Expression of aryl hydrocarbon receptor (AHR) and AHR-interacting protein in pituitary adenomas: pathological and clinical implications

Marie-Lise Jaffrain-Rea¹,²,³, Mariolina Angelini¹, Donatella Gargano¹, Maria A Tichomirowa⁴, Adrian F Daly⁴, Jean-François Vanbellinghen⁵, Emanuela D’Innocenzo¹, Anne Barlier⁶, Felice Giangaspero²,⁷, Vincenzo Esposito², Luca Ventura⁸, Antonietta Arcella², Marily Theodoropoulou⁹, Luciana A Naves¹⁰, Carmen Fajardo¹¹, Sabina Zachariева¹², Vincent Rohmer¹³, Thierry Brue⁶, Alberto Gulino⁷, Giampaolo Cantore², Edoardo Alesse¹ and Albert Beckers⁴

¹Department of Experimental Medicine, University of L’Aquila, via Vetoio, Coppito 2, 67100 L’Aquila, Italy
²Neuromed Institute, Istituto di Ricovero e di Ricerca a Carattere Scientifico, Via Atinense 18, 86077 Pozzilli, Italy
³Fondazione ‘Carlo Ferreri’ per la prevenzione e la cura dei tumori, via Edmondo Riva 42, 00015 Monterotondo, Italy
⁴Departments of Endocrinology and Molecular Genetics, Centre Hospitalier Universitaire de Liège, Université de Liège, 4000 Liège, Belgium
⁵Department of Endocrinology, Hôpital de la Timone, Centre de Référence des maladies rares d’origine hypophysaire, Assistance Publique-Hôpitaux de Marseille, and Centre de Recherche en Neurobiologie - Neurophysiologie de Marseille (CRN2M), Unité Mixte de Recherche 6231, Université de la Méditerranée - Université Paul Cézanne - CNRS, 13284 Marseille, France
⁶Department of Experimental Medicine and Pathology, University of Rome ‘La Sapienza’, Viale dell’Università, 00161 Rome, Italy
⁷Pathology, San Salvatore Hospital, Coppito, 67100 L’Aquila, Italy
⁸Max Planck Institute of Psychiatry, 80804 Munich, Germany
⁹Endocrinology Unit, Faculty of Medicine, University of Brasilia, 70910-900 Brasilia, Brazil
¹⁰Department of Endocrinology, Hospital Universitario de La Ribera, 46600 Alzira, Spain
¹¹Department of Endocrinology, Sofia University, 1303 Sofia, Bulgaria
¹²Endocrinology, Centre Hospitalier Universitaire de Angers, 49033 Angers, France

(Correspondence should be addressed to M-L Jaffrain-Rea; Email: jaffrain.ml@libero.it)

Abstract

Germline mutations of the aryl hydrocarbon receptor (AHR)-interacting protein (AIP) gene confer a predisposition to pituitary adenomas (PA), usually in the setting of familial isolated PA. To provide further insights into the possible role of AIP in pituitary tumour pathogenesis, the expression of AIP and AHR was determined by real-time RT-PCR and/or immunohistochemistry (IHC) in a large series of PA (n=103), including 17 with AIP mutations (AIPmut). Variable levels of AIP and AHR transcripts were detected in all PA, with a low AHR expression (P<0.0001 versus AIP). Cytoplasmic AIP and AHR were detected by IHC in 84.0 and 38.6% of PA respectively, and significantly correlated with each other (P=0.006). Nuclear AHR was detected in a minority of PA (19.7%). The highest AIP expression was observed in somatotrophinomas and non-secreting (NS) PA, and multivariate analysis in somatotrophinomas showed a significantly lower AIP immunostaining in invasive versus non-invasive cases (P=0.019). AIP expression was commonly low in other secreting PA. AIP immunostaining was abolished in a minority of AIPmut PA, with a frequent loss of cytoplasmic AHR and no evidence of nuclear AHR. In contrast, AIP overexpression in a subset of NS PA could be accompanied by nuclear AHR immunopositivity. We conclude that down-regulation of AIP and AHR may be involved in the aggressiveness of somatotrophinomas. Overall, IHC is a poorly sensitive tool for the screening of AIP mutations. Data obtained on AHR expression suggest that AHR signalling may be differentially affected according to PA phenotype.

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Introduction

Germline mutations of the aryl hydrocarbon receptor (AHR)-interacting protein (AIP) gene confer a predisposition to pituitary adenomas (PA; Vierimaa et al. 2006), usually in the setting of familial isolated PA (FIPA; Daly et al. 2006, 2007, Beckers & Daly 2007). Because mutations are likely to be inactivating and associated with tumour loss of heterozygosity (LOH), AIP is viewed as a new pituitary tumour suppressor gene associated with tumour loss of heterozygosity (LOH), because mutations are likely to be inactivating and associated with tumour loss of heterozygosity (LOH), which is underscored by its involvement in normal ontogeny and tumourigenesis (Gasiewicz et al. 2008). Dioxin is carcinogenic (Popp et al. 2006), and AHR can be overexpressed in human tumours (Harper et al. 2006, Schlezinger et al. 2006). Yet, the effects of dioxin exposure on the incidence of pituitary tumours remain uncertain (Pesatori et al. 2008), and the expression of AHR in the normal human pituitary and in PA has not been reported to date.

We wished to further characterize AIP expression and assess AHR expression and cellular localization in a representative series of PA. We also aimed to further characterize AIPmut PA in order to provide new insights into their pathogenesis and possibly help identify patients who could benefit from AIP mutational screening.

