGC AGG TTC TC</td>
<td></td>
</tr>
<tr>
<td>TG</td>
<td>+</td>
<td>AGG CCC TGC TCT CTA ACT CC</td>
<td>445</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>GCC AAA GGA GTG CTG AAG TC</td>
<td></td>
</tr>
<tr>
<td>NIS</td>
<td>+</td>
<td>CTCCCTGTAAACGACTCCAG</td>
<td>412</td>
</tr>
<tr>
<td></td>
<td>−</td>
<td>GACCACCATCATGTCCAACA</td>
<td></td>
</tr>
</tbody>
</table>

+/− Means that the oligonucleotide is sense or antisense relative to cDNA.
tissues based on histological examination (including 15 paired samples with 2 FTA, 3 FTC, 9 PTC, and 1 ATC).

Total RNA was extracted from frozen tissue samples with Trireragent (Sigma–Aldrich) and then purified on Rneasy columns (Qiagen) according to the manufacturer’s protocols. Quality of RNA preparation, based on the 28S/18S rRNAs ratio, was assessed with the RNA 6000 Nano Lab-On-chip (Agilent Technologies, Palo Alto, CA, USA). One microgram of total RNA was reverse transcribed by Moloney murine leukemia virus reverse transcriptase in the presence of random primers as previously described (Applied Biosystems).

Oligonucleotide primers and Taqman probes specific for the NOXes, including NOX4 and p22phox, were designed to be intron spanning by the Primer-Express computer software (Applied Biosystems). Sequences were obtained from the GenBank database, and the oligonucleotides were purchased from MWG Biotech (Courtaboeuf, France); these sequences are available on demand. Primers and probes for 18S were obtained from Assays-On-Demand (Applied Biosystems). Q-PCRs were performed on the equivalent of 10 ng total RNA per tube in a final volume of 18 μl (Lacroix et al. 2005). Each primers and probes have been controlled not to cross-react, to avoid amplification dimmers, and to provide optimal amplification efficiency tested with standard curves constructed from pool of cDNA from several tissues and cell lines that were serially diluted in nuclease-free RNAse-free water. Moloney murine leukemia virus reverse transcriptase has been therefore used. To avoid amplification dimmers, and to provide optimal amplification efficiency, standard curves were constructed from pool of cDNA from several tissues and cell lines that were serially diluted in nuclease-free RNAse-free water. Moloney murine leukemia virus reverse transcriptase (M-MLV) was obtained from Promega (Madison, WI, USA). Quality of RNA was assessed with the RNA 6000 Nano Lab-On-chip (Agilent Technologies, Palo Alto, CA, USA). One microgram of total RNA was reverse transcribed by Moloney murine leukemia virus reverse transcriptase in the presence of random primers as previously described (Applied Biosystems).

Oligonucleotide primers and Taqman probes specific for the NOXes, including NOX4 and p22phox, were designed to be intron spanning by the Primer-Express computer software (Applied Biosystems). Sequences were obtained from the GenBank database, and the oligonucleotides were purchased from MWG Biotech (Courtaboeuf, France); these sequences are available on demand. Primers and probes for 18S were obtained from Assays-On-Demand (Applied Biosystems). Q-PCRs were performed on the equivalent of 10 ng total RNA per tube in a final volume of 18 μl (Lacroix et al. 2005). Each primers and probes have been controlled not to cross-react, to avoid amplification dimmers, and to provide optimal amplification efficiency tested with standard curves constructed from pool of cDNA from several tissues and cell lines that were serially diluted in nuclease-free RNAse-free water. Moloney murine leukemia virus reverse transcriptase (M-MLV) was obtained from Promega (Madison, WI, USA). Quality of RNA was assessed with the RNA 6000 Nano Lab-On-chip (Agilent Technologies, Palo Alto, CA, USA). One microgram of total RNA was reverse transcribed by Moloney murine leukemia virus reverse transcriptase in the presence of random primers as previously described (Applied Biosystems).

