ORIGINAL ARTICLE

Constitutive Activation of PKA Catalytic Subunit in Adrenal Cushing's Syndrome

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ABSTRACT

BACKGROUND

Corticotropin-independent Cushing's syndrome is caused by tumors or hyperplasia of the adrenal cortex. The molecular pathogenesis of cortisol-producing adrenal adenomas is not well understood.

METHODS

We performed exome sequencing of tumor-tissue specimens from 10 patients with cortisol-producing adrenal adenomas and evaluated recurrent mutations in candidate genes in an additional 171 patients with adrenocortical tumors. We also performed genomewide copy-number analysis in 35 patients with cortisol-secreting bilateral adrenal hyperplasias. We studied the effects of these genetic defects both clinically and in vitro.

RESULTS

Exome sequencing revealed somatic mutations in *PRKACA*, which encodes the catalytic subunit of cyclic AMP–dependent protein kinase (protein kinase A [PKA]), in 8 of 10 adenomas (c.617A→C in 7 and c.595_596insCAC in 1). Overall, *PRKACA* somatic mutations were identified in 22 of 59 unilateral adenomas (37%) from patients with overt Cushing's syndrome; these mutations were not detectable in 40 patients with subclinical hypercortisolism or in 82 patients with other adrenal tumors. Among 35 patients with cortisol-producing hyperplasias, 5 (including 2 first-degree relatives) carried a germline copy-number gain (duplication) of the genomic region on chromosome 19 that includes *PRKACA*. In vitro studies showed impaired inhibition of both PKA catalytic subunit mutants by the PKA regulatory subunit, whereas cells from patients with germline chromosomal gains showed increased protein levels of the PKA catalytic subunit; in both instances, basal PKA activity was increased.

CONCLUSIONS

Genetic alterations of the catalytic subunit of PKA were found to be associated with human disease. Germline duplications of this gene resulted in bilateral adrenal hyperplasias, whereas somatic *PRKACA* mutations resulted in unilateral cortisol-producing adrenal adenomas. (Funded by the European Commission Seventh Framework Program and others.)

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Endogenous hypercortisolism, referred to as Cushing's syndrome, is associated with substantial morbidity and mortality.[1] When Cushing's syndrome is severe, patients have catabolic symptoms such as muscle weakness, skin fragility, osteoporosis, and severe metabolic sequelae.[2] Hypersecretion of cortisol can be driven by an excess of pituitary or ectopic corticotropin or can be due to adrenocortical tumors or hyperplasias with corticotropin-independent cortisol production. Adrenal adenomas are common, with a prevalence of at least 3% among persons older than 50 years of age.[3] Whereas only a subset of these tumors is associated with overt Cushing's syndrome, some degree of cortisol excess is present, depending on the diagnostic criteria applied,[4] in up to 47% of patients with adrenal adenomas and is associated with a range of phenotypes, from hypertension to the metabolic syndrome and osteoporosis.[5]

The molecular pathogenesis of cortisol-producing adrenal adenomas is not well understood. Whereas somatic mutations in the gene encoding beta-catenin (*CTNNB1*) have been found primarily in nonsecreting adrenocortical adenomas,[6] there is some evidence that increased endocrine activity may be linked to aberrant cyclic AMP (cAMP) signaling.[7,8] For instance, ectopic expression of G-protein–coupled receptors for neuroendocrine hormones or neurotransmitters that mediate their effects through cAMP has been implicated in syndromes such as food-dependent hypercortisolism and related conditions[9,10] that are caused by cortisol-producing adenomas or bilateral hyperplasias of the adrenal cortex. Moreover, somatic mutations in the gene encoding the α subunit of the stimulatory G protein (*GNAS1*) cause adenomas or hyperplasias leading to Cushing's syndrome in patients with McCune–Albright syndrome[11] or macronodular hyperplasia.[12,13] Finally, mutations in the genes encoding the cAMP-degrading phosphodiesterase 11A (*PDE11A*)[14] and phosphodiesterase 8B (*PDE8B*)[15] and in the gene encoding the regulatory subunit of the cAMP-dependent protein kinase (protein kinase A [PKA]) (*PRKAR1A*)[16,17] have been identified in patients with Cushing's syndrome due to primary pigmented nodular adrenocortical disease and in a small number of cortisol-producing adrenal adenomas. These genetic alterations, however, explain only a small fraction of cases. The observation that a subset of adrenal adenomas is characterized by abnormal PKA activity, despite the absence of mutations in these candidate genes,[18] suggests yet unknown alterations in the cAMP–PKA signaling cascade in these tumors.

