Molecular analysis of CDKN1C and TP53 in sporadic adrenal tumors

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Abstract

Objective: To evaluate the roles of the CDKN1C (P57KIP2) gene, which encodes for the cyclin-dependent kinase inhibitor CDNC, and the TP53 tumor suppressor gene in adrenal tumorigenesis, as a means of investigating the molecular basis of sporadic adrenal tumors, which is unknown.

Design: Screening for the presence CDKN1C and TP53 mutations and analyzing the expression pattern of CDNC, P53 and its downstream effector CDN1 (P21WAF1/CIP1) in a series of 79 sporadic adrenal tumors.

Methods: Single-strand conformation polymorphism and sequencing were used for mutation analysis of CDKN1C and TP53 in blood and adrenal tissue samples. In a subgroup of 48 tissues, CDKN1C expression was evaluated by RT-PCR and immunohistochemistry. Immunohistochemical analysis of P53 and CDN1 was performed.

Results: No somatic mutations of CDKN1C were found in the tumors analyzed, in spite of low/absent CDNC expression in adrenocortical adenomas and carcinomas. Mutations in the TP53 gene were present in 70% of adrenocortical carcinomas, associated with abnormal P53 and CDN1 expression, but not in benign neoplasms. In the normal adrenal cortex, CDNC expression was strictly nuclear and confined to the cortical zone (i.e. zona glomerulosa and reticularis), with no staining in the medulla.

Conclusions: Mutations in the TP53 gene are frequent in adrenocortical carcinomas and might be used as a marker of malignancy. In the normal adrenal cortex, the zone-specific pattern of expression of CDNC suggests a role in adrenal differentiation.

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Introduction

Management of adrenocortical masses still raises much concern about the diagnosis of malignancy. Indeed, clinical and morphological data cannot reliably distinguish between benign and malignant adrenal masses, and often the nature of a localized tumor cannot be assessed even at histology. Identification of molecular markers of malignancy has been demonstrated to be helpful in the diagnosis and characterization of several haematologic and solid neoplasms. However, the molecular events leading to malignancy are largely unknown for adrenal tumors, even though a multi-step model with a sequence of genetic events, involving overexpression of proto-oncogenes or inactivation of tumor suppressor genes, or both, have been hypothesized (1). Rearrangements, loss of heterozygosity and abnormal imprinting at the 11p15.5 chromosomal region, associated with low CDKN1C (P57KIP2) and H19 RNA expression and increased IGF2 mRNA levels, have been reported in adrenocortical carcinomas (1). Mutations within candidate genes, such as TP53, have also been demonstrated in adrenocortical carcinomas (1). A putative role for these alterations in adrenal tumorigenesis is suggested also by the association, although rare, of adrenocortical carcinomas with familial tumor syndromes, such as the Beckwith–Wiedemann syndrome and the Li–Fraumeni syndrome. The molecular basis of these syndromes is represented by abnormalities within 11p15.5, including CDKN1C mutations, and germline TP53 mutations respectively (1).

It is against this background that the CDKN1C and the TP53 genes have been considered as candidate genes for adrenal tumorigenesis. In the present study we screened a large series of sporadic adrenal tumors for mutations in the CDKN1C gene and for expression of CDKN1C mRNA and the
encoded protein CDNC. In the same tumor samples, we performed mutational analysis of TP53 and immunohistochemical evaluation of the expression of P53 and of its downstream effector CDN1 (P21WAF1/CIP1).

Materials and methods

Patients and tissues

A total of 79 patients with sporadic adrenal tumors were investigated. Clinical and pathologic data are summarized in Table 1. Normal adult adrenals were obtained from 10 patients who underwent nephrectomy for kidney cancer. Patients underwent clinical, radiological, and hormonal evaluation as previously described (2). They were considered to have functioning tumors on the basis of the clinical picture and of abnormal hormone levels. Staging of adrenocortical carcinomas was performed according to the MacFarlane criteria (3). Diagnosis of benign, suspect and malignant adrenocortical tumors was based on widely accepted criteria, including tumor mass, presence of metastasis or recurrence, mitotic rate, nuclear grade, necrosis and capsula and/or vascular invasion (4). Tissue specimens, removed at surgery, were snap-frozen in liquid nitrogen and stored at −80 °C until required for DNA extraction. To avoid contamination with surrounding tissue, non-neoplastic areas were removed macroscopically, and only a central portion of each tissue specimen was used. Blood samples from all patients were available. Blood and tissues were collected after informed consent had been given by the patients and with the approval of the local ethics committee.