Oligonucleotide primers and Taqman probes specific for the NOXes, including NOX4 and p22phox, were designed to be intron spanning by the Primer-Express computer software (Applied Biosystems). Sequences were obtained from the GenBank database, and the oligonucleotides were purchased from MWG Biotech (Courtaboeuf, France); these sequences are available on demand. Primers and probes for 18S were obtained from Assays-On-Demand (Applied Biosystems). Q-PCRs were performed on the equivalent of 10 ng total RNA per tube in a final volume of 18 μl (Lacroix et al. 2005). Each primers and probes have been controlled not to cross-react, to avoid amplification dimmers, and to provide optimal amplification efficiency tested with standard curves constructed from pool of cDNA from several tissues and cell lines that were serially diluted in nuclease-free RNAse-free water. Moloney murine leukemia virus reverse transcriptase (M-MLV) was obtained from Promega (Madison, WI, USA). Quality of RNA was assessed with the RNA 6000 Nano Lab-On-chip (Agilent Technologies, Palo Alto, CA, USA). One microgram of total RNA was reverse transcribed by Moloney murine leukemia virus reverse transcriptase in the presence of random primers as previously described (Applied Biosystems).

Oligonucleotide primers and Taqman probes specific for the NOXes, including NOX4 and p22phox, were designed to be intron spanning by the Primer-Express computer software (Applied Biosystems). Sequences were obtained from the GenBank database, and the oligonucleotides were purchased from MWG Biotech (Courtaboeuf, France); these sequences are available on demand. Primers and probes for 18S were obtained from Assays-On-Demand (Applied Biosystems). Q-PCRs were performed on the equivalent of 10 ng total RNA per tube in a final volume of 18 μl (Lacroix et al. 2005). Each primers and probes have been controlled not to cross-react, to avoid amplification dimmers, and to provide optimal amplification efficiency tested with standard curves constructed from pool of cDNA from several tissues and cell lines that were serially diluted in nuclease-free RNAse-free water. Moloney murine leukemia virus reverse transcriptase (M-MLV) was obtained from Promega (Madison, WI, USA). Quality of RNA was assessed with the RNA 6000 Nano Lab-On-chip (Agilent Technologies, Palo Alto, CA, USA). One microgram of total RNA was reverse transcribed by Moloney murine leukemia virus reverse transcriptase in the presence of random primers as previously described (Applied Biosystems).

Oligonucleotide primers and Taqman probes specific for the NOXes, including NOX4 and p22phox, were designed to be intron spanning by the Primer-Express computer software (Applied Biosystems). Sequences were obtained from the GenBank database, and the oligonucleotides were purchased from MWG Biotech (Courtaboeuf, France); these sequences are available on demand. Primers and probes for 18S were obtained from Assays-On-Demand (Applied Biosystems). Q-PCRs were performed on the equivalent of 10 ng total RNA per tube in a final volume of 18 μl (Lacroix et al. 2005). Each primers and probes have been controlled not to cross-react, to avoid amplification dimmers, and to provide optimal amplification efficiency tested with standard curves constructed from pool of cDNA from several tissues and cell lines that were serially diluted in nuclease-free RNAse-free water. Moloney murine leukemia virus reverse transcriptase (M-MLV) was obtained from Promega (Madison, WI, USA). Quality of RNA was assessed with the RNA 6000 Nano Lab-On-chip (Agilent Technologies, Palo Alto, CA, USA). One microgram of total RNA was reverse transcribed by Moloney murine leukemia virus reverse transcriptase in the presence of random primers as previously described (Applied Biosystems).

Oligonucleotide primers and Taqman probes specific for the NOXes, including NOX4 and p22phox, were designed to be intron spanning by the Primer-Express computer software (Applied Biosystems). Sequences were obtained from the GenBank database, and the oligonucleotides were purchased from MWG Biotech (Courtaboeuf, France); these sequences are available on demand. Primers and probes for 18S were obtained from ...
medium (5H); 1 mU/ml TSH was then added to the medium for 48 h as required. The knockdown efficiency was checked by real-time QPCR.

