Epigenetic Inactivation of the RASSF1A 3p21.3 Tumor Suppressor Gene in Both Clear Cell and Papillary Renal Cell Carcinoma

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ABSTRACT

Renal cell carcinoma (RCC), the most common adult kidney neoplasm, is histopathologically heterogeneous, with most sporadic RCCs (~80%) classified as clear cell (CC) tumors. Chromosome 3p allele loss is the most frequent genetic alteration in RCC but is associated specifically with sporadic and hereditary forms of clear cell RCC (CC-RCC) and is not a feature of non-CC-RCC, such as papillary (chromophilic) RCC. The VHL tumor suppressor gene (TSG) maps to chromosome 3p25, and somatic inactivation of the VHL gene occurs in up to 70% of CC-RCC tumors and cell lines. However, VHL inactivation is not sufficient for CC-RCC tumorigenesis, and inactivation of 3p12-p21 TSG(s) appears to be necessary in CC-RCC irrespective of VHL gene inactivation status. Recently, we demonstrated that the candidate 3p21 TSG, RASSF1A, is hypermethylated in most small cell lung cancers. We have now investigated the role of RASSF1A inactivation in primary RCC tumors, RASSF1A promoter methylation was detected in 23% (32 of 138) of primary CC-RCC tumors. In CC-RCC cell lines, RASSF1A methylation was associated with silencing of RASSF1A expression and restoration of expression after treatment with 5-azacytidine. The frequency of RASSF1A methylation was similar in CC-RCC with and without VHL gene inactivation (24% versus 21%), and there was no association between epigenetic silencing of the RASSF1A and VHL TSGs, because 0 of 6 tumors with VHL hypermethylation had RASSF1A methylation, and VHL was not methylated in 26 CC-RCCs with RASSF1A methylation. Although 3p allele loss has been reported rarely in papillary RCC, we identified RASSF1A methylation in 44% (12 of 27) of papillary RCCs analyzed. Thus: (a) inactivation of RASSF1A is a frequent event in both CC-RCC and papillary RCC tumors; (b) there is no relationship between epigenetic silencing of RASSF1A and VHL inactivation status in CC-RCC. Fifty-four CC-RCCs analyzed for RASSF1A methylation were informative for 3p21 allele loss, and 20% (7 of 35) with 3p21 allele loss demonstrated RASSF1A methylation. All informative CC-RCCs with 3p21 allele loss and no RASSF1A methylation also demonstrated allele losses at other regions of 3p so that tumorigenesis in these cases may result from: (a) haploinsufficiency of RASSF1A; (b) inactivation of other 3p21 TSGs; or (c) inactivation of 3p TSGs from outside of 3p21. RASSF1A is the first TSG to be inactivated frequently in both papillary and CC-RCCs. The finding of frequent epigenetic inactivation of RASSF1A in papillary RCCs despite previous studies reporting infrequent 3p21 allele loss in this tumor type illustrates how the systematic identification of all major human cancer genes will require detailed analysis of the cancer genome and epigenome.

INTRODUCTION

RCC3 accounts for ~2% of adult malignancies and is the most common adult kidney neoplasm. Histopathologically, most sporadic RCCs (~80%) are classified as CC-RCCs, and papillary (chromophilic) tumors are the most common form of non-CC-RCC (1). Deletions of the short arm of chromosome 3 are the most widely observed genetic aberration in RCC. Although 3p allele loss is reported in 45–90% of sporadic RCCs, it is associated specifically with hereditary and sporadic CC-RCCs and is infrequent in non-CC-papillary RCC (2–8). Germ-line mutations in the VHL TSG are associated with a high risk of CC-RCCs, and somatic inactivation of the VHL gene (by loss, mutation, or epigenetic silencing) occurs in up to 70% of CC-RCCs (9–14). However, VHL gene mutations are rare in non-CC-RCCs. In contrast, germ-line mutations in the MET proto-oncogene lead to hereditary papillary (chromophilic) RCCs, and somatic MET gene mutations are rare in CC-RCCs (15).

