Germline PRKACA amplification causes variable phenotypes that may depend on the extent of the genomic defect: molecular mechanisms and clinical presentations

Maya B Lodish, Bo Yuan¹, Isaac Levy, Glenn D Braunstein², Charalampos Lyssikatos, Paraskevi Salpea, Eva Szarek, Alexander S Karageorgiadi, Elena Belyavskaya, Margarita Raygada, Fabio Rueda Fauze, Louise Izatt³, Caroline Brain⁴, James Gardner⁵, Martha Quezado⁶, J Aidan Carney⁷, James R Lupski¹,⁸,⁹ and Constantine A Stratakis

Section on Endocrinology and Genetics, Program on Developmental Endocrinology and Genetics, National Institute of Child Health and Human Development, National Institutes of Health, Building 10-CRC, Room 9D42, 10 Center Drive, MSC, 1103, Bethesda, Maryland 20892, USA, ¹Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, Texas, USA, ²Department of Medicine, Cedars–Sinai Medical Center, Los Angeles, California, USA, ³Department of Clinical Genetics, Guy's Hospital, London, UK, ⁴Department of Endocrinology, Great Ormond Street Hospital for Children, London, UK, ⁵Department of Pediatrics, Our Lady of the Lake Children's Hospital, Baton Rouge, Louisiana, USA, ⁶Department of Pathology, National Cancer Institute, Bethesda, Maryland, USA, ⁷Emeritus Member, Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, Minnesota, USA, ⁸Department of Pediatrics, Baylor College of Medicine, Houston, Texas, USA and ⁹Texas Children's Hospital, Houston, Texas, USA

Correspondence should be addressed to M B Lodish
Email lodishma@mail.nih.gov

Abstract

Objective: We have recently reported five patients with bilateral adrenocortical hyperplasia (BAH) and Cushing's syndrome (CS) caused by constitutive activation of the catalytic subunit of protein kinase A (PRKACA). By doing new in-depth analysis of their cytogenetic abnormality, we attempted a better genotype-phenotype correlation of their PRKACA amplification.

Design: This study is a case series.

Methods: Molecular cytogenetic, genomic, clinical, and histopathological analyses were performed in five patients with CS. Reinvestigation of the defects of previously described patients by state-of-the-art molecular cytogenetics showed complex genomic rearrangements in the chromosome 19p13.2p13.12 locus, resulting in copy number gains encompassing the entire PRKACA gene; three patients (one sporadic case and two related cases) were observed with gains consistent with duplications, while two sporadic patients were observed with gains consistent with triplications. Although all five patients presented with ACTH-independent CS, the three sporadic patients had micronodular BAH and underwent bilateral adrenalectomy in early childhood, whereas the two related patients, a mother and a son, presented with macronodular BAH as adults. In at least one patient, PRKACA triplication was associated with a more severe phenotype.

Conclusions: Constitutional chromosomal PRKACA gene amplification is a recently identified genetic defect associated with CS, a trait that may be inherited in an autosomal dominant manner or occur de novo. Genomic rearrangements can be complex and can result in different copy number states of dosage-sensitive genes, e.g., duplication and triplication. PRKACA amplification can lead to variable phenotypes clinically and pathologically, both micro- and macro-nodular BAH, the latter of which we speculate may depend on the extent of amplification.
Introduction
Inactivating mutations of PRKARIA, the main regulatory subunit (R1a) of protein kinase A (PKA), cause primary pigmented nodular adrenocortical disease (PPNAD), a bilateral adrenocortical hyperplasia (BAH) leading to Cushing’s syndrome (CS) (1). PRKARIA maps to 17q24.2 and is frequently deleted in patients with PPNAD with and without Carney complex (CNC), as well as in sporadic patients with cortisol-secreting adrenal adenomas (2, 3, 4). Inactivation of PRKARIA leads to increased PKA activity that is due to lack of regulation of the PKA’s main catalytic subunit (Cz) coded by the PRKACA gene (3).