**Measurement of intracellular ROS**

Intracellular ROS levels were measured by flow cytometry in cells loaded with the redox-sensitive dye 2',7'-dichlorofluorescin diacetate (DCFH-DA; Invitrogen Molecular probe). The nonfluorescent DCFH-DA readily diffuses into the cells, where it is hydrolyzed to the polar derivative DCFH, which is oxidized in the presence of H$_2$O$_2$ to the highly fluorescent DCF. Approximately 5×10$^5$ cells were harvested by trypsinization, resuspended in 0.5 ml culture medium (Ham’s F-12) supplemented with 0.2% (v/v) FCS and incubated with 10 μM DCFH-DA for 30 min in the dark at 37 °C. Fluorescence was recorded on FL-1 channel of FACScan (Becton Dickinson, Le pont-de-Clai, France).

**Western blots**

Human thyrocytes were washed twice with PBS and directly solubilized in denaturing sample buffer (Tris/HCl 10 mM pH 7, 2.5% (w/v) SDS, 1 mM EDTA, 1 mM EGTA, 4 M urea and protease inhibitors (0.1 mM phenylmethylsulphonyl fluoride, 5 μg/ml aprotinin, 5 μg/ml leupeptine, 157 μg/ml benzamidine and 1 μg/ml pepstatine)). Protein samples (20 μg) supplemented with 2.5% (w/v) β-mercaptoethanol and 10% glycerol were sonicated for 15 s and denatured at 70 °C during 10 min. They were then subjected to SDS-PAGE on a 4–12% acrylamide slab minigel (NUPAGE, Invitrogen) and electrotransferred to SDS-PAGE on a 4–12% acrylamide slab minigel 8 at 70 and 10% glycerol were sonicated for 15 s and denatured b

**Immunohistochemistry**

Forty-one thyroid samples were obtained from patients who underwent surgery at Institut Gustave Roussy. Informed consent was obtained from all patients. These samples included normal thyroid tissue (n = 8); nodular and/or diffuse hyperplasia (n = 11); follicular adenoma (n = 4); papillary carcinoma (n = 11); follicular carcinoma (n = 3); and poorly differentiated follicular carcinoma (n = 4).

Immunochemical staining was performed on formaldehyde-fixed, paraffin-embedded tissues, as previously described (Caillou et al. 2001). Briefly, 5-micron sections were deparaffinized. Endogenous peroxidase activity was quenched by incubation in 0.03% hydrogen peroxide, in 0.1 mol/l Tris–HCl buffer 1× (pH 7.6) for 5 min. Microwave/pressure cooker pretreatment was performed in 1 mmol/l EDTA buffer (pH 8). Sections were subsequently incubated for 60 min at room temperature with the rabbit polyclonal anti-NOX4 antiserum (1:100), with the anti-DUOX antiserum (1:100 dilution) (Caillou et al. 2001) that cross-reacted with DUOX1 and DUOX2 proteins (Morand et al. 2003), with the anti-Na/I symporter (NIS) serum (1:500) (Caillou et al. 2001), with the monoclonal anti-CD34 (NOVO/MENARINI; clone QB END/10; dilution: 1:60), and with the monoclonal anti-human-p22 phox (p22 phox) (1:50) (mouse monoclonal antibody 449, Verhoeven et al. 1989). Sections were then washed in Tris–HCl 1× buffer for 5 min and incubated with a peroxidase-conjugated goat anti-rabbit antibody for 30 min (ENVISION; DAKO Corp., Carpinteria, CA, USA). After further washes, peroxidase staining was revealed in diaminobenzidine tetrahydrochloride (Polysciences Inc., Warrington, PA, USA) with 0.1% (w/v) of hydrogen peroxide, in Tris buffer, 0.01 mol/l (pH 7.2). Sections were counterstained and mounted. Negative controls were obtained by replacing the specific primary antibody by an irrelevant antibody. Kidney tissue was used as positive controls for NOX4 antibody (Shiose et al. 2001).

The percentage of positively stained cells was assessed semiquantitatively, being 0–25; 25–50; 50–75; or 75–100%, as well as the intensity of staining in NOX4-positive cells.

**Statistical analysis**

The tests were performed using the GraphPad InStat software (La Jolla, CA, USA) for ANOVA, Student $t$-test with the level of significance set at $P<0.05$.