Material and methods

Patients and samples

A series of 103 PA have been studied for AIP and AHR expression by real-time RT-PCR (n=66) and/or IHC (n=94). There were 46 GH-, 22 PRL-, 7 ACTH-, 2 TSH-secreting and 26 NS adenomas respectively. Unselected sporadic adenomas were operated on for medical reasons at the Neuromed Institute (Italy). Seventeen FIPA samples were collected in 14 FIPA patients who came from eight international centres (Italy, Belgium, France, Brazil, Spain and Bulgaria), out of which 10 PA were operated on in 8 patients with a germline AIP mutation. The study was approved by local ethical committees. Clinical, biological and neuroradiological data, as well as intra-operative findings and pre-operative pharmacological treatment, were systematically recorded. Invasiveness was defined according to pre-operative neuroradiological imaging and intra-operative findings, including macroscopic evidence of dural infiltration. Tumour phenotype was defined on the basis of pre-operative endocrine evaluation and immunohistochemical characterization of hormone secretion. This latter was available in all but two cases and performed with the commercial anti-PRL, anti-GH, anti-FSH, anti-LH, anti-ACTH and anti-TSH antibodies in use in the participating centres (in Italy, polyclonal antibodies from Orthodiagnostic Systems, Raritan, NJ, USA).
Cell proliferation was evaluated in 77 PA by Ki-67 immunostaining with the monoclonal MIB-1 antibody (DBA Italia srl, Milan, Italy), as previously described (Jaffrain-Rea et al. 2002). Tumours showing microscopic evidence of contamination by normal pituitary fragments were considered for immunohistochemical studies only. In addition, normal human pituitary glands were collected at autopsy in four patients who died from non-endocrine diseases and divided into frozen and formalin-fixed paraffin-embedded fragments, as previously described (Fratticci et al. 2007).

**Molecular and genetic analysis**

Methodological details on RT-PCR and real-time RT-PCR protocols are provided in the Supplementary Materials and methods, which can be viewed online at [http://erc.endocrinology-journals.org/supplemental/](http://erc.endocrinology-journals.org/supplemental/). Briefly, after preliminary, RT-PCR experiments allowed the exclusion of tumour samples with potential contamination with normal pituitary cells according to cell-specific transcription factors’ criteria and revealed an almost universal AIP and AHR gene expression; AIP and AHR transcripts were quantified by real-time RT-PCR based on a Taqman methodology and corrected for β-actin expression. Leukocyte genomic AIP sequencing (gDNA) was performed in 28 patients, as previously described (Daly et al. 2007). Searches for somatic mutations, or LOH in AIPmut tumours, were performed by direct sequencing of tumour cDNA and/or DNA (tDNA) in 35 and 6 cases respectively. Procedures for AIP cDNA sequencing are described in the electronic Supplementary Materials and methods. Overall, the AIP gene status could be determined in 67 cases. Wherever new changes in AIP sequencing were identified, AIP variations were considered as AIP mutations for statistical purposes and their potential biological significance further analysed in the Supplementary Materials and methods and in the Discussion section.

**Immunohistochemistry**

Tissue sections were dewaxed in xylene and rehydrated through a descending ethanol series, and antigen retrieval was performed by microwave boiling at 850 W in citrate buffer 0.1 M, pH 6.0. Mouse monoclonal antibodies directed against AIP (clone 35-2) and AHR (clone RPT9, referred to as ‘N-mAb’) were purchased from Novus (Novus Biologicals LLC, Littleton, CO, USA) and both used at a 1:500 dilution, in 94 and 83 PA respectively. A polyclonal rabbit anti-AHR antibody was also used in 61 PA (17 PRL-, 21 GH-, 3 ACTH-secreting and 20 NS respectively) at a 1:50 dilution (sc-5579, referred to as ‘C-pAb’, Santa Cruz Biotechnology, Santa Cruz, CA, USA). This antibody proved to be more sensitive than the N-mAb in the detection of nuclear AHR in positive control sections (human invasive breast cancer samples and rat liver), and cytoplasmic background could be reduced by introducing a further blocking step with 5% milk in PBS. IHC was performed with a multilink biotinylated antibody and the avidin–biotin peroxidase system according to the manufacturer’s instructions (LSAB+ kit, DAKO Cytomation, Milan, Italy). Negative controls were performed omitting the primary antibody. Topographical localization of AIP-expressing cells in normal pituitaries was performed...
Table 1 Aryl hydrocarbon receptor-interacting protein (AIP) expression in the whole series of pituitary adenomas (PA) according to patients and tumours characteristics

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Age (years)</th>
<th>Pre-operative treatment</th>
<th>Invasiveness</th>
<th>SSE</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>All</td>
<td>&lt; 30</td>
<td>≥ 30</td>
</tr>
<tr>
<td>All PA</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AIP/β-actin mRNA (66)</td>
<td>0.8 ± 0.9</td>
<td>0.3 ± 0.4</td>
<td>0.9 ± 1.0</td>
<td>0.015</td>
</tr>
<tr>
<td>AIP staining (94)</td>
<td>39.4%</td>
<td>34.4%</td>
<td>41.9%</td>
<td></td>
</tr>
<tr>
<td>GH-secreting</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AIP/β-actin mRNA (20)</td>
<td>0.9 ± 0.9</td>
<td>0.5 ± 0.6</td>
<td>1.0 ± 1.0</td>
<td>NS</td>
</tr>
<tr>
<td>AIP staining (44)</td>
<td>52.3%</td>
<td>47.4%</td>
<td>56.0%</td>
<td></td>
</tr>
<tr>
<td>PRL-secreting</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AIP/β-actin mRNA (12)</td>
<td>0.5 ± 0.5</td>
<td>0.1 ± 0.1</td>
<td>0.6 ± 0.5</td>
<td>NS</td>
</tr>
<tr>
<td>AIP staining (21)</td>
<td>14.3%</td>
<td>12.5%</td>
<td>15.4%</td>
<td></td>
</tr>
<tr>
<td>ACTH-secreting</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AIP/β-actin mRNA (7)</td>
<td>1.0 ± 1.3</td>
<td>0.3 ± 0.1</td>
<td>1.0 ± 1.3</td>
<td>NS</td>
</tr>
<tr>
<td>AIP staining (21)</td>
<td>42.8%</td>
<td>33.3%</td>
<td>47.0%</td>
<td></td>
</tr>
<tr>
<td>TSH-secreting</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AIP/β-actin mRNA (2)</td>
<td>0.7 ± 0.3</td>
<td>0.4</td>
<td>0.7 ± 0.3</td>
<td>–</td>
</tr>
<tr>
<td>AIP staining (6)</td>
<td>16.7%</td>
<td>0/1</td>
<td>1/5</td>
<td>–</td>
</tr>
</tbody>
</table>