We have recently reported gain-of-function mutations in PRKACA that lead to increased cAMP signaling in adrenal CS associated with BAH (when PRKACA defects are present in the germline) and sporadic cortisol-producing adrenal adenomas (CPAs) (when PRKACA defects are present in the somatic state, i.e., somatic events confined to the tumor tissue) (4). Thus, gain of function of PRKACA appears to lead to benign adrenal tumors without any other manifestations of CNC (such as skin pigmentation, myxomas, and other neoplasms), suggesting that increased activity of this catalytic subunit of CPA is associated with abnormalities specific to adrenocortical tissue, whereas inactivating mutations of the PKA regulatory subunit R1a (encoded by PRKARIA) result in the full spectrum of findings associated with CNC.

All patients had been sequenced for PRKARIA, PRKACA and PRKACB and their sequences were normal (4). In the present investigation, using in-depth probes, we investigated the nature of the cytogenetic defects in all patients with germline PRKACA amplification. We also collected additional phenotypic information on the probands and their families. Surprisingly, our new data suggest that there might be a dosage-dependent effect on the phenotype, as both duplications and triplications encompassing PRKACA were observed, and those patients with triplications presented at a younger age. In addition, one patient developed breast cancer that was found to express PRKACA. The type of BAH varied from PPNAD, to non-pigmented isolated micronodular adrenocortical disease (iMAD) and micronodular adrenocortical disease also known as primary macronodular adrenocortical hyperplasia (PMAH).

Subjects and methods
Patients
The Institutional Review Boards of all the participating institutions approved the investigation. Written informed consent was obtained from all patients and/or their guardians. In our previous report, the details of the clinical presentation of the patients with germline amplification of the PRKACA gene were not included (4).

Array comparative genomic hybridization
DNA samples from subjects CAR54.03, CAR615.01, CAR696.01, and CAR767.03 were studied by array comparative genomic hybridization (aCGH). Customized high-density (HD) aCGH (Agilent Technology, Santa Clara, CA, USA) in an 8X60K format was designed to interrogate the 19p13.2p13.12 critical region (chr19: 12 907 616–15 565 924, GRCh37/hg19). The probe density averaged five oligonucleotides per kilobase for the critical region identified with copy number alterations. The array was also designed to interrogate the flanking genomic regions of up to 6 Mb in size with a probe density of 1–2/kb. Previously described protocols (5) with minor modifications were followed for aCGH’s experimental procedures, including DNA fragmentation, labeling and hybridization, array scanning, and data processing. We excluded 19p duplication in the parents of patients 1 and 2, and DNA was not available for patient 3.

Breakpoint junction analysis
Breakpoint junction analysis was performed to examine rearrangement product structures and surmise the potential underlying mechanisms for the complex genomic rearrangements observed from the aCGH data. Long-range (LR) PCRs were used to amplify the breakpoint junctions. Forward and reverse primers were designed using the sequences from the estimated copy number variant (CNV) boundaries as determined by changes in copy number states on the aCGH log2 ratio plot. TaKaRa LA Taq (Clontech, #RR002A) was used for the PCR amplifications. Sanger sequencing was performed for the PCR products, and the DNA sequences were compared with the reference genome (hg19) in order to precisely map the breakpoint junctions.

CNV analyses
Individual CNV assays were performed by duplex TaqMan real-time PCR assays in order to independently verify the aCGH results in the patients and to extend the analysis in a cohort of patients with sporadic BAH. CNV assays for
**Clinical Study**