METHODS

STUDY PATIENTS AND DNA EXTRACTION

Patients were recruited at three centers that participate in the European Network for the Study of Adrenal Tumors and at the U.S. National Institutes of Health. We evaluated 139 patients with adrenal adenoma, 42 patients with adrenocortical carcinoma, and 35 patients with corticotropin-independent bilateral adrenal hyperplasia who did not have germline mutations in *PRKAR1A*, *PDE11A*, or *PDE8B* or somatic *GNAS* mutations (33 with micronodular hyperplasia [31 with primary pigmented nodular adrenocortical disease and 2 with isolated micronodular adrenocortical disease] and 2 with macronodular hyperplasia) (Fig. S1 and Table S1 in the Supplementary Appendix, available with the full text of this article at NEJM.org). In all cases, the diagnosis was histologically confirmed after surgical resection. All the patients gave written informed consent, and the study was approved by the ethics committee at each participating institution.

The diagnosis of corticotropin-independent Cushing's syndrome was based on a combination of biochemical hallmarks of hypercortisolism — elevated urinary excretion of free cortisol, increased late-night salivary or serum cortisol levels, suppressed plasma corticotropin levels (<10 pg per milliliter [<2.2 pmol per liter]), and nonsuppressible serum cortisol levels (>5 μg per deciliter [>138 nmol per liter]) after the administration of 1 mg of dexamethasone — as well as on the presence of catabolic signs of hypercortisolism. Patients were classified as having overt Cushing's syndrome if they had at least three abnormal biochemical test results or if they had typical catabolic features (i.e., muscle weakness, skin fragility, and osteoporosis) plus at least two abnormal biochemical test results. Patients were considered to have endocrine-inactive adrenal lesions if they had normal biochemical test results and no catabolic signs. All patients who had no catabolic signs but had at least one abnormal result in the abovementioned tests were classified as having subclinical Cushing's syndrome.

DNA was extracted as described previously[19-21] from unilateral adrenocortical tumors in 181 patients and from corresponding normal tissue

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in 26 of these patients. Furthermore, germline DNA was available for all 35 patients with bilateral hyperplasia, and DNA from adrenal-tissue samples obtained during surgery was available for 10 of these 35 patients.

EXOME AND *PRKACA* SEQUENCING

Exomes were enriched in solution and indexed with the use of the SureSelect XT Human All Exon 50Mb kit, version 4 (Agilent Technologies). Sequencing was performed as paired-end reads of 100 bp on HiSeq2000 systems (Illumina). Pools of 12 indexed libraries were sequenced on four lanes. Image analysis and base calling were performed with the use of Real-Time Analysis software (Illumina). Methods of variant detection and *PRKACA* sequencing are described in the Supplementary Appendix.

COMPARATIVE GENOMIC HYBRIDIZATION

Array-based comparative genomic hybridization analysis was performed with the use of commercial arrays (Agilent Technologies), according to the manufacturer's instructions and as described previously.[22] Technical details are provided in the Supplementary Appendix.

IN SILICO ANALYSIS OF HUMAN MUTATIONS

Structural images were prepared with the use of PyMOL software (www.pymol.org). The structure of the mouse full-length tetrameric RIIβ(2):Cα(2) holoenzyme[23] (Protein Data Bank entry 3TNP) was used to display the structures of the PKA catalytic subunit (Cα) and regulatory subunit (RIIβ).

DNA CONSTRUCTS AND SITE-DIRECTED MUTAGENESIS

Plasmids encoding nonmutant human RIIβ or Cα subunits were purchased from OriGene Technologies. The *PRKACA*-containing plasmid was used for site-directed mutagenesis, with the c.617A→C and the c.595_596insCAC mutation introduced with the use of the QuikChange II Site-Directed Mutagenesis Kit (Agilent Technologies), according to the manufacturer's protocol. The mutation was confirmed by means of sequencing.