For raw data, the number of studied cases is indicated within brackets. The AIP/β-actin ratio was defined according to real-time RT-PCR experiments. AIP staining refers to significant AIP immunostaining (+ diffuse, moderate and ++ diffuse, strong) – as compared with very low or absent staining. SSE, suprasellar extension; N/A, not applicable; NS, non-significant data.
using pre-diluted mouse mAbs for pituitary hormones (DAKO Cytomation). Semi-quantitative analysis of cytoplasmic AIP and AHR immunostaining was performed at 20× and 40× magnifications and semiquantitatively scored as follows: − (negative); +/− (weak immunostaining and/or scattered positive cells); + (diffuse, moderate immunostaining); ++ (diffuse, strong immunostaining). In the presence of heterogeneous staining, the areas obtaining the highest score were considered for statistical purposes. Nuclear staining for AHR (C-pAb) was further evaluated at high magnification (100×) in all cases. A double step immunohistochemical study was also performed as previously described (Fratticci et al. 2007) to first detect cytoplasmic AIP or the pituitary hormones GH, PRL, ACTH and FSH respectively using 3-3′-diaminobenzidine (DAB) as a chromogen, followed by a second step for the detection of nuclear AHR (C-pAb) using Novored as a chromogen (Vector, DBA Italia), introducing a further blocking step with milk as indicated hitherto. Photographs of slides were taken using a Zeiss Axioplan 2 microscope and a Leica DFC 320 digital camera.