M B Lodish and others

**PRKACA amplification in Cushing's syndrome**

172:6 | 805

---

**PRKACA** utilized a pair of unlabeled primers, and a FAM-labeled MGB probe was supplied from Life Technologies. RNase P (Life Technologies, #4403328) with a VIC-labeled TAMRA probe was used as a reference gene. TaqMan CNV assays were performed according to the manufacturer's protocol (Life Technologies). Briefly, experiments were prepared in 96-microwell plates and consisted of 20 µl reaction volumes containing 20 ng genomic DNA, 10 µl TaqMan Genotyping Master Mix (Life Technologies, catalog number 4371355), and 1 µl each of one target gene and reference CNV assay mixes. All reactions were run in triplicate on a ViiA 7 Real-Time PCR System (Life Technologies) and thermal cycling conditions were 95 °C for 10 min followed by 40 cycles of 95 °C for 1 min. All data were analyzed using the CopyCaller Software version 2.0 (Life Technologies). The copy number was determined by the relative relationship between the quantity of the target gene and the reference gene, using a female calibrator sample known to have two copies of each gene as the basis for comparison.

**Immunohistochemistry and clinical assays**

The adrenal glands from all patients were processed as per routine histopathological procedures for diagnostic purposes. Hematoxylin and eosin (H&E)-stained slides and other appropriate immunohistochemical (IHC) stainings (for example, inhibin-A dilution 1:100, Biogenex, Inc. (Fremont, CA, USA) and synaptophysin, dilution 1:100, Zymed, Inc. (Carlsbad, CA, USA)) were reviewed. Detailed analysis of the pathology of these patients has been reported previously (6). IHC on unstained slides from breast tumor tissue for patient CAR615.05 was performed in collaboration with Histoserve, Inc. (Germantown, MD, USA) using standard procedures. The primary antibody used was rabbit anti-Ca, sc903 (Santa Cruz Biotechnology) and the secondary antibody was rabbit polyclonal anti-IgG (Sigma–Aldrich, Inc.). Adrenocorticotropic hormone (ACTH) was measured using the chemiluminescence immunoassay on an Immulite 200 XPi analyzer (Siemens, Malvern, PA, USA). Serum cortisol was measured using the chemiluminescence immunoassay on the Siemens Immulite 2500 analyzer (Siemens).

**Results**

**Clinical history and manifestations**

Patient 1 (CAR54.03) presented at the age of 8 with a year-long history of progressive facial swelling, prominent hirsutism on the face and back, decreased linear growth, 9 kg weight gain in 1 year, facial plethora, and hypertension. During the preceding 6 months, he complained of intermittent headaches and decreased energy. The patient had no significant past medical history; his maternal grandfather died at the age of 39 due to a myocardial infarction. Physical examination revealed a pigmented left inner canthus, as well as pigmented spots on the vermilion border and facial freckling (Fig. 1). He was hypertensive with systolic blood pressures ranging from 125 to 140 mmHg (normal range (NR) for an eight year old is > 116/77). An evaluation for hypercortisolemia showed that he failed to suppress to 1 mg overnight dexamethasone, with a post-dexamethasone cortisol level remaining elevated (Table 1); ACTH was undetectable. Further evaluation confirmed hypercortisolemia with elevated urinary free cortisol (UFC), and loss of diurnal cortisol variation with a midnight cortisol of 974.3 (NR: < 121 nmol/l) and morning cortisol of 1010.2 nmol/l (NR: 138–690 nmol/l). Corticotropin-releasing hormone (CRH) stimulation test was flat with a baseline cortisol of 1037.8 nmol/l and a peak of 1035 nmol/l; ACTH remained suppressed throughout the test. There was a paradoxical increase in UFC levels in response to the Liddle’s test (2 days of low-dose dexamethasone 0.5 mg by mouth every 6 h, followed by 2 days of high-dose dexamethasone 2 mg by mouth every 6 h). The patient had a baseline UFC of 1821.6 nmol/day, rising to a peak of 2484 nmol/day at the end of high-dose dexamethasone, corresponding to a 73.4% increase in UFC. A computed tomography (CT) scan revealed bilateral adrenal nodularity with slight thickening and irregularity of both glands with multiple nodules < 5 mm; the pituitary magnetic resonance imaging (MRI) was normal. The patient underwent bilateral adrenalectomy and pathological findings were consistent with a form of BAH characterized by cytomegaly, persistence of the transient cortex, and hyperplasia of the permanent cortex that has been reported previously in other patients with similar clinical presentation (Fig. 2) (7). No sequence change in **PRKACA** was identified, but combined commercially available aCGH and custom designed HD-aCGH revealed a 2.7 Mb duplication encompassing **PRKACA** on chromosome 19p13.2p13.12 (4). The patient was screened for manifestations of CNC including thyroid and testicular ultrasounds and echocardiogram; all were normal. He continues to do well 5 years after adrenalectomy.