PCR-single-strand conformation polymorphism analysis and sequencing

DNA was isolated from leukocytes and tissue specimens by standard procedures using proteinase k digestion and the phenol–chloroform method. All samples were screened for mutations in the coding sequence of the CDKN1C and the TP53 genes by single-strand conformation polymorphism (SSCP) analysis, direct sequencing, or both. Oligonucleotide primer sequences used for PCR and sequencing are available on request. Sequencing was performed on an ABI PRISM 310 DNA sequencer (Applied Biosystem, Foster City, CA, USA) using ABI PRISM BigDye Terminator Cycle Sequencing Reaction Kit with AmpliTaq DNA Polymerase FS (Applied Biosystem).

Immunohistochemistry

CDNC expression was investigated in situ in a subgroup of 48 adrenal tissues, including normal adult (10

<table>
<thead>
<tr>
<th>Diagnosis</th>
<th>No.</th>
<th>Sex (F/M)</th>
<th>Median age (yr)</th>
<th>Median size (cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adrenocortical carcinoma†</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Non-functioning</td>
<td>3</td>
<td>2/1</td>
<td>45 (43–65)</td>
<td>8 (5–12)</td>
</tr>
<tr>
<td>Functioning†</td>
<td>7</td>
<td>6/1</td>
<td>46 (27–69)</td>
<td>9.5 (8–20)</td>
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<tr>
<td>Suspect adrenocortical carcinoma</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Non-functioning</td>
<td>3</td>
<td>2/1</td>
<td>52 (35–68)</td>
<td>4.5 (4–6)</td>
</tr>
<tr>
<td>Androgen-secreting</td>
<td>1</td>
<td>1</td>
<td>44</td>
<td>8</td>
</tr>
<tr>
<td>Adrenocortical adenoma</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Non-functioning</td>
<td>17</td>
<td>11/6</td>
<td>58 (46–70)</td>
<td>3.5 (2.5–5)</td>
</tr>
<tr>
<td>Aldosterone-producing</td>
<td>16</td>
<td>10/6</td>
<td>36 (28–57)</td>
<td>2 (0.5–3)</td>
</tr>
<tr>
<td>Cortisol-producing</td>
<td>8</td>
<td>7/1</td>
<td>47 (19–58)</td>
<td>3 (2.5–5)</td>
</tr>
<tr>
<td>ACTH-dependent adrenal hyperplasia</td>
<td>6</td>
<td>5/1</td>
<td>36 (17–48)</td>
<td></td>
</tr>
<tr>
<td>Pheochromocytoma</td>
<td>17</td>
<td>7/10</td>
<td>20 (12–52)</td>
<td>5 (3–8)</td>
</tr>
<tr>
<td>Malignant pheochromocytoma</td>
<td>1</td>
<td>0/1</td>
<td>35</td>
<td>8</td>
</tr>
</tbody>
</table>

†Stage I–II = three patients; stage III–IV = six patients.
‡Local recurrences of adrenocortical carcinoma in two patients.

Table 1  Clinical and pathological data of adrenal tumors (n = 79). Values in parentheses are ranges.

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samples) and fetal (one sample) adrenals, ACTH-dependent adrenocortical hyperplasia (four samples), functioning and non-functioning adrenocortical adenomas (five samples), functioning and non-functioning adrenocortical tumors (suspect malignant, four samples; malignant, seven samples) and pheochromocytomas (17 samples).

The immunohistochemical analysis for CDNC was performed on formalin-fixed paraffin-embedded sections using microwave antigen retrieval and a streptavidin–biotin peroxidase technique (LSAB Dako, Carpinteria, CA, USA), as described previously (5). A goat affinity-purified polyclonal antibody raised against a peptide corresponding to amino acids 286–305 mapping at the carboxy terminus of human CDNC was used (C-20 cat. No. sc-1040 Santa Cruz Biotechnology, Santa Cruz, CA, USA).

The immunohistochemical analysis for P53 and CDKN1C was performed as previously described (6) using DO-1 MoAb (Dako, Glostrup, Denmark) specific for P53 and EA10 MoAb (Oncogene Science, Uniondale, NY, USA) recognizing CDKN1C.

**Results**

**Mutations of the CDKN1C gene in sporadic adrenal tumors**

SSCP analysis and sequencing of CDKN1C revealed several neutral or conservative polymorphisms in 18 of 79 adrenal tumors (three adrenocortical carcinomas, six non-functioning adrenocortical adenomas, four aldosterone-producing adenomas, one cortisol-producing adenoma, four pheochromocytomas) and in one normal adrenal sample. Polymorphisms were found also in the corresponding blood samples. These included the PAPA-repeat length polymorphism in exon 2 (1715–1727del) in six cases, 1776C → T transition in exon 2 (A183A) in nine cases, 2773–2774insG in intron 3 in 12 cases (which have been reported also by others (7), and three novel polymorphisms: 1407C → T (R60R) in exon 3 in one case, 2708C → G (G305G) and 2726G → A (P311P) in exon 3 in the other two. At variance with the benign tumors, the three adrenocortical carcinomas showed 1776C → T and 2773–2774insG heterozygous polymorphisms in blood DNA, but were hemizygous in tumor DNA, suggesting loss of heterozygosity. No relationships between DNA polymorphism and phenotype (including age, sex, functioning status, size, histological diagnosis) were apparent from our data. All samples showed both 2079G → C transversion and 2600–2601insC in exon 2, confirming previous reports (7). None of the adrenal tumors contained CDKN1C somatic coding or splice-signal mutations.