**Statistical analysis**

All data are expressed in mean ± S.D. and statistical analyses were performed using Statview 5.01 software for PC (SAS Institute, Cary, NC, USA). Continuous values were analysed by non-parametric analysis, using Mann–Whitney and Kruskal–Wallis test for 2 and ≥3 group comparisons respectively and the Spearman test for correlation studies. Distribution of nominal values was compared by the χ²-test, logistic regression being used for multivariate analysis. For logistic regression and analysis of subgroups, the immunostaining scores for cytoplasmic AIP and AHR were transformed into binary parameters as follows: significant (scores + and ++) versus low (− and +/−) AIP immunostaining; and
<table>
<thead>
<tr>
<th>Patients surgery&lt;sup&gt;a&lt;/sup&gt;</th>
<th>AIP mutation</th>
<th>Country</th>
<th>Sex</th>
<th>Age (years)</th>
<th>Symptoms&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Tumour&lt;sup&gt;c&lt;/sup&gt;</th>
<th>Hormone values at diagnosis (ng/ml)</th>
<th>Pre-op treatment</th>
<th>Pre-op hormone values (ng/ml)</th>
<th>Plutitary hormones IHC</th>
<th>AIP IHC&lt;sup&gt;d&lt;/sup&gt;</th>
<th>AHR IHC&lt;sup&gt;e&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fam 1&lt;sup&gt;(c,i)&lt;/sup&gt;</td>
<td>R304X</td>
<td>Italy</td>
<td>F</td>
<td>19</td>
<td>Amenorrhoea–galactorrhea, visual loss, bitemporal haemianopsia, weight gain and hydrocephalus requiring emergency surgery for ventricular derivation (VD)</td>
<td>Giant-SSE (52 mm), Inv+ (CS)</td>
<td>PRL 99, Post-VD, GH 15.8, IGF-I 420, PRL 32</td>
<td>OCT up to 200 µg t.i.d. CAB 0.5 mg ×2/w</td>
<td>PRL 9.1, GH 16.0, IGF 900</td>
<td>GH, FSH (±), Ki-67, 0.5%</td>
<td>+/−</td>
<td>(scattered cells +)</td>
</tr>
<tr>
<td>Fam 1B&lt;sup&gt;1st TS&lt;/sup&gt;</td>
<td>R304X</td>
<td>Italy</td>
<td>F</td>
<td>21</td>
<td>Amenorrhoea, weight gain, mild acromegaly, DH 164 cm and headache</td>
<td>Giant-SSE (41 mm), Inv+ (CS)</td>
<td>GH 33, IGF-I 630, PRL 5</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>GH, PRL (±), Ki-67, 6.0%</td>
<td>+/−</td>
<td>C − N ND</td>
</tr>
<tr>
<td>2&lt;sup&gt;nd TS&lt;/sup&gt;</td>
<td>R304X</td>
<td>Italy</td>
<td>F</td>
<td>22</td>
<td>Evolutve disease and pharmacological resistance</td>
<td>Ma-SSE (27 mm), Inv+ (CS)</td>
<td>Post-TS1 GH 4.0, IGF-I 400, PRL 7.2</td>
<td>LAN 30 mg /14 d. CAB 0.5 mg ×2/w.</td>
<td>GH 5.8, IGF-I 598 PRL 1.3</td>
<td>GH, FSH, LH (±), Ki-67, 2.7%</td>
<td>+/−</td>
<td>C − N ND</td>
</tr>
<tr>
<td>Fam 1C&lt;sup&gt;TS&lt;/sup&gt;</td>
<td>R304X</td>
<td>Italy</td>
<td>M</td>
<td>8</td>
<td>Incipient gigantism</td>
<td>Ma-IS (12 mm), Inv−</td>
<td>GH 48.2, IGF-I 1070, PRL 11.8</td>
<td>OCT-LAR 10 mg/28 d.</td>
<td>GH 65.9, IGF-I 1294 PRL 21.9</td>
<td>GH, Ki-67, 5.0%</td>
<td>+/−</td>
<td>(scattered cells +)</td>
</tr>
<tr>
<td>Fam 2&lt;sup&gt;(i)&lt;/sup&gt;</td>
<td>Q285fs17X</td>
<td>Italy</td>
<td>M</td>
<td>21</td>
<td>Gigantism − DH 208 cm, headache and visual fields’ defects</td>
<td>Ma-SSE (28 mm), Inv+</td>
<td>GH &gt; 30.0, PRL 7.4, IGF-I N/A</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>GH, PRL (±), Ki-67, 0.7%</td>
<td>+/−</td>
<td>C − N</td>
</tr>
<tr>
<td>Fam 2B&lt;sup&gt;1st TS&lt;/sup&gt;</td>
<td>Q285fs17X</td>
<td>Italy</td>
<td>M</td>
<td>33</td>
<td>Acromegaly − DH 185 cm</td>
<td>Ma-SSE (30 mm), Inv+ (CS)</td>
<td>GH 74.0, IGF-I 664, PRL 35.4</td>
<td>OCT-LAR 20 mg/28 d.</td>
<td>GH 3.5, IGF-I 414, PRL 4.4</td>
<td>GH, PRL, FSH (±), Ki-67, 0%</td>
<td>+/−</td>
<td>(large areas −)</td>
</tr>
<tr>
<td>2&lt;sup&gt;nd TS&lt;/sup&gt;</td>
<td>Q285fs17X</td>
<td>Italy</td>
<td>M</td>
<td>34</td>
<td>Evolutve acromegaly</td>
<td>Ma-IS (15 mm), Inv+ (CS)</td>
<td>GH 6.0, IGF-I 540, PRL 7.0</td>
<td>OCT-LAR 10 mg/28 d.</td>
<td>GH 19.6, IGF-I 449, PRL 6.7</td>
<td>GH, PRL (±), Ki-67, 0%</td>
<td>−</td>
<td>C−</td>
</tr>
<tr>
<td>Fam 3&lt;sup&gt;(i)&lt;/sup&gt;</td>
<td>K241E</td>
<td>Belgium</td>
<td>M</td>
<td>53</td>
<td>Visual loss and bitemporal haemianopsia. Visual loss</td>
<td>Ma-SSE (30 mm), Inv+</td>
<td>PRL 41, IGF-I 50</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>FSH, LH +</td>
<td>C − N−</td>
<td></td>
</tr>
<tr>
<td>Fam 3B&lt;sup&gt;TS&lt;/sup&gt;</td>
<td>K241E</td>
<td>Belgium</td>
<td>M</td>
<td>53</td>
<td>Visual loss</td>
<td>Ma-SSE (34 mm), Inv+ (CS)</td>
<td>PRL 2333, GH 0.2, IGF-I 100</td>
<td>CAB 0.5 mg ×2/w.</td>
<td>PRL 12.5, GH 0.2</td>
<td>PRL</td>
<td>−</td>
<td>C − N ND</td>
</tr>
</tbody>
</table>