Deletions of 3p are frequent in many adult cancers including lung, breast, ovary, testicular, and head and neck carcinomas (16). VHL TSG inactivation does not occur in these tumor types; therefore, several TSGs map to 3p. In addition to the FHIT TSG at 3p14, the finding of homozgyous deletions in lung and breast cancers has mapped additional TSGs to 3p21 and 3p12. In detailed 3p allele-loss studies of CC-RCCs, we found evidence that loss of 3p12–p21 TSGs is required for tumor development in CC-RCCs with and without VHL gene inactivation, and that VHL inactivation alone was not sufficient for tumorigenesis (14, 17, 18). Furthermore, chromosome transfer experiments demonstrated that 3p fragments not containing the VHL gene (e.g., 3p12–p14 and 3p12–p22) can suppress RCC tumorigenicity (19, 20).

Within 3p12–p21, several distinct regions are proposed to contain TSGs. The FHIT gene has been reported to suppress RCC tumorigenicity in nude mouse assays, and reduced expression and hemizygous deletions involving FHIT may occur in the majority of CC-RCCs (21–24). However, the role of FHIT in RCC tumorigenesis has been questioned (25), and 3p allele loss analysis in CC-RCCs suggests a primary role for 3p21 TSG(s) (14, 18, 26). A critical 120-kb interval for a lung and breast cancer TSG was identified by overlapping homozgyous deletions (27, 28). We identified eight genes within this interval, and although mutation analysis of these candidate TSGs in lung tumors and tumor lines revealed only rare inactivating mutations, we and others have demonstrated promoter methylation and absent expression of RASSF1A in many lung cancer cell lines and tumors (29–31). In view of the evidence for a 3p21 TSG in CC-RCCs, we have investigated RASSF1A as a candidate gene in RCC.

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3 The abbreviations used are: RCC, renal cell carcinoma; CC-RCC, clear cell RCC; VHL, von Hippel-Lindau; TSG, tumor suppressor gene; RT-PCR, reverse transcription-PCR; LOH, loss of heterozygosity.

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MATERIALS AND METHODS

Patients and Samples

Two hundred eleven sporadic primary RCC tumor and normal (blood or kidney) DNA pairs were analyzed for RASSF1A promoter methylation. In addition, we also examined 13 RCC cell lines that had been described previously (11). Tumors were histopathologically classified according to the criteria of Thoenes et al. (1). One hundred eighty-one tumors (mostly CC-RCCs) had been analyzed previously for VHL gene mutation and methylation status (10, 13, 14). DNA samples from a panel of primary papillary RCCs and corresponding normal tissues were provided by P. Schraml and have been described previously (32).

Molecular Genetic Studies

Bisulfite modification of the DNA was carried out as described previously (30). Briefly, 0.5–1 μg of DNA was denatured by incubation with 0.3 M NaOH for 15 min at 37°C, before sulfonation of unmethylated cytosines by incubation in 3.12 μM sodium bisulfite/1 mM hydroquinone (pH 5) at 99°C (for 30 s) and 50°C (for 15 min) × 20 cycles. The sulfonated DNA was recovered using the Wizard DNA clean-up system (Promega) in accordance with the manufacturer’s instructions. The DNA was then desulfonated by incubation in 0.3 M NaOH for 10 min at room temperature, before ethanol precipitation and resuspension in water.

DNA sequences specific for the RASSF1A promoter region were amplified using primers and conditions described previously (30). Dose-response experiments showed no evidence of significant amplification bias for either methylated or unmethylated DNA (data not shown). Methylated cytosine residues were identified by restriction enzyme digestion. Briefly, 16 μl of the 204-bp PCR product were incubated with 20 units of TaqI (Roche) or BstUI (New England Biolabs) for 2 h at 65°C and 60°C, respectively. The possible sizes of the TaqI restriction enzyme digestion products are 173, 112, 92, 81, and 31 bp; the sizes of the BstUI digestion products are 172, 121, 89, 83, and 32 bp (30). The restriction enzyme digestion products were then visualized by separation in a 3% agarose gel, and the presence of methylation was verified in a limited number of samples by direct sequencing of the PCR product.