QUANTIFICATION OF PKA ACTIVITY IN INTACT CELLS

Human embryonic kidney 293 cells were transfected with the AKAR4-NES (a protein activity reporter 4 with a nuclear export signal) sensor[24] so that PKA activity could be monitored by means of fluorescence resonance energy transfer (FRET) imaging. Transfection and FRET imaging were performed as described previously.[25] Equimolar concentrations of a cell-permeable pair of synergistic cAMP analogues were used to activate PKA II.[26]

QUANTIFICATION OF PRKACA PROTEIN AND PKA ENZYMATIC ACTIVITY

Whole-cell or tissue lysates were studied for PKA Cα subunit expression by means of Western blotting with the use of a specific antibody (sc-903, Santa Cruz Biotechnology). COS-7 cells were transfected with the use of the X-tremeGENE HP DNA Transfection Reagent (Roche) and 500 ng of plasmid DNA per well for 24 hours. For transfections including both PKA Cα (nonmutant or Leu206Arg variant) and RIIβ subunits, a molar ratio of 1:8 was used. In lysed cells from the transfection experiments or patient-derived cells, PKA activity was determined by means of an enzymatic assay (Enzo Life Sciences).

GENE-EXPRESSION MICROARRAY ANALYSIS AND REAL-TIME POLYMERASE-CHAIN-REACTION (PCR) ANALYSIS

An earlier microarray analysis of 22 adenomas[27] was expanded to include 39 adenomas in the current study (see Table S1 in the Supplementary Appendix). For quantification of *PRKACA* expression, real-time quantitative PCR analysis was used. Details of the microarray experiments and real-time PCR analysis are provided in the Supplementary Appendix.

STATISTICAL ANALYSIS

Data were compared between two groups with the use of the Mann–Whitney U test and among three groups with the use of the Kruskal–Wallis test. All comparisons were two-sided, and P values of less than 0.05 were considered to indicate statistical significance. The analyses were performed with the use of SPSS software, version 20 (IBM).

RESULTS

SOMATIC *PRKACA* MUTATIONS AND GERMLINE DUPLICATIONS IN CORTISOL-PRODUCING LESIONS

Exome sequencing was performed in samples from 10 patients with unilateral cortisol-producing adenomas and overt Cushing's syndrome (Table S2 in the Supplementary Appendix) and revealed a low number of somatic mutations per adenoma (median, 5; range, 1 to 14) (Table S3 in the Supplementary Appendix). Within this small set of genetic alterations, somatic variants in *PRKACA*, encoding the PKA Cα subunit, were found in

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8 of 10 tumors (c.617A→C, p.Leu206Arg in 7 and c.595_596insCAC, Leu199_Cys200insTrp in 1). The affected amino acids were highly conserved across a variety of species (Fig. S2 in the Supplementary Appendix).

On the basis of these initial results, *PRKACA* was sequenced in 129 additional adenomas (including 89 cortisol-producing, 20 aldosterone-producing, and 20 inactive adenomas). In 33 of these samples, the entire coding sequence was investigated, and in the remaining 96 samples, sequencing of hot-spot regions was performed. The Leu206Arg variant was identified in 14 of these 129 adenomas, and all 14 patients with this variant also had overt Cushing's syndrome, according to the predefined criteria. Whole-exome and targeted sequencing indicated that both the nonmutated and mutated alleles were present in tumor tissue, consistent with a heterozygous state of *PRKACA* mutations (Fig. 1A and 1B, and Fig. S3 in the Supplementary Appendix). In the affected patients, there were no *PRKACA* mutations in DNA derived from leukocytes (19 patients) or fat tissue (1 patient) or in adjacent normal adrenal tissue (6 patients).

Comparative genomic hybridization of samples from 35 patients with cortisol-secreting bilateral adrenal hyperplasias and overt Cushing's syndrome identified 5 patients (4 kindreds) with copy-number gains (duplications) of the genomic region on chromosome 19p that includes *PRKACA* (Fig. 1C, and Table S4 in the Supplementary Appendix). In one case, the defect was inherited: a mother and son, both carriers of the same *PRKACA* duplication, were affected by bilateral macronodular hyperplasia. In another case, that of a 3-year-old boy with Cushing's syndrome due to bilateral micronodular hyperplasia, the defect was de novo, because neither parent carried the *PRKACA* duplication. No amplification of *PRKACA* was found in 24 cortisol-producing adrenal adenomas analyzed by means of single-nucleotide polymorphism array profiling.[28]

No *PRKACA* mutations were detected in 1600 in-house exomes or in the 1000 Genomes Project data set (version 0.0.14). Although *PRKACA* duplications are reported in public databases of copy-number variants in at least six instances (occurring in patients referred for genetic testing because of developmental delay), no *PRKACA* whole-gene duplications are included in the Database of Genomic Variants, which is based on the general population. Moreover, no *PRKACA* duplications were found in 2000 persons with intellectual disability, congenital malformations, or both in an internal database.