<sup>a</sup>Table 2 Characteristics of pituitary adenomas (PA) with AIP mutations and immunohistochemistry (IHC) for aryl hydrocarbon receptor (AHR)-interacting protein (AIP) and AHR.
<table>
<thead>
<tr>
<th>Patients surgery</th>
<th>AIP mutation</th>
<th>Country</th>
<th>Sex</th>
<th>Age (years)</th>
<th>Symptoms</th>
<th>Tumour</th>
<th>Hormone values at diagnosis (ng/ml)</th>
<th>Pre-op treatment</th>
<th>Pre-op hormone values (ng/ml)</th>
<th>Pituitary hormones IHC</th>
<th>AIP IHC</th>
<th>AHR IHC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fam 4</td>
<td>E174fs21X</td>
<td>Brazil</td>
<td>M</td>
<td>17</td>
<td>Gigantism, DH 193 cm, headache and visual field's defect</td>
<td>Giant-SSE (46 mm), Inv+ (CS)</td>
<td>GH 51, IGF-I 778, PRL 50</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>GH, PRL, Ki-67, 0%</td>
<td>Het +, +/−</td>
<td>C +/−</td>
</tr>
<tr>
<td>Spor 1</td>
<td>V195A</td>
<td>Brazil</td>
<td>M</td>
<td>12</td>
<td>Visual loss and pre-puberal, post-operative resistance to dopamine-agonists Incipient gigantism and visual defect</td>
<td>Giant-SSE (40 mm), Inv+ (CS)</td>
<td>PRL 10 561, GH 0.06, IGF-1 147</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>PRL, Ki-67, 0%</td>
<td>+</td>
<td>C − N ND</td>
</tr>
<tr>
<td>Spor 2</td>
<td>A277P</td>
<td>Italy</td>
<td>M</td>
<td>12</td>
<td>None</td>
<td>Ma-SSE (27 mm), Inv+ (CS)</td>
<td>GH 13.6, IGF-I 530, PRL 52.5</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>GH, PRL, Ki-67, 15.0%</td>
<td>+/−</td>
<td>C − N −</td>
</tr>
<tr>
<td>Spor 3</td>
<td>IVS3 (c.468 + 16G &gt; T)</td>
<td>Italy</td>
<td>F</td>
<td>15</td>
<td>None</td>
<td>Ma-SSE (20 mm), Inv+ (CS)</td>
<td>N/A</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>GH, Ki-67, 0.5%</td>
<td>(in part necrotic)</td>
<td>ND</td>
</tr>
<tr>
<td>Spor 4</td>
<td>IVS3 (c.468 + 15C &gt; T)</td>
<td>Spain (Ecuador)</td>
<td>F</td>
<td>17</td>
<td>None</td>
<td>Ma-IS (13 mm), Inv−</td>
<td>GH 54.8, IGF-I 635, PRL ↑</td>
<td>LAN-60 mg i.m. /28 d.</td>
<td>N/A</td>
<td>GH, PRL, FSH, LH, ACTH (±)</td>
<td>Het +/−, −</td>
<td>C +/− N ND</td>
</tr>
<tr>
<td>Spor 5</td>
<td>Q82fsX7</td>
<td>Bulgaria</td>
<td>M</td>
<td>15</td>
<td>Gigantism, headache and hydrocephalus</td>
<td>Giant-SSE (60 mm), Inv−</td>
<td>N/A</td>
<td>None (RxT)</td>
<td>GH 42.3, IGF-1 ↑, PRL 60 IGF-I 1090</td>
<td>GH</td>
<td>−</td>
<td>C − N ND</td>
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<tr>
<td>Spor 6</td>
<td>R128H</td>
<td>Belgium</td>
<td>M</td>
<td>27</td>
<td>Acromegaly</td>
<td>Ma-SSE (20 mm), Inv−</td>
<td>GH 58.7, IGF-I 909, PRL N/A</td>
<td>OCT 100 μg i.d. CAB 0.5 mg 2/w</td>
<td>GH</td>
<td>Het ++/+</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>Spor 7</td>
<td>IVS2 (c.279 + 23C &gt; T)</td>
<td>Italy</td>
<td>F</td>
<td>43</td>
<td>Secondary amenorrhea, headache and transient visual defects</td>
<td>Ma-SSE (18 mm), Inv−</td>
<td>PRL 30, GH 0.2, IGF-I 152</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>PRL, GH (±), Ki-67, 3.0%</td>
<td>+/−</td>
<td>C − N −</td>
</tr>
<tr>
<td>(T) Spor 8</td>
<td>R304X</td>
<td>Italy</td>
<td>F</td>
<td>17</td>
<td>Visual defects, headache, secondary amenorrhoea and DH 171 cm</td>
<td>Ma-SSE, Inv−</td>
<td>GH 9.0, IGF-I 905, PRL 57</td>
<td>None</td>
<td>See values at diagnosis</td>
<td>GH, Ki-67, 3.0%</td>
<td>+/−</td>
<td>ND</td>
</tr>
</tbody>
</table>

a(i) Previously reported in Daly et al. (2007), (ii) clinical details on Fam1 A and B previously reported in Ferretti et al. (2001), (iii) previously reported in details in Naves et al. (2007), (T) only tumour available.

bDH, definitive height.
cMa, macroadenoma; SSE, suprasellar extension; maximal tumour diameter within brackets; Inv−, non-invasive; Inv+, invasive; CS, cavernous sinus.
dAIP staining with semi-quantitative score. + + strong, diffuse; + moderate, diffuse; +/− weak or scattered positive cells; − negative.
eAHR staining; C, cytoplasmic staining with an N-terminal monoclonal antibody; N, nuclear staining with a C-terminal polyclonal antibody respectively; ND, not done (unavailable material).
AHR expression

Weak immunostaining and/or scattered positive cells; semi-quantitative AIP and AHR scores were defined by immunohistochemistry (mRNA ratios were obtained by real-time RT-PCR (the number of studied tumours is indicated in italicized text within brackets).

P-subset of cases, a polyclonal anti-AHR antibody (C-pAb) recognizing the C-terminal half of AHR respectively. Nearly significant values are indicated in italics; NS, non-significant.

Suprasellar extension

10/14 (71.4%) 16/32 (50.0%) NS

Invasive

10/14 (71.4%) 12/32 (37.5%) \( \chi^2 = 4.49, P = 0.034 \)

Ki-67, \( > \) 3.0%

5/11 (45.4%) 6/29 (20.7%) NS

Pre-operative treatment

7/14 (50.0%) 13/32 (40.6%) NS

AIP expression

Detectable AHR (N-mAb) \( (c) \)

0/7 2/13 NS

Nuclear AHR (C-pAb) \( (c) \)

0/7 2/13 NS

Groups A and B refer to patients and tumours with or without documented AIP mutations respectively. AIP/\( \beta \)-actin and AHR/\( \beta \)-actin mRNA ratios were obtained by real-time RT-PCR (the number of studied tumours is indicated in italicized text within brackets).

Semi-quantitative AIP and AHR scores were defined by immunohistochemistry (+ + diffuse, strong; + diffuse, moderate; ++− weak immunostaining and/or scattered positive cells; − negative), using anti-AIP and AHR (N-mAb) monoclonal antibodies and, in a subset of cases, a polyclonal anti-AHR antibody (C-pAb) recognizing the C-terminal half of AHR respectively. Nearly significant \( P \) values are indicated in italics; NS, non-significant.

detectable (scores +/− and +) versus undetectable AHR immunostaining respectively. The level of significance was set at \( P < 0.05 \).