Briefly, PCR products containing bisulfite-resistant cytosines were purified using the Qiaquick gel extraction kit (Qiagen) and ligated into the pGEM-T Easy Vector system (Promega) according to the manufacturer’s instructions. Clones were then isolated and sequenced using a dRhodamine sequence cycling kit (Perkin-Elmer) on an ABI 3700 automated sequencer (Applied Biosystem).

RASSF1A Mutation Analysis and Allele Loss Studies

Mutation screening in primary tumor DNA was performed using the PCR-single strand conformation polymorphism method using intronic primers as described previously (30). Ablerrantly migrating bands were sequenced on an ABI 377 automated sequencer. Results of detailed 3p LOH analysis on many samples have been reported previously, but alleleyotyping at D3S4064, which maps close to RASSF1A, was performed in a subset of samples. Allelic loss was considered to be present in tumor samples when there was a 50% or greater reduction in signal intensity of an allele in tumor DNA compared with normal DNA.

RASSF1A Expression Analysis

5’-Azacytidine Treatment.

Cell lines KTCL-26, SKRC 39, and SKRC 47 where treated with 5 μM 5’-azacytidine (Sigma Chemical Co.) for 5, 7, and 9 days. The cells were then harvested, and RNA was extracted using the RNeasy Extraction kit (Qiagen). Prior to RT-PCR, the RNA was treated with 10 units of DNase (Sigma Chemical Co.) and incubated at 37°C for 10 min, before re-extraction, as described in the Qiagen RNA clean-up protocol.

RT-PCR of RASSF1A. RT-PCR was carried out using the Ready-To-Go RT-PCR bead system (Amersham Pharmacia Biotech) as described in the manufacturer’s instructions. Briefly, 0.5 μg of RNA from treated and untreated cell lines was reverse transcribed as described previously (31).

As a control, we also assayed levels of the shorter RASSF1 isoform C, which has been shown previously to be widely expressed and not susceptible to methylation (31, 33). 123F2E2RT-PCR (5’-ACC TGA CCT TTC TCA AGC TG-T-3’) was used as the forward primer, with 123F2E31R (5’-CAT CCT TGG GGA GGT AAA AG-3’) used as the reverse primer. Conditions were 95°C for 5 min and a sequence of 95°C (for 30 s), 60°C (for 30 s), and 72°C (for 30 s) 40 cycles, and 72°C for 3 min for 1 cycle.

Cell Culture. RCC cell lines were grown in DMEM supplemented with 10% FCS at 37°C and 5% CO2.

Statistical Analysis

Comparisons were made by Fisher’s exact test. P < 0.05 was considered statistically significant.

RESULTS

Initially, we investigated the frequency of RASSF1A promoter methylation in 211 RCCs of known and unknown histopathology. Overall, we identified RASSF1A promoter methylation in 59 of 211 (28%) primary tumors. In view of the strong correlations between molecular pathology and histopathological subtypes, we then proceeded to concentrate on 165 RCCs of confirmed histopathology representing the two most common forms of RCC (138 CC-RCCs and 27 papillary tumors).

RASSF1A Methylation and Mutation Status in CC-RCC.

Twenty-three % (32 of 138) CC-RCC tumor samples demonstrated RASSF1A hypermethylation (Fig. 1). To determine the precise pattern of CpG methylation within the RASSF1A CpG island, we directly sequenced 23 clones from 3 CC tumors with RASSF1A methylation from nucleotides −110 to +41 bp after sodium bisulfite modification (see “Materials and Methods”). Two tumor samples demonstrated methylation of all 16 CpGs within the amplified fragment (Fig. 2b), and 1 had methylation at 14 of 16 CpGs. In addition to the promoter fragments demonstrating complete CpG methylation, there were also clones of unmethylated DNA that were attributed to the presence of contaminating normal tissue (tumor samples were not microdissected). For each of the 106 CC-RCCs that did not demonstrate RASSF1A methylation, we also analyzed the methylation status of the corresponding blood (n = 26) or normal renal tissue (n = 80) DNA. In 2 normal samples (both extracted from renal tissue), RASSF1A methylation was detected by the TaqI restriction digest assay. After excluding a sample switch (by demonstrating the presence of a previously characterized tumor VHL mutation in the tumor sample but not in the donor blood sample), we concluded that for the 106 nonmethylating tumors, RASSF1A methylation was a tumorigenic event.