**CDKN1C expression in normal adrenal tissues and sporadic adrenal tumors**

In normal adrenal gland (10 samples) a number of CDNC expressing cells were observed at immunohistochemistry, confined to the cortical zone, with completely negative results in the medulla. The immunostaining was strictly nuclear, and variable in intensity. The proportion of CDNC expressing cells was highly variable and related to the location within the cortex. In the zona glomerulosa 5–10% CDNC positive cells were present. The zona fasciculata was devoid of positive cells in all samples, with the exception of few scattered nuclei observed in a minority of samples. The proportion of positive cells reached the greatest values in the zona reticularis, with 10–20% cells expressing CDNC (Fig. 1). Similar levels of CDNC expression were observed in a single sample of fetal adrenal (12 weeks old). In all samples of cortical hyperplasia, a pattern of CDNC expression similar to that observed in normal adrenal tissue was observed, with variable levels of expression in different zones. In contrast, most samples of adenoma (four of five) showed very few positive cells, with a single case expressing a proportion of positive cells akin to normal adrenal cortex. A low level of CDNC expression was documented in most adrenocortical tumors (six of seven) clearly defined as malignant on the basis of pathological and clinical criteria, and in most adrenal tumors characterized by atypical morphology, but lacking consistent clinico-pathological features of malignancy (Table 2). Nevertheless, a focal immunostaining was observed in two out of four of these cases. No particular features could be documented (including sex, age, morphology, tumor dimension, or functioning status) to account for this phenotypic heterogeneity. Most cells in pheochromocytomas were devoid of CDNC expression, with the exception of focal collections of strongly staining cells in four of 17 investigated cases.

Densitometric analysis of RT-PCR for CDKN1C mRNA showed greatest expression in normal adrenal gland and adrenocortical hyperplasia. At variance with this, CDKN1C mRNA levels were lower or absent in functioning and non-functioning adenomas (5–70% and 0–30% of that of normal adrenal respectively) and in adrenocortical carcinomas (0–15% of that of normal adrenal) (Fig. 2).

**Mutations of the TP53 gene in sporadic adrenal tumors**

PCR-SSCP analysis and sequencing of TP53 showed mutations in tumor DNA from six of seven (86%) functioning adrenocortical carcinomas, in one of three (33%) non-functioning adrenocortical carcinomas, and in one of four (25%) suspect non-functioning adrenocortical carcinomas. Sequencing of paired leukocyte
DNA revealed a wild-type sequence. In particular, missense mutations were identified in five stage II-III adrenocortical carcinomas (A161V, I162M, E180A, D208G, G245S) and in the suspect adrenocortical carcinoma (S185R). These included a female patient who, after 1 year of follow-up, exhibited an increase in tumor mass size from 3.5 to 4.5 cm, associated with subclinical hypercortisolism (8). Deletions were demonstrated in two recurrences from two aggressive stage IV adrenocortical carcinomas: the first tumor had a heterozygous 3 bp in-frame deletion (P191del); the second had two distinct hemizygous deletions in exon 8 (14571delC; 14575delG), leading to a frame-shift that modified the three amino acids downstream and resulted in a premature translation termination. Germ-line genetic polymorphisms (13342T → C (L194L) in exon 6 and 12139G → C (R72P) in exon 4) were also observed in an adrenocortical carcinoma and in four adrenocortical adenomas (one androgen-secreting and three non-functioning) respectively.

**Table 2** CDNC, P53 and CDN1 expression in sporadic adrenal tumors.

<table>
<thead>
<tr>
<th>Sample</th>
<th>CDNC expression†</th>
<th>P53 expression†</th>
<th>CDN1 expression†</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No.</td>
<td>++</td>
<td>+</td>
</tr>
<tr>
<td>Normal adrenocortical tissue</td>
<td>10</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td>Adrenocortical hyperplasia</td>
<td>4</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Adrenocortical adenoma</td>
<td>5</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>Suspect adrenocortical carcinoma</td>
<td>4</td>
<td>4†</td>
<td></td>
</tr>
<tr>
<td>Adrenocortical carcinoma</td>
<td>7</td>
<td>1</td>
<td>6</td>
</tr>
<tr>
<td>Pheochromocytoma</td>
<td>16</td>
<td>4</td>
<td>12</td>
</tr>
<tr>
<td>Malignant pheochromocytoma</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
</tbody>
</table>