Results

Normal pituitary

AIP and AHR transcripts were detected in normal pituitary samples, with a significantly lower expression of AHR \( (P < 0.0001 \) versus AIP). Accordingly, AIP-immunopositive cells were largely present in the adenohypophysis (see Supplementary Fig. 1A, which can be viewed online at http://erc.endocrinology-journals.org/supplemental/), with topographical studies arguing for a preferential strong and diffuse expression in somatotrophs (see Supplementary Fig. 1B), and to a lesser extent by lactotrophs (data not shown). AHR (N-mAb) immunostaining was less intense, with a roughly similar, although more scattered and diffuse, cell distribution (see Supplementary Fig. 1C). AIP and AHR (N-mAb) immunostaining was confined to the cytoplasm (see Supplementary Fig. 1D and E), although some degree of AHR nuclear positivity was revealed by C-pAb immunostaining (see Supplementary Fig. 1F). Some scattered AIP- and AHR-immunopositive cells were observed in the pars intermedia, containing ACTH-secreting cells (see Supplementary Fig. 1G–I). Double immunostaining with AHR C-pAb revealed co-localization of AHR with AIP (see Supplementary Fig. 1J), nuclear AHR immunostaining being observed in a subset of somatotrophs (see Supplementary Fig. 1K) and a few corticotrophs (data not shown), whereas in lactotrophs, AHR appeared to be mostly perinuclear (see Supplementary Fig. 1L). FSH-secreting cells were virtually negative for nuclear AHR (data not shown).

Pituitary adenomas

The expression of AIP and AHR has been first performed on the entire series of PA. AIP and AHR transcripts were detected in all PA (Fig. 1), with a markedly lower AHR expression \( (P < 0.0001 \) versus AIP). Accordingly, AIP and AHR proteins were detected in 84.0 and 38.6% of the cases respectively. Marked individual variations were observed in AIP gene expression and immunostaining (Fig. 1A; Table 1) – examples of IHC scoring are shown in Fig. 2A–C, including one microprolactinoma with a normal pituitary fragment shown as an internal control (Fig. 2D). The AIP immunostaining score was significantly correlated with AIP expression \( (P = 0.0014) \) and with the AHR (N-mAb) score \( (\chi^2 = 18.1, P = 0.006) \). However, cytoplasmic AHR...
immunostaining (N-mAb) was generally weak, and nuclear immunostaining (C-pAb) was observed in a minority of cases (12/61 Z 19.7%; Fig. 2E–I), including a familial NS PA with normal AIP sequencing (Fig. 2I). Correlation with clinical characteristics

A series of factors were found to account for the variations in AIP mRNA and AIP immunostaining observed on the entire series of PA, including tumour phenotype and aggressiveness (Table 1). Briefly, both were found to be highly variable in somatotrophinomas, generally low in prolactinomas and in other secreting PA, but paradoxically high in a subset of NS adenomas (Fig. 1A; Table 1). AIP mRNA was significantly lower in invasive PA (P = 0.0197 versus non-invasive), which were also more likely to show a low AIP immunostaining (χ² = 6.91, P = 0.009 versus non-invasive). Overall, no significant difference in AIP expression was observed according to the AIP gene status (data not shown). AHR mRNA was poorly influenced by phenotype (Fig. 1B), but complete loss of AHR immunostaining (N-mAb) was significantly more frequent in invasive (71.4 vs 47.4% in non-invasive, χ² = 5.2, P = 0.022) and in AIP mut PA (86.7 vs 58.7% in non-mutated PA, χ² = 3.92, P = 0.048). Nuclear AHR immunostaining (C-pAb) was observed in three somatotrophinomas, three prolactinomas and six NS adenomas respectively, but in none of the AIP mut PA included in this study.

Correlation with clinical characteristics

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Analysis of PA subgroups

Because the proportion of AIP mut tumours varied according to phenotype, data obtained in all somatotrophinomas, prolactinomas and NS adenomas have been further analysed as distinct subgroups.

Somatotrophinomas

As most AIP mut tumours were somatotrophinomas, data were analysed according to the presence (group A) or the absence (group B) of documented AIP mutations.
respectively. In group A, AIP mutations were identified on patient’s leukocyte DNA in six FIPA patients (eight PA) and in five sporadic cases, respectively, and on tumour cDNA and DNA in an additional sporadic case where no leukocyte DNA was available. Individual data are shown in Table 2 (Family 1, 2 and 4; Spor 2–6 and 8). Germline mutations were heterozygous whereas only the mutated allele was detected in cDNA/tDNA where available, thereby indicating somatic loss of heterozygosity in four out of five cases (Fam 1B and C, Fam 2B; Spor 2) and strongly suggesting hemizygosity in the other case (Spor 8). In group B, the lack of detectable AIP mutations was confirmed in most cases by sequencing of gDNA (n = 7), tumour cDNA (n = 12) and/or tDNA (n = 4) respectively. Data observed in group A and group B are summarized in Table 3. Somatotrophinomas occurred in group A at a significantly younger age (P < 0.0001) were more frequently invasive (P = 0.034) and more likely to display decreased AIP immunostaining (P = 0.031) than those in group B respectively. Of note, the pattern of AIP immunostaining could differ according to the mutation (Fig. 3A, D, E and G). Similarly, there was a trend towards cytoplasmic AHR (N-mAb) being less likely to be detected in group A (Fig. 3B and F) than in group B (P = 0.059). Further evaluation with the AHR C-pAb confirmed the lack of nuclear immunostaining in group A (Fig. 3C).