PRKACA MUTATIONS AND REGULATION OF CATALYTIC SUBUNITS BY REGULATORY SUBUNITS

Analysis of the mouse full-length tetrameric RIIβ(2):Cα(2) holoenzyme structure[23] revealed that this mutation is located in the highly conserved core of the interaction between the regulatory (RIIβ) and catalytic (Cα) subunits of PKA — a finding that supports a functional relevance of the Leu206Arg variant. Leu206 is part of the active-site cleft of the catalytic subunit to which the inhibitory sequence of the regulatory subunit binds, mimicking a substrate for the catalytic subunit. This interaction keeps the catalytic subunit inactive in the absence of cAMP. Exchanging Leu206 with the bulky and positively charged amino acid Arg in silico yields steric hindrance between the side chain of the mutated Arg206 in the Cα subunit and Val115 and Tyr228 in the RIIβ subunit (Fig. 2A and 2B).[29]

The functional consequences of the two detected variants (Leu206Arg and Leu199_Cys200insTrp) were investigated in intact cells by means of FRET microscopy with the use of a sensor for PKA activity (AKAR4-NES).[24] The PKA activity in cells transfected only with either nonmutant Cα or the variants was high and was not further stimulated by cAMP analogues, indicating preservation of the catalytic activity in the mutants (Fig. 2C, and Fig. S4A and S4C in the Supplementary Appendix). However, after cotransfection with excess nonmutant RIIβ, basal PKA activity was decreased in cells transfected with nonmutant Cα and became responsive to cAMP analogues, whereas PKA activity in the cells transfected with the mutants remained high and was not responsive to cAMP analogues (Fig. 2C, and Fig. S4B and S4D in the Supplementary Appendix). This finding indicates that the mutations made the catalytic subunit resistant to the physiologic suppression by the regulatory subunit. The lack of suppression remained when an equal amount of nonmutant Cα was cotransfected, indicating a dominant effect of the mutations (Fig. 2D).

Similarly, transfection of the mutant Cα Leu206Arg variant caused a profound increase in PKA activity under basal conditions so that PKA activity was in the same range as that in cells

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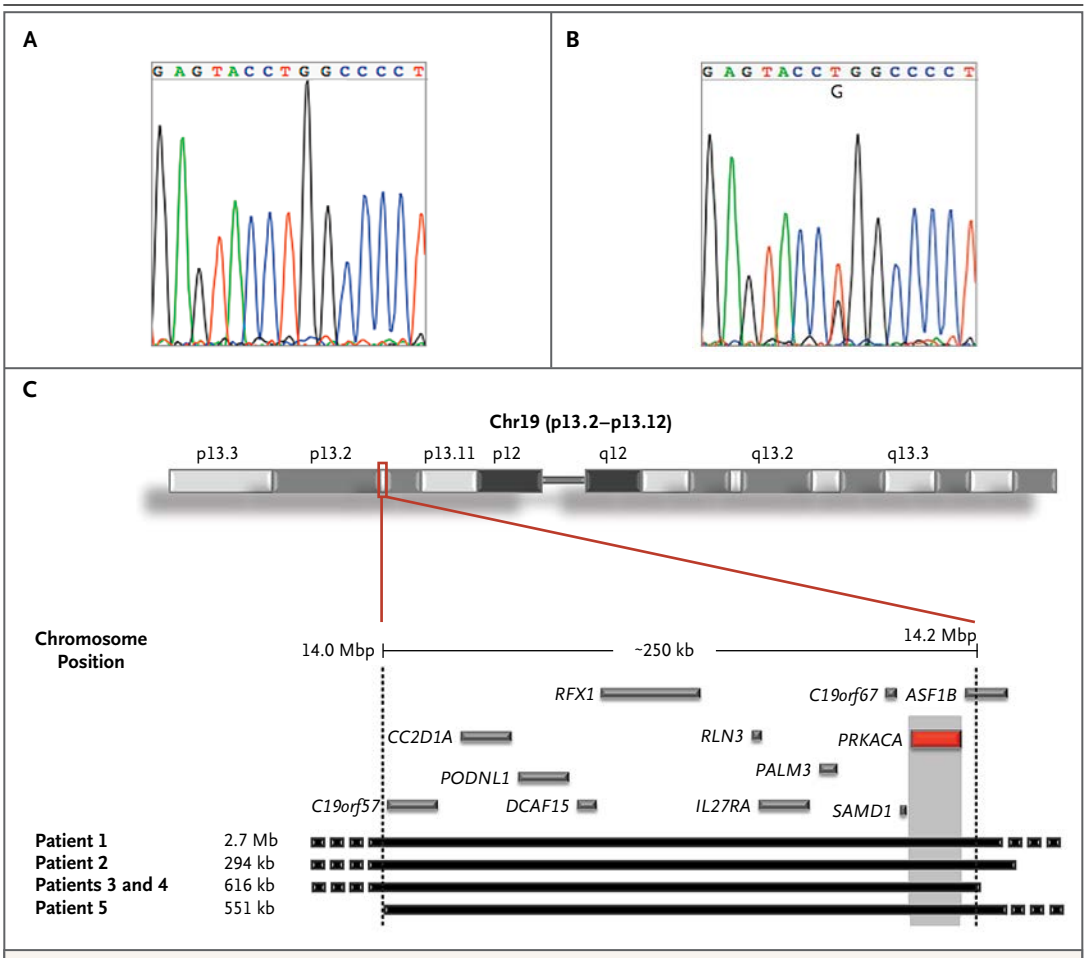