Patient 2 (CAR696.01) presented at the age of 2 years and 6 months with rapid weight gain and centripetal obesity, hirsutism, moon faces, posterior cervical fat pad, flushed cheeks, muscle weakness, fatigue, and easy irritability. He had mild developmental delay. He was...
delivered at 36 weeks gestation and had neonatal hypoglycemia. He had a healthy older brother and no family history of endocrinopathy. On examination, his height was in the 25% with weight >99%; no skin lesions consistent with CNC were noted (Fig. 1). Biochemical evaluation confirmed hypercortisolemia with an elevated 24-h UFC (Table 1), and absent diurnal variation (midnight serum cortisol 811.4 nmol/l and 8-h cortisol 850.1 nmol/l). ACTH remained undetectable, consistent with an adrenal source of CS. Dexamethasone administration in the Liddle’s test (2 days of 20 μg/kg per day followed by 2 days of 80 μg/kg per day) did not cause suppression of cortisol. ACTH levels remained low throughout the CRH test, while cortisol levels remained elevated, both consistent with primary adrenal disease. Adrenal CT scan was read as normal. The patient

Figure 1

Facial appearance of patients 1–3 before and after adrenalectomy and their corresponding HD-aCGH results. The photographs of the patients are shown in the left column, and their HD-aCGH studies are shown accordingly in the right column. aCGH plots covering the critical region (chr19: 12 346 258–16 058 758) are shown. Red dots, probes with log2 ratio >0.25; black dots, probes with log2 ratio between −0.25 and 0.25; and green dots, probes with log2 ratio smaller than −0.25. The vertical red bar represents the position of PRKACA, and the log2 ratios of the amplified segments encompassing PRKACA are listed under each aCGH plot.
underwent bilateral adrenalectomy and pathological findings were diffuse cortical hyperplasia and prominent capsular and extra-capsular micronodular cortical hyperplasia, consistent with iMAD (6). No sequence change in PRKACA was identified, but, on a commercially available aCGH, a 294 kb gain at chromosome 19p13.13p13.12 was found (4). Follow-up HD-aCGH study revealed a complex genomic gain of distal duplication followed by a proximal triplication (dup–trp); PRKACA was included in the triplicated segment (see also below and Supplementary Figure 1, see section on supplementary data given at the end of this article). Most recently, at the age of 5 years and 9 months, his height had improved to the 75th percentile and there were no signs of CNC or any other conditions.

Patients 4 and 5 are a mother and son who presented at different times with CS. Patient 4 (CAR615.05) was

Table 1  Patients' baseline characteristics.