Excluding somatotrophinomas with undetermined AIP gene status, AIP mutations were estimated to account for AIP gene down-regulation in 3 out of 4 cases and for low AIP immunostaining in 10 out of 19 cases respectively. Low AIP immunostaining tended to be more frequent in AIPmut somatotrophinomas than in those with normal AIP sequencing (10 out of 14 vs 9 out of 22, \( \chi^2 = 3.20, P = 0.074 \)), indicating a sensitivity of IHC in detecting AIP mutations of 71.4% and a specificity of 40.9% respectively. According to logistic regression analysis, tumour invasiveness was the only independent predictor of AIP down-regulation in somatotrophinomas (P = 0.019), whereas young age was the only independent predictor of AIP mutations (P = 0.002; see Supplementary Table 2, which can be viewed online at http://erc.endocrinology-journals.org-supplemental/). Complete loss of AHR (N-mAb) immunostaining was significantly more frequent in invasive than in non-invasive somatotrophinomas (78.9 vs 35.7%, \( \chi^2 = 4.7, P = 0.012 \)), while a trend was confirmed in AIPmut somatotrophinomas as compared with those with normal AIP sequencing (83.3 vs 52.4%, \( \chi^2 = 2.76, P = 0.096 \)).

Prolactinomas

Both AIP mRNA and AIP immunostaining were generally low in prolactinomas (Table 1; Figs 1 and 2C and E). The AIP gene status was available in most cases (15 out of 22), according to AIP sequencing performed on gDNA (n = 8) or tumour cDNA (n = 7). Germline AIP mutations were identified in three cases (Table 2, Fam 3B; Spor 1 and 7), although no splicing alteration was found by tumour cDNA sequencing in Spor 7. Low AIP immunostaining occurred in prolactinomas with normal AIP sequencing (10 out of 12) as well as in AIPmut (2 out of 3). Excluding AIPmut tumours, low AIP immunostaining was confirmed to be significantly more frequent in prolactinomas than in somatotrophinomas (\( \chi^2 = 16.5, P = 0.0009 \)). Cytoplasmic (N-mAb) and nuclear (C-pAb) AHR immunostaining could be detected in 11 out of 21 (52.3%) and 3 out of 17 (17.6%) prolactinomas respectively.

NS adenomas

The mean AIP mRNA in NS adenomas was similar to that observed in somatotrophinomas, 42.3% of PA in this group also displaying significant AIP immunostaining (Table 1; Figs 1 and 2B). A germline AIP mutation was identified in one FIPA patient (Table 2, Fam 3A), and normal AIP sequencing was documented in 11 cases on tumour cDNA (n = 8) or tDNA (n = 3) – including all NS occurring in patients aged ≤ 50 years old. Surprisingly, a significant AIP immunostaining was observed in the AIPmut NS adenoma (Fig. 3I), but not in the prolactinoma that was surgically resected in her brother (Fig. 3H). AIP immunostaining was frequently associated with nuclear AHR (55.5 vs 9.0% according to the presence or the absence of significant AIP respectively, \( \chi^2 = 5.09, P = 0.02 \)), which in turn was significantly correlated with cytoplasmic AHR (\( \chi^2 = 11.6, P = 0.0007 \)). No significant correlation was found between AIP and AHR immunostaining and tumour volume, invasiveness or immunostaining for gonadotrophins.

Discussion

This study shows for the first time that both AHR and AIP are expressed in the normal human pituitary and frequently down-regulated in PA. In normal pituitaries, topographical studies indicated a preferential expression of AIP by somatotrophs, which display a strong and diffuse expression, and to a lesser extent by lactotrophs. These findings are in agreement with recent work by Leontiou et al. (2008), which also localized AIP within GH and PRL-containing...
secretory granules in normal cells. Scattered AIP-expressing cells were also observed in the pars intermedia. AHR was expressed at lower transcriptional levels and with a lower immunostaining intensity than AIP, with scattered AHR-expressing cells being more widely distributed than AIP-expressing cells. AIP and AHR were first observed in the cytoplasm only. However, further evaluation with an antibody directed against the C-terminal part of the AHR protein revealed moderate nuclear immunostaining in a subset of somatotrophs and in some corticotrophs. Differences between cytoplasmic and nuclear staining may reflect variations in protein–protein interactions involving AHR in subcellular compartments, which may in turn influence epitope recognition and modify the sensitivity of the corresponding IHC assays. As DNA binding and basic-helix-loop-helix (bHLH) -interacting domains of AHR are located N-terminal (Fukunaga et al. 1995, Fukunaga & Hankinson 1996), the N-mAb epitope of AHR may be masqueraded in its transcriptionally active conformation. Thus, nuclear immunostaining with the C-terminal antibody alone may indicate some degree of endogenous AHR activity. Supporting a role for AHR in pituitary development and/or cell differentiation, binding sites for the pituitary transcription factors Lhx3 and Pit-1 are present in the promoter of the AHR gene (Harper et al. 2006). Constitutive expression of AHR and ARNT has been shown in the rat hypothalamus (Korkalainen et al. 2005). These data suggest a physiological role for AHR in the human hypothalamus–pituitary unit, further extending the spectrum of bHLH transcription factors expressed in the normal pituitary and PA (Jackson et al. 1993, Ferretti et al. 2001, Huang et al. 2002, Fratticci et al. 2007).

In agreement with a recent report (Leontiou et al. 2008), AIP was found by real-time RT-PCR to be expressed at a transcriptional level in all PA, with a relative overexpression in a subset of somatotrophinomas and NS adenomas. Accordingly, significant AIP immunostaining was observed in about half of somatotrophinomas and NS adenomas, but in ≤15% of other PA. Thus, AIP expression can be either retained or down-regulated in somatotrophinomas and is frequently decreased in prolactinomas, whereas abnormal AIP expression may occur in a subset of NS adenomas.