Figure 1. Identification of Somatic *PRKACA* Mutation and Germline Genetic Duplications.

Panel A shows a sequence chromatogram of normal adrenal tissue, and Panel B a chromatogram of a cortisol-producing adrenal adenoma. A somatic mutation in *PRKACA* (c.617A→C) was identified in the cortisol-producing adenoma, resulting in a Leu206Arg substitution that is not present in the adjacent normal tissue. Panel C shows an ideogram of chromosome 19 (top) with the genes included in the p13.2–p13.12 band (GRCh37/h19). The black blocks (bottom) represent the size and position of the duplications. The gray blocks represent the genes included only in the shared region of duplication. The red block represents *PRKACA*.

transfected with the nonmutant Cα on cAMP stimulation, and this activity was not suppressed by cotransfection with RIIβ, indicating again a lack of suppression of the activity of the mutant catalytic subunit by the regulatory subunit (Fig. 2E). Consistent with these findings, basal PKA activity in tumor tissue was found to be higher in adenoma samples with *PRKACA* mutations than in those without such mutations (Fig. S5 in the Supplementary Appendix). Taken together, these data indicate that the Leu206Arg mutant protein is constitutively active and is not suppressed by the regulatory subunit.

ASSOCIATION OF GERMLINE DUPLICATION OF *PRKACA* WITH INCREASED PROTEIN LEVELS AND PKA ACTIVITY

As compared with tumor-tissue samples from patients without any known genetic defects, tumor-tissue samples from patients with duplications of *PRKACA* had higher PKA Cα messenger RNA and protein levels (Fig. S6A and S6B, respectively, in the Supplementary Appendix). Immunohistochemical experiments confirmed higher expression of the PKA Cα subunit in adrenal tissue from these patients (Fig. S6C in the Supplementary Appendix). The higher expression of the PKA Cα subunit was associated with higher basal and cAMP-