**Results**

NOX mRNAs expression was analyzed by RT-PCR in normal human thyroid tissue and in human thyrocytes in culture (Fig. 1). All NOX genes, except NOX3 gene, were expressed in the thyroid tissue. NOX2, referred to as the phagocyte NOX, was detected in thyroid tissues and is known to be expressed in phagocytic cells and endothelial cells. The expression levels of NOX1 and
and p22phox mRNA was also detected at a low level but only NOX4 mRNA levels showed greater variation in human thyrocytes. However, during TSH stimulation, TSH increased the expression of these two genes (2- to 45-fold) at 48 h as compared with NOX4 levels increased after exposure to TSH, with a greater increase of p22phox protein level. NOX4 protein had an apparent molecular mass of 75 kDa, corresponding to its expected molecular weight (Wingler et al. 2001, Hilenski et al. 2004). Expression of the thyroid-specific protein TPO was shown as control (Fig. 2B). Because the NADPH oxidase NOX4 was described to play a role in superoxide and hydrogen peroxide production, we evaluated its contribution of increased intracellular ROS in TSH-stimulated thyrocytes. Figure 2C shows that TSH treatment for 48 h increased intracellular ROS levels (DCF fluorescence). Transfection of human thyrocytes with short interfering RNAs to NOX4 abolished the increase in intracellular ROS indicating that NOX4 was responsible for ROS generation elicited by TSH. Determination of the NOX4 and p22phox mRNA levels in normal and tumor tissues was done by real-time QPCR.

As shown in Fig. 3A, the expression levels of NOX4 and p22phox mRNA varied only by eight- and five-fold among normal thyroid tissues respectively but by 54- and 95-fold among malignant thyroid tumors.

In benign thyroid tumors, NOX4 and p22phox gene expression levels were not significantly different from those observed in normal thyroid tissues. However, the expression levels of NOX4 and p22phox mRNA were significantly higher in all cancers than in normal tissues (P = 0.0006 and P = 0.0136). The increased NOX4 expression level was significant in the PTC group (P < 0.0001), and of borderline significance in FTC (P = 0.05). In the 15-paired normal and tumor tissues (Fig. 3B), a significantly increased NOX4 mRNA expression was found in tumors (P = 0.0006).

The p22phox mRNA expression was significantly increased in the PTC and in ATC groups (P = 0.0031 and P = 0.0257), but differences between paired normal/tumor samples were not significant (P = 0.3028). Finally, Fig. 4 shows that the expression of NOX4 and p22phox genes was significantly correlated (r² = 0.425; P < 0.0001) in normal and in tumors tissues.

Expression of NOX4 protein was analyzed by immunohistochemistry (Fig. 5 and Table 2). NOX4 immunostained thyrocytes were found in all normal and pathological human thyroid specimens. In normal thyroid tissue, NOX4 immunostaining was intracytoplasmic and appeared granular on a faint diffuse positive background (Fig. 5A). Staining was clearly different to that of DUOX that is exclusively localized at the apical membrane (Fig. 5B). NOX4 immunostaining was heterogeneous. In the majority of cases, staining was present in activated tall columnar cells and absent in quiescent flat cells. Heterogeneity was found from one follicle to another and inside a given follicle (Fig. 5D). On serial sections immunostained for NOX4, CD34 (a vascular marker) and the NIS follicle (Fig. 5D). Staining was heterogeneous. In the majority of cases, staining was present in activated tall columnar cells and absent in quiescent flat cells. Heterogeneity was found from one follicle to another and inside a given follicle. In the same tall columnar cells and negative or weakly positive in flat cells. Positive cells were usually located in close contact with blood vessels (Fig. 5D–F).

In hyperplastic multinodular thyroid tissue, the same cell type heterogeneity was found. The so-called ‘Sanderson pollsters’ constituted of intraluminal papillary structures (Fig. 5C) and microfollicular structures budding from larger follicles were strongly stained. ‘Sanderson pollsters’ are accumulation of follicular cells in a small part of a follicle. This accumulation can be either solid or constituted by microfolicles. It is likely due to TSH stimulation heterogeneously distributed in thyroid follicles because variations of vascularization according to follicle area. At the subcellular level, NOX4 immunostaining was usually distributed in thyroid follicles because variations of vascularization according to follicle area. At the subcellular level, NOX4 immunostaining was usually...
dispersed in the whole cytoplasm but in some cells it could be confined to the apical and/or basal cellular parts of the cytoplasm.