<table>
<thead>
<tr>
<th>Patient number</th>
<th>Patient code</th>
<th>Sex</th>
<th>PRKACA CNV</th>
<th>Age at diagnosis (years)</th>
<th>ACTH (pmol/l)</th>
<th>Midnight salivary cortisol (nmol/l)</th>
<th>Midnight serum cortisol (nmol/l)</th>
<th>Serum cortisol after Dex (nmol/l)</th>
<th>24-h urinary cortisol (nmol/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>CAR54.03</td>
<td>Male</td>
<td>dup</td>
<td>8</td>
<td>&lt;1.10</td>
<td>974.3</td>
<td>786.6</td>
<td>651.4</td>
<td>1322–2221.8</td>
</tr>
<tr>
<td>2</td>
<td>CAR696.01</td>
<td>Male</td>
<td>trp</td>
<td>2.5</td>
<td>&lt;1.10</td>
<td>811.4</td>
<td>640.4</td>
<td>604.4</td>
<td>703.8</td>
</tr>
<tr>
<td>3</td>
<td>CAR767.03</td>
<td>Male</td>
<td>trp</td>
<td>2.6</td>
<td>1.58</td>
<td>43.33</td>
<td>648.6</td>
<td>604.4</td>
<td>568.6</td>
</tr>
<tr>
<td>4</td>
<td>CAR615.05</td>
<td>Female</td>
<td>dup</td>
<td>39</td>
<td>&lt;2.20</td>
<td>43.33</td>
<td>648.6</td>
<td>604.4</td>
<td>568.6</td>
</tr>
<tr>
<td>5</td>
<td>CAR615.01</td>
<td>Male</td>
<td>dup</td>
<td>23</td>
<td>&lt;1.10</td>
<td>43.33</td>
<td>648.6</td>
<td>604.4</td>
<td>568.6</td>
</tr>
</tbody>
</table>

dup, duplication; trp, triplication.

growth and normal appetite, with weight decreasing to the 50% and height back up to the 25%. No sequence change in PRKACA was identified, but a commercially available aCGH showed a 551 kb gain on chromosome 19p13.13p13.12 (4). Follow-up HD-aCGH study revealed a complex genomic gain of a pattern of a distal duplication followed by a proximal triplication subsequently followed by another proximal duplication (dup–trp–dup) with PRKACA residing within the triplicated segment (Supplementary Figure 1); the rearrangement was complex (see above) and similar to what has been observed in other genomic disorders (8).

Patients 4 and 5 are a mother and son who presented at different times with CS. Patient 4 (CAR615.05) was
a 39-year-old woman who presented with hypertension, weight gain, hirsutism, bruising, depression, irritability, moon facies, buffalo hump, and headaches. Biochemical evaluation revealed hypercortisolism with an elevated UFC with low ACTH levels (Table 1). The serum cortisol did not suppress to high-dose (8 mg) dexamethasone (Table 1). Adrenal CT revealed an enlarged left adrenal, 1.2 cm in maximum diameter, and a normal appearing right adrenal. Following left adrenalectomy, the CS remitted, but recurred at the age of 43, prompting a right adrenalectomy. Pathological examination of both adrenal glands was consistent with macronodular hyperplasia (PMAH). The patient developed a well-differentiated infiltrating tubular breast carcinoma, 4 mm in size, and extensive ductal carcinoma in situ at the age of 49 years; she is currently well. Genetic testing showed no sequence changes in known genes, but a commercially available aCGH/chromosomal microarray analysis revealed a 616 kb gain on chromosome 19p13.2 (4). Subsequent IHC of the patient’s breast carcinoma for the PRKACA subunit was positive (Supplementary Figure 2, see section on supplementary data given at the end of this article).

Patient 5 (CAR615.01) is the son of patient 4; he presented at the age of 23 years with avascular necrosis of the left femoral head and hypertension. CS was suspected; biochemical analysis confirmed hypercortisolism with elevated cortisol after a high-dose (8 mg) dexamethasone suppression test (Table 1). Baseline ACTH was undetectable; adrenal MRI with contrast showed an enhancing left adrenal ovoid mass measuring 2.6 × 2.4 cm with an irregular periphery. The patient underwent left adrenalectomy; pathological findings were consistent with PMAH. At the age of 29, BMI was 27.6 kg/m², there was hypertension, and borderline elevation of morning cortisol following a 1 mg overnight dexamethasone suppression test, but UFC was normal (Table 1). He had the maternally inherited 616 kb gain on 19p13.2 by the suppression test, but UFC was normal (Table 1). He had cortisol following a 1 mg overnight dexamethasone.