†Immunohistochemical semi-quantitative evaluation of CDNC, P53 and CDN1 positive cells: –, negative; +, 5–10%; ++, 10–20% for CDNC, 10–15% for P53 and CDN1.
‡Focal expression of CDNC in two cases.
was very low in most adrenocortical adenomas and that paralleled that of normal adrenal tissue, whereas it was increased in an adrenocortical carcinoma bearing an A161V missense mutation (Table 2). This tumor was characterized by complete lack of CDN1, suggesting that non-functional P53 protein was accumulated in neoplastic nuclei. All other investigated malignant cases did not contain a significant number of P53 positive nuclei (<5%), whereas CDN1 was variably expressed regardless of molecular abnormalities. All four investigated suspect adrenocortical tumors were P53-negative; overexpression of CDN1 was demonstrated in two. All 17 samples of pheochromocytoma were negative for P53, whereas CDN1 was overexpressed in a single malignant pheochromocytoma (Table 2).

**Discussion**

Previous reports have suggested a role for genes located in the 11p15.5 region, including CDKN1C, in adrenal tumorigenesis (1, 9–11). To our knowledge, the present report is the first on mutational analysis of CDKN1C and immunohistochemical evaluation of its expression in normal and neoplastic adrenal tissues.

Our results indicate that mutations within the CDKN1C gene are rare events and do not account for reduced CDKN1C mRNA and protein levels observed in adrenocortical tumors. However, we cannot exclude the presence of mutations in the non-coding region of the gene, influencing expression or altering the start site, or hemizygous deletions of one allele, or other mutations missed by SSCP analysis. In accordance with others (9–11), our data showed a pattern of expression of CDKN1C mRNA and CDNC in hyperplastic adrenal that paralleled that of normal adrenal tissue, whereas it was very low in most adrenocortical adenomas and carcinomas. As the majority of these tumors are known to be monoclonal in origin (12), low expression of CDKN1C may indeed reflect a growth advantage of a particular clone. Decrease in both RNA and protein expression in adrenal tumors suggests that post-translational modifications by the ubiquitin–proteasome system may not be important in regulating CDKN1C expression (13). At variance with this, loss of heterozygosity, imprinting abnormalities, or both, reported in most adrenocortical carcinomas (10, 11), could explain low CDKN1C expression. In our patients, immunohistochemical analysis demonstrated that CDNC is expressed in the normal adrenal cortex, but not in the medulla. Immunostaining of CDNC was strictly nuclear and, interestingly, was zone-specific – that is, negative in the adrenal zona fasciculata. This pattern of expression seems to reflect the differential regulation of cell proliferation, maturation and apoptosis in the normal adrenal gland, with cell proliferation predominant in the zona fasciculata and programmed cell death predominant in the zona reticularis and in the zona glomerulosa (14, 15). These data suggest that CDNC might play a part in the differentiation of the normal adrenal cortex (16).

TP53 somatic mutations were observed in 70% adrenocortical carcinomas, but not in benign lesions, suggesting that it may be possible to use their presence as a marker of malignancy. Although our analysis was performed in a relatively small series of adrenocortical carcinomas, the prevalence of mutations was greater than had been observed in other studies reporting TP53 mutations in 20–30% of sporadic adrenocortical carcinomas, but rarely in adenomas (1, 17–20). Environmental factors or methodological aspects such as the scanning of the entire rather than the partial sequence of the gene may account for this difference. At variance with this, but in agreement with previous findings (20, 21), no TP53 gene mutations were observed in pheochromocytomas, suggesting that TP53 mutations are not important in the pathogenesis of these tumors, although a role in the development of malignant pheochromocytomas cannot be excluded (20). Immunohistochemical analysis of P53 and of its downstream effector CDN1 in adrenal cortical and medullary tumors showed a poor concordance with TP53 sequence data. Only one adrenocortical carcinoma with a TP53 mutation had the typical immunohistochemical pattern of P53 overexpression and decreased CDN1 expression. Discordant results between TP53 mutations and immunohistochemical staining have been reported in other types of malignancy (22). In fact, deletion mutations, as in our two samples with negative staining, may not result in a P53 protein with increased stability, and, in the case of missense mutations, additional cellular events may be required for P53 overexpression (22). Thus immunohistochemical analysis alone (23, 24) does not detect all genetic alterations affecting TP53 in adrenal tumors.
In conclusion, reduced CDKN1C expression occurs in the majority of adrenocortical adenomas and carcinomas, but is not due to genetic mutations. Mutations in the TP53 gene are frequent in adrenocortical carcinomas and might be used as a marker of malignancy. Further investigations on the mechanisms of CDKN1C downregulation in adrenal tumors and on its role in the development of the normal adrenal cortex are required.

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References

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