In follicular adenoma, heterogeneous staining was found, with a strong staining of the majority of small follicles (Fig. 5G).

In papillary carcinoma, immunostaining was homogeneous, being present in all malignant cells. Interestingly, staining was usually found at the apical and basal parts of the cytoplasm (Fig. 5H).

In poorly differentiated follicular carcinoma, NOX4 immunostaining was homogeneous, being present in all malignant cells. Staining was diffuse in the cytoplasm (Fig. 5I).

We also analyzed the expression of the integral membrane protein p22phox and as expected, p22phox displayed an identical cellular expression pattern and was also mainly present in the cytoplasm (Fig. 6). A strong immunoreactivity for p22phox was also seen in macrophages, which contain the oxidase complex NOX2–p22phox (Fig. 6D and F).

**Discussion**

A high concentration of ROS, resulting either from an increased production or/and from a reduced antioxidant activity, triggers an ‘oxidative stress’. ROS are involved in several physiological processes, such as
host defense, cell growth, differentiation, protein synthesis, and angiogenesis (Bedard & Krause 2007, Lambeth 2007, Mittal et al. 2007). ROS are seen as intra- and extracellular messengers with a tightly controlled production. This concept was reinforced by the discovery of six NOXes, with the presence of several NOXes in the same cells, suggesting different intracellular H$_2$O$_2$-producing compartments with specific functions (Hilenski et al. 2004).

In this study, for the first time, we demonstrate the presence of NOX4 and its partner p22phox that is required for its catalytic activity and forms a heterodimeric enzyme complex with NOX4 and, that is localized and produces ROS inside the thyroid cell. TSH stimulation increases ROS production by thyrocytes in culture and siRNA to NOX4 prevent the increase in intracellular ROS, indicating that NOX4 was responsible for ROS generation. Importantly, we

![Figure 3](image-url)

**Figure 3** Comparative expression of NOX4 and p22phox genes in human thyroid tissues analyzed by real-time quantitative reverse transcription PCR. Data are expressed as mRNA relative expression levels determined as X fold of calibrator corresponding to a pool of thyroid tissue samples and cell lines. Expression values (y-axis) are displayed on based 2 logarithmic scale. (A) Comparative expression of NOX4 and p22phox genes in several human thyroid tissue types: nontumoral (NT); follicular thyroid adenomas (FTA); follicular thyroid carcinomas (FTC); papillary thyroid carcinoma (PTC); and anaplastic thyroid carcinoma (ATC); (Table): distribution of mRNA relative expression levels of NOX4 and p22phox according to the histological type. Nb, number of cases in each histological group; Min/Max, minimum and maximum of mRNA relative expression levels in each histological group; > 75% Perc. NT, number of cases (percentage) displaying a mRNA relative expression level higher than the 75% percentile expression level of normal tissues; > Max of NT, number of cases (percentage) displaying a mRNA relative expression level higher than the higher expression level in normal tissues. (B) Comparative expression of NOX4 and p22phox genes in 15 paired samples of normal and tumor tissues. (NT, paired normal counterpart; T, tumors, corresponding to 2 (FTA), 3 FTC, 9 PTC, and 1 ATC. Each value represents the mRNA relative expression level.)