Genomic gains revealed by HD-aCGH

The critical region with genomic gains shared, among the subjects, including CAR54.03, CAR615.01, CAR696.01, and CAR767.03, was identified previously by genome-wide aCGH (4). Customized HD-aCGH interrogating the critical region delineated the genomic gains in the DNA samples from these four families, and revealed complex genomic gains based on the HD-aCGH data: a distal duplicated segment followed by a normal segment subsequently followed by a proximal duplicated segment (dup–nml–dup) was observed in CAR54.03; a distal duplication followed by a proximal triplication (dup–trp) was observed in CAR696.01; and a distal duplication followed by a proximal triplication subsequently followed by another proximal duplication (dup–trp–dup) was observed in CAR767.03 (Fig. 1). The genomic gain in subject CAR615.01 was barely visible due to the low quality of the aCGH result, which might result from the low quality of the DNA sample from this subject (data not shown). Therefore, details of the gain in the genome of CAR615.01 could not be fully ascertained.

All the genomic gains observed in the four individuals were complex genomic rearrangements (CGRs) with variable breakpoint junctions, and these gains encompassed the gene PRKACA. The PRKACA gene resided on duplication segments in subject CAR54.03, while it was triplicated in subjects CAR696.01 and CAR767.03. Although a chromosomal gain could be observed based on the aCGH data of subject CAR615.01, the exact copy number state of the PRKACA gene could not be estimated.

Breakpoint junction analyses of the genomic gains

LR-PCR and Sanger sequencing were attempted for the breakpoint junction (Jct) analyses of all the genomic gains. In the ‘dup–nml–dup’ observed in CAR54.03, at least two breakpoint junctions (Jct1 and Jct2) are expected to be involved in the rearrangement. Breakpoint analyses revealed Jct1, which connected the proximal end of the distal duplicated segment and the distal end of the proximal duplicated segment. A 2 bp microhomology (GG) was observed at the breakpoint junctions, suggesting the Fork Stalling and Template Switching/Microhomology-Mediated Break-Induced Replication (FoSTeS/MMBIR) as the potential mechanism for the formation of Jct1 (9, 10, 11). Attempts to map the other breakpoint(s) in the ‘dup–nml–dup’ were unsuccessful. The breakpoint mapping for the ‘dup–trp’ rearrangement in CAR696.01 was also not successful. These results might suggest potential invisible complexity underlying the rearrangement that generated the ‘dup–nml–dup’ and ‘dup–trp’ complex structure observed in subjects CAR54.03 and CAR696.01. Regarding the ‘dup–trp–dup’ observed in CAR767.03, two breakpoint junction clusters were revealed by breakpoint analysis (Jct1 and Jct2). Two Alu repetitive elements, AluSx3 and AluSx1, were found at the Jct1. These two Alus, sharing 73.7% identity with direct orientation, might serve as substrates for Alu-Alu mediated recombinational rearrangement (8). A 6 bp microhomology (TACAGG) was identified at the Jct1, which was flanked by highly

www.eje-online.org

Downloaded from Bioscientifica.com at 06/16/2022 08:07:32PM via free access
identical sequences. In Jct2, a 3 bp insertion (ACA) was identified at the junction. It might be explained by the FoSTeS/MMBIR mechanism by two potential template switches to generate the insertion.

The Jct1 observed in the ‘dup–nml–dup’ of subject CAR54.03 might be part of the CGR, or it might be a breakpoint junction of a deletion of a genomic segment on the homologous chromosome. However, the parental DNA was not available for testing the actual mechanism. According to the Jct1 and Jct2 observed in the ‘dup–trp–dup’ of subject CAR767.03, the gains were likely to result from CGRs: the two Alus (AluSx1 and AluSx3) aligned at the Jct1 indicated an Alu-mediated recombination, while the observance of the 3 bp insertion (ACA) at the Jct2 favored the FoSTeS/MMBIR as the mechanism.