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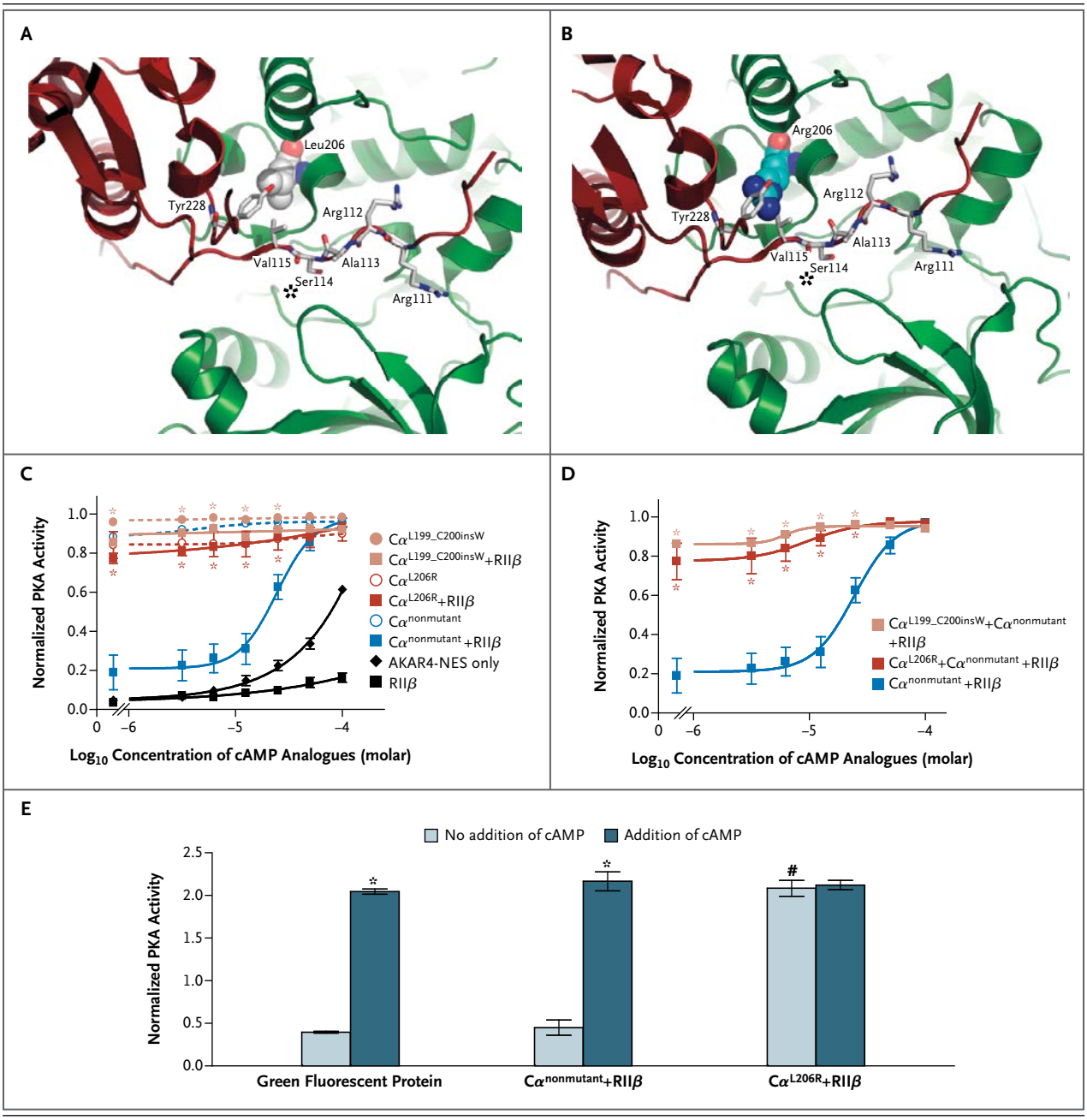

stimulated PKA activity (Fig. S6D in the Supplementary Appendix).

CLINICAL PHENOTYPES AND *PRKACA* MUTATION STATUS

Whereas 22 of 59 patients (37%) with overt Cushing's syndrome due to a unilateral adenoma harbored a *PRKACA* mutation, this alteration was not present in any adenoma associated with subclinical Cushing's syndrome (40 patients), nor was it present in inactive adrenal adenomas (20 patients), aldosterone-producing adrenal adenomas (20 patients), or adrenocortical carcinomas (42 patients) or in adrenal tissue (10 patients) or lymphocytic DNA (35 patients) from patients with corticotropin-independent adrenal hyperplasia (35 patients). Furthermore, in the group of patients with overt Cushing's syndrome, the presence of *PRKACA* mutations was associated with a more severe phenotype (Table 1). Accordingly, expression levels of a variety of steroidogenic enzymes in mutant ade-

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Figure 2 (facing page). Functional Characterization of *PRKACA* Variants.