Statistical Analysis

Comparisons were made by Fisher’s exact test. P < 0.05 was considered statistically significant.
CC-RCCs with 3p21 allele loss had RASSF1A methylation, exhibiting CpG methylation. DNA showing full methylation of the CpG island (16 of 16 CpGs methylated; not the normal kidney sample), we proceeded to sequence 16 clones of the 3p21.3 region, showing partial methylation at 10 of 16 CpGs, including those constituting one TaqI digestion product. This explains the presence of TaqI digestion products, although only partial methylation of the fragment had occurred. Sequencing of 2 normal samples not exhibiting restriction digest products revealed minimal methylation of the CpG island in these samples (1 had no CpG methylation (Fig. 2c), and 1 had only 2 CpGs methylated).

Eight CC-RCCs with RASSF1A methylation were informative for 3p21 allele loss studies. Seven (87%) demonstrated 3p21 allele loss compared with 28 of 46 (61%) informative CC-RCCs without RASSF1A methylation (P = 0.24). Seven of 35 (20%) informative CC-RCCs with 3p21 allele loss had RASSF1A methylation. However, all of the 25 CC-RCCs with 3p21.3 allele loss and no RASSF1A methylation that were informative at 3p25 and/or 3p12 showed allele loss in at least one of these additional regions (therefore, there were no informative tumors without RASSF1A methylation in which allele loss was limited to 3p21).

Although RASSF1A mutations appear to be rare in other tumor types in which epigenetic inactivation is common (29, 30, 32), we proceeded to analyze: (a) 1 CC-RCC with RASSF1A methylation and no 3p21 LOH; and (b) 10 CC-RCCs with 3p21 LOH and no RASSF1A methylation for somatic RASSF1A mutations. No RASSF1A sequence variants were identified in the 11 tumors.

**Relationship between RASSF1A and VHL Gene Mutation and Methylation Status in CC-RCC.** The frequency of RASSF1A methylation in CC-RCCs without VHL gene inactivation was 21% (9 of 43), similar to the 24% (17 of 71) observed in CC-RCC with VHL mutations (P = 0.82). There was no association between epigenetic inactivation of RASSF1A and VHL in CC-RCCs; 0 of 6 CC-RCCs with VHL methylation demonstrated RASSF1A methylation, and 0 of 26 CC-RCCs with RASSF1A methylation had VHL gene methylation.

**RASSF1A Methylation in Papillary RCCs.** We detected RASSF1A promoter methylation in 12 of 27 (44%) papillary RCCs analyzed. The identification of RASSF1A methylation in papillary RCCs was surprising, given the well-recognized rarity of 3p allele loss in this tumor type. Detailed information on the subtype of papillary RCC was available for 19 tumors, and the incidence of RASSF1A methylation was similar in type 1 (3 of 10) and type 2 (5 of 9) papillary RCCs. Four papillary RCCs with RASSF1A methylation were informative for 3p21 allele loss analysis, and 1 tumor demonstrated allele loss at D3S4604 close to RASSF1A.

Sequencing analysis of methylated clones was carried out to establish the extent of methylation of the positive papillary tumors as described previously. Sequencing of 2 clones of 1 methylated tumor sample showed methylation at 14 of 16 CpGs (Fig. 2a).