**Discussion**

The five patients had CS in association with a germline copy number gain resulting in amplification of the PRKACA gene encoding the most important catalytic subunit of the cAMP-dependent protein kinase or PKA. They are the first reported patients with a CNV involving this locus and implicated in a specific phenotype. As we have reported previously (4, 6), it appears that germline amplification of PRKACA leads to BAH, both macro- and micronodular and micronodular forms. In this study, we reexamined the genetics and genomics of these patients with in-depth genomic analysis and found that there were differences in the degree of amplification: PRKACA triplications were identified in patients 2 and 3, both of whom had clinical presentation at a younger age, when compared with the other patients. However, this observation needs to be repeated in a larger sample size before definitive conclusions are drawn. A similar genomic dosage-dependent phenotype has been described in Charcot–Marie–Tooth disease type 1A (CMT1A): in CMT1A, patients with triplications presented at an earlier age with a more severe distal symmetric polyneuropathy phenotype than those with duplications (12).

These data also demonstrate that amplifications of PRKACA at the genomic level, at least up to triplications, are compatible with life (13). No PRKACA-activating mutations associated with CS have been identified in the germline (4, 13), whereas such mutations have now been confirmed in the somatic state by five more studies of hundreds of patients with adrenal CS (14, 15, 16, 17, 18). Similarly, in the only cancer where PRKACA is reported to be involved, its activation is also somatic and is caused by genomic rearrangements of the 19p13 locus resulting in recurrent DNAJB1–PRKACA chimeric transcripts found in fibrolamellar hepatocellular carcinoma (19).

The somatic PRKACA mutations identified to date (4, 14, 15, 16, 17, 18) are all present in a location of the Cz protein that is responsible for binding to the regulatory subunit(s). They, as a result, lead to activation of PKA by making the catalytic subunit of the enzyme largely inaccessible to its main controller and binding partner, the PKA regulatory subunit(s) (20, 21). The cAMP-dependent protein kinase or PKA is a tetramer that consists of two inactive catalytic subunits and two regulatory subunits (20, 22). The major regulatory subunit of PKA is PRKAR1A, the gene responsible for CNC (there are three other regulatory subunits, PRKAR1B, PRKAR2A, and PRKAR2B), and the major catalytic subunit of PKA is PRKACA (there are three other catalytic subunits, PRKACB, PRKACG, and PRKX); in the inactive tetramer, each molecule of Cz is bound by a regulatory subunit (3).

The two heterodimers are mainly held together by the two inactivating regulatory subunits; when two molecules of cAMP bind to each regulatory subunit, the tetramer dissolves and the catalytic subunits are free to phosphorylate downstream targets (3, 22). Thus, the only controller of the catalytic subunit’s activity is its interaction with its binding partner, the regulatory subunit (3, 20, 22). It should be noted that PRKACA mutations that were predicted to lose interaction with the regulatory subunit while maintaining enzymatic activity had been studied in vitro in the early 1990s (23, 24, 25). Additional PRKACA sequences that had similar effects in vitro have been described recently, and the first PRKACA mutations in humans with predicted functional effects were reported in 2012 with no association with an obvious phenotype (26).

The first study to investigate the presence of PRKACA mutations in endocrine lesions failed to show any defects in a large collection of thyroid and pituitary adenomas (27). More recently, 92 specimens from sporadic somatotrope adenomas were screened for mutations of PRKACA or PRKACB, and none were identified (28).

The data presented here and those reported earlier (4, 14, 15, 16, 17, 18) show that PRKACA is a relatively unique endocrine tumor gene: it causes rare forms of BAH leading to CS in children and young adults when it is part of increased dosage of chromosome 19p13.2p13.12 genomic material; triplications appear to convey a more severe phenotype than duplications. It then causes the relatively common CPA leading to CS in older age when it acquires mutations in the somatic state within the adrenal cortex of one gland. The Leu206Arg and the other activating PRKACA mutations identified to date (4, 14, 15, 16, 17, 18) may not