<table>
<thead>
<tr>
<th>NOX4</th>
<th>NT</th>
<th>FTA</th>
<th>FTC</th>
<th>PTC</th>
<th>ATC</th>
<th>All cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nb</td>
<td>25</td>
<td>15</td>
<td>26</td>
<td>19</td>
<td>4</td>
<td>40</td>
</tr>
<tr>
<td>Mean (median)</td>
<td>0.26 (0.25)</td>
<td>0.38 (0.31)</td>
<td>0.42 (0.36)</td>
<td>1.05 (0.77)</td>
<td>0.40 (0.31)</td>
<td>0.67 (0.42)</td>
</tr>
<tr>
<td>Min/Max</td>
<td>0.07/0.94</td>
<td>0.06/2.12</td>
<td>0.06/1.21</td>
<td>0.14/0.81</td>
<td>0.17/0.81</td>
<td>0.06/1.51</td>
</tr>
<tr>
<td>P-value</td>
<td>0.1711</td>
<td>0.0512</td>
<td>&lt;0.0001</td>
<td>0.4671</td>
<td>0.0006</td>
<td></td>
</tr>
<tr>
<td>&gt; 75% perc. NT</td>
<td>7 (47%)</td>
<td>14 (53%)</td>
<td>15 (79%)</td>
<td>2 (50%)</td>
<td>31 (63%)</td>
<td></td>
</tr>
<tr>
<td>&gt; Max. NT</td>
<td>3 (20%)</td>
<td>8 (31%)</td>
<td>14 (73%)</td>
<td>1 (25%)</td>
<td>23 (47%)</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>p22phox</th>
<th>NT</th>
<th>FTA</th>
<th>FTC</th>
<th>PTC</th>
<th>ATC</th>
<th>All cancer</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nb</td>
<td>25</td>
<td>15</td>
<td>26</td>
<td>19</td>
<td>4</td>
<td>49</td>
</tr>
<tr>
<td>Mean (median)</td>
<td>0.95 (0.75)</td>
<td>1.41 (1.09)</td>
<td>1.35 (1.07)</td>
<td>1.29 (1.30)</td>
<td>1.46 (1.42)</td>
<td>1.34 (1.23)</td>
</tr>
<tr>
<td>Min/Max</td>
<td>0.45/2.37</td>
<td>0.15/6.15</td>
<td>0.06/3.99</td>
<td>0.45/1.78</td>
<td>1.07/1.93</td>
<td>0.06/2.61</td>
</tr>
<tr>
<td>P-value</td>
<td>0.3282</td>
<td>0.0031</td>
<td>0.0034</td>
<td>0.0136</td>
<td></td>
<td></td>
</tr>
<tr>
<td>&gt; 75% perc. NT</td>
<td>8 (53%)</td>
<td>14 (53%)</td>
<td>15 (79%)</td>
<td>4 (100%)</td>
<td>33 (67%)</td>
<td></td>
</tr>
<tr>
<td>&gt; Max. NT</td>
<td>2 (13%)</td>
<td>5 (19%)</td>
<td>7 (37%)</td>
<td>0 (0%)</td>
<td>5 (10%)</td>
<td></td>
</tr>
</tbody>
</table>
found that NOX4 and p22phox expressions are both positively regulated by TSH, with a highest regulation for p22phox, which is known to stabilize and increase NOX4 at the protein level (Ambasta et al. 2004). This result suggests a role for ROS in TSH signaling, which is mediated through NOX4.

Its intracellular localization probably corresponds to the endoplasmic reticulum where it was recently found in other cell types (Chen et al. 2008). This localization also suggests a role of NOX4 in cell signaling, unlike DUOX which are only active at the apical cell surface of thyrocytes where they produce H2O2 in the extracellular colloid space. Furthermore, thyroid cells possess very potent H2O2 degradation systems, which prevent the intracytoplasmic diffusion of extracellular H2O2 and intracellular iodide organification (Björkman & Ekholm 1995, Ekholm & Björkman 1997). The strong NOX4 staining in activated columnar thyrocytes and in their hyperplastic protrusion in the follicular lumen suggests a relationship with proliferation and functional activity. The presence of NOX4 in solid cell aggregation or microfollicles budding from larger follicles might be related with follicle replication. Basal localization of NOX4 in close relation with blood vessels could be in agreement with the described angiogenic properties of NOX4, through HIF-1 and VEGF (Xia et al. 2007).

![Figure 4](image_url)  
**Figure 4** Correlation between NOX4 and p22phox mRNA levels in normal and tumor tissues. Correlation between expression profiles was studied using Spearman’s rank-order correlation coefficient. The level of significance chosen was 5%.