We first focused our attention on the significance of AIP down-regulation in somatotrophinomas. In these tumours, decreased gene and protein expression of AIP were significantly associated with the presence of aggressive features and, although AIP immunostaining tended to be lower in AIPmut somatotrophinomas, only invasiveness was an independent predictor of AIP loss. On the other hand, young age (<30 years of age) was an independent predictor for the presence of AIP mutations, but not for low AIP immunostaining. These findings may have interesting pathogenetic and clinical implications. First, they strongly suggest that AIP down-regulation may be involved in the progression of somatotrophinomas, regardless of detectable germline AIP mutations. Although we cannot exclude the presence of large AIP genomic deletions, this is unfrequent (Georgitsi et al. 2008b), and additional mechanisms of AIP silencing may be present. Second, such data contrast with those obtained in prolactinomas, where a low AIP expression could be observed at early stages of the disease, suggesting a peculiar role for AIP in somatotrophs. This could explain the large predominance of somatotrophinomas among PA developing in patients with germline AIP mutations, as reported in this and other studies (Cazabat et al. 2007, Daly et al. 2007), and the frequent aggressiveness of AIPmut somatotrophinomas (Daly et al. 2007, Iwata et al. 2007, Toledo et al. 2007, this study). This is consistent with the high expression of AIP in normal somatotrophs, and supported by functional experiments on GH3 cells (Leontiou et al. 2008). Third, IHC may not be as suitable as previously suggested for the pre-screening of patients with germline AIP mutations (Georgitsi et al. 2007). Indeed, our data support recent evidence that AIP can frequently be detected in AIPmut tumours (Leontiou et al. 2008). Such discrepancies may depend on the type of mutation and, to a lesser extent, antibody characteristics. Due to somatic hemizygosity for the mutated AIP allele, as further supported by cDNA sequencing in this study, IHC data will depend on epitope expression by the mutated protein, if actually transcribed. In fact, AIP immunostaining can theoretically be retained unless early stop mutations are present. Early data on IHC were obtained in series where Finnish patients and their distinctive Q14X early stop mutation were largely represented (Georgitsi et al. 2007). Although the AIP immunoscore in AIPmut somatotrophinomas can also be low due to mono-allelic gene expression, this is of limited diagnostic interest, since semi-quantitative interpretation of IHC is difficult to standardize and can be confounded readily. Thus, evidence of AIP immunostaining should not discourage AIP gene sequencing in acromegals with a familial history of FIPA or a young age at disease onset. Furthermore, IHC is unsuitable as a pre-screening tool in prolactinomas, due to the frequent loss of significant AIP immunostaining in this group.
The familial AIP mutations reported herein (E174fs, K241E, Q285fs and R304X) were previously published (Daly et al. 2007, Naves et al. 2007), whereas seven out of the eight nucleotide changes identified in patients with sporadic PA were undescribed. They consisted of one frameshift (Q82fs) and three missense (R128H, V195A and A277P) mutations respectively, three intronic changes (IVS2 c.279+23C>T, IVS3 c.468+16 G>T and IVS3 c.468+15C>T) being also recognized. None was observed in controls and comparison with available SNPs, and orthologue sequences’ databases were performed (see the electronic Supplementary Materials and methods). Briefly, the Q82fs frameshift mutation is expected to encode for a truncated protein after seven amino acids. None of the novel missense changes has been identified as a SNP to date, the amino acid residues K(241), V(195) and A(277) are highly conserved among species, and loss of the wild-type allele could be verified by cDNA sequencing in the latter case. In contrast, the presence of an arginine or a histidine at position 128 variant might explain normal AIP immunostaining in this case. However, the exclusion of this case from which might explain normal AIP immunostaining in controls and AIP immunostaining in the presence of low AIP levels, thereby supporting a role for AIP in AHR cytoplasmic stabilization in the human pituitary, as observed in most tissues. In AIPmut PA, AHR can be further destabilized by a defective interaction with the AIP protein. As the C-terminal half of AIP is critical for interaction with AHR, which is abolished by truncation of the last five amino acids (Bell & Poland 2000), AIP-truncating mutations are expected to prevent the constitution of the cytoplasmic complex. The functional implications of each missense mutation would need specific in vitro experiments, but a number of single amino acid changes occurring in the TPR region can abolish AIP binding to hsp90 and/or strongly reduce AIP/AHR interaction (Bell & Poland 2000, Petrulis & Perdew 2002). The N-terminal part of AIP may also contribute to the cytoplasmic stabilization of AHR (Kazlauskas et al. 2002). Accordingly, none of the AIPmut PA showed nuclear AHR staining, suggesting that increased AHR nuclear signalling is not implicated in AIP-related tumorigenesis. Hence, AHR down-regulation may be involved in AIPmut and/or invasive somatotrophinomas, although we cannot exclude a non-specific bystander effect of AIP down-regulation. In contrast, AHR appears to be up-regulated in a subset of NS overexpressing AIP. Of note, NS but not GH-secreting PA have been reported after Seveso’s exposure (Pesatori et al. 2008). These findings suggest a differential role of AHR in pituitary cells, and further in vitro investigations should help clarifying these issues.

In addition to AHR modulation, AIP is known to interact with a number of cytoplasmic proteins including phosphodiesterases (Bolger et al. 2003, de Oliveira et al. 2007), thereby possibly modulating...
cAMP concentration, survivin, an anti-apoptotic protein (Kang & Altieri 2006), and Ret (Vargioli et al. 2009). Interactions with phosphodiesterases can be altered by AIP mutations (Bolger et al. 2003, de Oliveira et al. 2007). Possible alterations in cAMP signalling or apoptosis accompanying down-regulation of AIP in somatotrophinomas or increased AIP expression in NS PA should be further investigated.

In conclusion, this study supports the role of AIP in the cytoplasmic stabilization of AHR and shows that reduced AIP and AHR expression are frequently observed in PA, at least at a protein level, with the exception of NS adenomas, in which up-regulation of both proteins can be observed. It suggests a possible role for AIP and AHR down-regulation in the progression of somatotrophinomas, independently from germline mutations, and indicates that IHC is not a sufficiently sensitive tool for the detection of AIP mutations in somatotrophinomas, and is unsuitable to this purpose in prolactinomas or NS PA.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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