Panel A shows the structure derived from the protein kinase A (PKA) tetramer, with the nonmutant catalytic subunit (Cα) depicted in green and the regulatory subunit (RIIβ) depicted in red. A zoomed view into the region of Leu206 in the Cα subunit is shown. Leu206 is depicted as a space-filling representation; the two residues in close proximity (Val115 and Tyr228) and additional residues from the inhibitory site (Arg111–Ser114, marked with an asterisk) of the regulatory subunit are depicted as sticks. Panel B shows the same region of the PKA tetramer, with Leu206 in the Cα subunit replaced by Arg206, also depicted as a space-filling representation. Panel C shows PKA activity of nonmutant and mutant PKA Cα subunits transfected in human embryonic kidney 293 cells, as determined by means of fluorescence resonance energy transfer (FRET) assay with a PKA reporter (for details, see Fig. S4 in the Supplementary Appendix). The results indicate that the mutant variants are constitutively active. Asterisks indicate $P<0.05$ for the comparison with $C\alpha^{nonmutant}$ + RIIβ. AKAR4-NES denotes a protein activity reporter 4 with a nuclear export signal. Panel D shows that high constitutive PKA activity was maintained when either mutant was cotransfected with an equal amount of nonmutant Cα subunit. Asterisks indicate $P<0.05$ for the comparison with $C\alpha^{nonmutant}$ + RIIβ. The data in Panels C and D were compared by means of a two-way analysis of variance followed by Bonferroni's test. Panel E shows the quantification of enzymatic PKA activity; COS-7 cells were transfected with Cα (nonmutant or mutant) and RIIβ, with or without the addition of cyclic AMP (cAMP). Asterisks indicate $P<0.05$ for the comparison between samples with and those without the addition of cAMP. The hatch mark indicates $P<0.05$ for the comparison between samples transfected with nonmutant Cα subunit and those transfected with mutant Cα subunit without the addition of cAMP. In Panels C, D, and E, the I bars represent the standard error.

noma tissues were higher in the presence of a *PRKACA* mutation (Table S5 in the Supplementary Appendix).

There were no obvious phenotypic differences between patients with germline *PRKACA* duplications and those without duplications, although the number of patients with duplications was small. The affected mother and son had mild Cushing's syndrome of insidious onset, caused by bilateral macronodular hyperplasia manifesting in the third and fourth decade of life. The three young boys presenting with Cushing's syndrome due to bilateral hyperplasia (two with micronodular disease and one with macronodular disease) (Table S4 in the Supplementary Appendix) had severe disease similar to that of patients with somatic *PRKACA* mutations. One patient with *PRKACA* duplication had a paradoxical increase in cortisol secretion after administration of dexamethasone,[30] whereas the other four patients did not undergo a long-term dexamethasone suppression test (Liddle's test) before surgery.

DISCUSSION

Despite evidence that enhanced cAMP signaling is the culprit in many benign adrenal lesions leading to Cushing's syndrome,[8,18] the search for tumorigenic mutations in adrenal adenomas with the use of a candidate-gene approach has revealed only very rare mutations in a distinct subgroup of patients.[12,13,17,31] The current study suggests that more than one third of cortisol-producing adenomas associated with overt Cushing's syndrome have unique somatic mutations in *PRKACA* (which encodes the main catalytic subunit of PKA), resulting in constitutive PKA activation. Although the mutation is present only in tumor cells in these patients, germline duplication of *PRKACA* was identified in a group of patients with bilateral adrenal hyperplasias. Consistent with the hypothesis that the resulting increased PKA activity is responsible for adrenocortical tumor formation, patients with somatic defects had single adenomas, whereas patients with germline duplications presented with bilateral adrenal hyperplasias. All the patients with *PRKACA* defects, whether germline or somatic, had overt Cushing's syndrome, and none of the patients with subclinical Cushing's syndrome or other adrenal tumors had genetic *PRKACA* alterations.

Thus, our findings provide evidence that *PRKACA* activation leads to marked excess of cortisol, as one would expect from constitutive activation of the enzymes that mediate corticotropin-dependent effects on adrenal steroidogenesis. The findings also indicate that subclinical Cushing's syndrome is not an early form of overt disease but a pathophysiologically distinct entity. Because *PRKACA* mediates most of the effects of inactivating *PRKAR1A* mutations[32] and because mutations of *PRKAR1A* are associated with a variety of tumors in humans and mice,[33,34] we would speculate that somatic *PRKACA* defects might also play a role in other forms of endocrine and nonendocrine tumors.

PKA, a cAMP-dependent serine–threonine kinase, is perhaps the best characterized protein

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Table 1. Clinical Characteristics of Patients with Adrenal Adenomas in Relation to *PRKACA* Mutational Status.*