![Figure 5](image_url)  
**Figure 5** NOX4 protein expression in human thyroid tissues. (A) normal thyroid tissue. Note intracytoplasmic granular staining of NOX4 (arrows) on a diffusely stained background; FL, follicular lumen; magnification, ×1000. (B) DUOX immunostaining is essentially localized at the apical membrane (arrow). Note faint, diffuse, intracytoplasmic staining. FL, follicular lumen. Magnification, ×1000. (C) follicular hyperplasia. NOX4-positive intraluminal so-called ‘Sanderson pollster’ (solid arrow). Note negative flat quiescent cells in the same follicle (thin arrow). Magnification, ×200. (D–F) NOX4, CD34 and NIS immunostainings on serial sections from the same follicle at the junction of activated columnar cells (solid arrows) and flat quiescent cells (thin arrows). Note on (E) that activated columnar cells are pseudostratified and present nuclei much larger than flat cells. Moreover, these cells are in contact to vessel endothelium, in contrast to flat cells. NOX4 and NIS display a strong immunostaining in large activated cells (solid arrows), and a negative or weak signal in quiescent flat cells (thin arrows). In vessels, red blood cells display pseudo-peroxidase activity, which has not been removed. Magnification, ×400. (G) Follicular thyroid adenoma. Small follicles present a larger number of NOX4-positive cells than macrofollicles. Magnification, ×200. (H) Papillary carcinoma. All tumor cells are NOX4 positive. Most staining is localized at the apical side, but some staining can be seen at the basal part (arrows). Magnification, ×400. (I) Poorly differentiated follicular carcinoma. Diffuse staining is seen in all tumor cells. Magnification, ×200.
originally identified as a NOX homolog highly expressed in the kidney and has been postulated to be involved in oxygen sensing (Geiszt et al. 2000, Shiose et al. 2001).

NOX4 was shown to produce \( \text{H}_2\text{O}_2 \) continuously (Geiszt et al. 2000), and \textit{in vivo} increased activity was linked to elevated mRNA levels (Gorin et al. 2003). ROS are overproduced in cancer cells (Quinn et al. 2006, Lambeth 2007), and inhibitors of NOX decrease cell proliferation (Brar et al. 2002). Furthermore, NOX4 increases survival properties in pancreatic cancer cells (Edderkaoui et al. 2005). Importantly, we observed in this study that NOX4 and p22 phox mRNA were up-regulated in thyroid cancers, particularly in papillary thyroid cancers, suggesting that this \( \text{H}_2\text{O}_2 \)-generating system could be involved in the signaling mechanism in thyroid tumor cells. As shown by immunohistochemistry, NOX4 is specifically expressed at a high level in thyrocytes, unlike p22phox, which is highly expressed also in macrophages. This could explain the absence of differences observed for p22phox expression between paired normal/tumor samples.

An imbalance between the production of ROS and degradation leads to oxidative stress, which can damage cell components, including proteins, lipids, and DNA. Interestingly, in mice, the spontaneous mutation frequency is higher in the thyroid gland as compared with other organs (Maier et al. 2006). In human thyroid tissues, there is also a high frequency of somatic mutations of the TSH receptor (Krohn et al. 2007). Until now, DUOX1 and DUOX2, as the only known \( \text{H}_2\text{O}_2 \)-generating systems in the thyroid gland, were suspected to play a role in the mutagenesis in the thyroid gland, in particular under conditions of iodine and selenium deficiency (Song et al. 2007). The discovery of NOX4 expression in the thyroid gland and its intracytoplasmic localization open new avenues of research concerning the role of the NOX4-derived ROS in TSH signaling and in the mechanisms leading to oxidative stress, genetic instability, and mutagenesis that might contribute to the development and progression of thyroid tumors.

**Declaration of interest**

The authors declare that there are no conflicts of interest that would prejudice the impartiality of this study.
Funding
This work was supported by grants from Association pour la Recherche sur le Cancer (ARC) (grant number 3945), Agence Nationale de la Recherche (ANR) (grant number 238503), Ligue Contre le Cancer (comité du Val-de-Marne), and Electricité de France (EDF).

Author contribution statement
Urbain Weyemi and Bernard Caillou contributed equally to this study.

References
iodide on nicotinamide adenine dinucleotide phosphate oxidase activity and Duox2 protein expression in isolated porcine thyroid follicles. *Endocrinology* **144** 1241–1248.