Characteristic	Endocrine-Inactive Adenoma (N=20)	Subclinical Cushing's Syndrome (N=40)	Overt Cushing's Syndrome (N=59)			P Value	
			Total	No *PRKACA* Mutation	*PRKACA* Mutation	Comparison of Endocrine-Inactive Adenoma, Subclinical Cushing's Syndrome, and Overt Cushing's Syndrome†	Comparison of Overt Cushing's Syndrome with and without *PRKACA* Mutation‡
Age at diagnosis (yr)							
Median	49.5	54.0	41.0	41.0	41.0	<0.001	0.37
Interquartile range	39.3–59.0	48.3–66.0	34.0–49.0	35.0–50.0	33.0–47.3		
Adenoma size (mm)§							
Median	43.0	40.0	30.0	30.0	30.0	<0.001	0.86
Interquartile range	33.0–50.0	30.0–50.0	30.0–36.0	29.5–40.0	30.0–35.5		
Corticotropin (pg/ml)¶							
Median	14.0	6.0	2.5	2.3	2.5	<0.001	0.69
Interquartile range	11.0–18.0	5.0–12.9	1.0–5.0	1.0–5.0	1.0–6.0		
Serum cortisol after 1 mg of dexamethasone (μg/dl)‖							
Median	1.2	2.9	15.9	15.0	22.0	<0.001	0.005
Interquartile range	1.0–1.7	2.3–7.5	13.3–23.0	9.4–19.5	16.5–27.7		
Urinary cortisol ÷ ULN**							
Median	0.62	0.46	3.67	3.14	5.33	<0.001	0.03
Interquartile range	0.38–0.72	0.26–0.99	1.88–6.01	1.53–5.23	2.46–9.08		
Midnight cortisol ÷ ULN††							
Median	0.6	1.6	3.9	3.6	4.3	<0.001	0.02
Interquartile range	0.4–1.0	0.8–2.6	2.8–4.6	2.3–4.5	3.9–5.9		

* For reference ranges of the endocrine characteristics, see the Methods section in the Supplementary Appendix. ULN denotes upper limit of the normal range.
† Values were compared with the use of the Kruskal–Wallis test.
‡ Values were compared with the use of the Mann–Whitney U test.
§ Data were not available for 1 patient with endocrine-inactive adenoma, 2 patients with subclinical Cushing's syndrome, and 4 patients with overt Cushing's syndrome (3 with no *PRKACA* mutation and 1 with *PRKACA* mutation).
¶ Data were not available for 9 patients with endocrine-inactive adenoma, 9 patients with subclinical Cushing's syndrome, and 12 patients with overt Cushing's syndrome (9 with no *PRKACA* mutation and 3 with *PRKACA* mutation). To convert values for corticotropin to picomoles per liter, multiply by 0.22.
‖ Data were not available for 12 patients with endocrine-inactive adenoma, 11 patients with subclinical Cushing's syndrome, and 22 patients with overt Cushing's syndrome (14 with no *PRKACA* mutation and 8 with *PRKACA* mutation). To convert values for serum cortisol to nanomoles per liter, multiply by 27.6.
** Values are based on 24-hour urine samples. Data were not available for 3 patients with endocrine-inactive adenoma, 11 patients with subclinical Cushing's syndrome, and 6 patients with overt Cushing's syndrome (3 with no *PRKACA* mutation and 3 with *PRKACA* mutation).
†† Values are based on midnight salivary or serum cortisol levels. Data were not available for 12 patients with endocrine-inactive adenoma, 21 patients with subclinical Cushing's syndrome, and 23 patients with overt Cushing's syndrome (15 with no *PRKACA* mutation and 8 with *PRKACA* mutation).

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kinase and provides a clear example of allosteric regulation.[35] In its inactive state, it is a tetrameric holoenzyme consisting of a dimer of two regulatory and two catalytic subunits; under physiologic conditions, PKA activity is induced by G-protein–coupled receptors through increased levels of cAMP.[23,35] On binding of cAMP, the regulatory subunits dissociate from the catalytic subunits, allowing the enzyme to become active.[35] Although some randomly introduced mutations in *PRKACA* have been shown to result in unopposed catalytic activation in vitro,[36] such alterations have not been linked to human disease. The only naturally found gain-of-function *PRKACA* mutations are those described in the Cos1(A1) drosophila mutant.[37] The two *PRKACA* mutants identified in the current study alter the structure of the catalytic subunit at a site that is essential for interaction with the regulatory subunit, thus maintaining high activity of the catalytic subunit in the absence of cAMP.[23,35] The critical position of the Leu206Arg mutation at the core of the interaction between the catalytic subunit and the inhibitory site of the regulatory subunit, combined with the steric hindrance involving Val115 and Tyr228 in the regulatory subunit, may explain the high grade of specificity of this particular mutation.

In conclusion, the current study links genetic variants of the main catalytic subunit of PKA with both hyperplasias and adenomas of the adrenal cortex leading to corticotropin-independent Cushing's syndrome. These observations are consistent with the known role of the cAMP signaling pathway in adrenal lesions that have been associated with Cushing's syndrome.

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APPENDIX

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