**RASSF1A Methylation Is Associated with Transcriptional Silencing.** RT-PCR analysis of two RCC cell lines with RASSF1A methylation (SKRC 39 and SKRC 47) demonstrated transcriptional silencing, whereas RASSF1A expression was detected in a RCC cell line (KTCL-26) without RASSF1A methylation. All three cell lines were then treated with 5′-azacytidine for up to 9 days. 5′-Azacytidine treatment of the RASSF1A methylation-negative cell line KTCL-26 did not influence expression of the RASSF1A transcript (Fig. 3a). In contrast, 5′-azacytidine treatment of the two RCC cell lines with RASSF1A methylation resulted in restoration of RASSF1A expression after 5 days (Fig. 3, b and c). The methylation-insensitive RASSF1C transcript was present in all samples and was not influenced by treatment with 5′-azacytidine.

**RASSF1A Methylation and Clinicopathological Information.** To determine whether the presence of RASSF1A methylation was associated with significant differences in tumor grade and Tumor-
CC-RCCs without evidence of VHL addition, 3p12–p21 allele loss was also present in high frequency in RCCs (7, 8, 34 reported a high frequency of 3p allele loss in CC-RCCs but not papillary RCC. We and others have demonstrated loss (in particular 3p21) appeared to be a critical step in the development of all informative tumors analyzed had allele loss at 3p12 (29). In vivo studies (29, 31). These findings establish suppression of the wild-type TSG, hemizygous loss of 3p12–pter would promote tumorigenesis by inactivating both alleles of a 3p12–p14 TSG (often after inactivation of VHL) and by causing haploinsufficiency of RASSF1A. Certainly, TSG haploinsufficiency is emerging as a significant cause of tumorigenesis in some human and murine cancers (37–39).

Although TSG methylation is increasingly recognized as a major contributor to the pathogenesis of many human cancers, the precise etiology of epigenetic changes in cancer are enigmatic. It has been suggested that cis-, rather than trans-, acting factors are responsible for VHL gene methylation in CC-RCCs (40). However, in colorectal cancers, a subgroup of tumors demonstrates a methylator phenotype with a propensity to epigenetic alterations in multiple genes (41, 42). The absence of an association between VHL and RASSF1A methylation in CC-RCC provides no evidence for the existence of a subgroup of CC-RCCs with a methylator phenotype.

The RASSF1 gene has several major isoforms because of alternative splicing and promoter usage, but epigenetic silencing of the longer isoform, RASSF1A, is specifically associated with cancer. The RASSF1A M, 39,000 predicted peptide contains a RAS association domain, a diacylglycerol binding domain, and a region that is a putative substrate for ATM phosphorylation (33). RASSF1 was shown recently to be an effector of RAS both in vitro and in vivo studies (33).

The finding of RASSF1A inactivation in lung cancers was compatible with previous reports implicating mutations or alterations in activity of the RAS signal transduction pathways in the pathogenesis of these tumors. In contrast, RAS mutations are reported to be rare in RCC (43, 44), and the finding of frequent RASSF1A inactivation in CC-RCCs will provide new opportunities to develop therapeutic interventions targeted at reversing RASSF1A silencing or the downstream consequences of RASSF1A inactivation.

The finding of frequent RASSF1A methylation in papillary RCCs was unexpected in view of the infrequent reports of 3p allele loss in this tumor type. Furthermore, previous studies have demonstrated that VHL and FHIT inactivation is specifically associated with CC-RCC and not papillary RCC, whereas MET gene mutations are restricted to papillary tumors (15). Thus, RASSF1A inactivation provides an important link between the pathways of tumorigenesis in CC-RCCs and papillary RCCs. Nevertheless, the involvement of RASSF1A in both tumor types is consistent with the results of chromosome transfer experiments in which a chromosome 3p fragment suppressed tumorigenicity in both CC-RCC and papillary RCC (45). RAS signaling pathways have been implicated in the cellular responses to hepatocyte growth factor/scatter factor (the ligand for MET; Refs. 46, 47). Germ-line activating mutations of the MET proto-oncogene cause inherited susceptibility to type 1 papillary RCCs (15, 48), but we observed RASSF1A methylation in both type 1
(paclitaxel, small cell) and a type 2 (eosinophilic cytoplasm, large cell) subtype by papillary RCCs.

Traditionally, the detection of cytogenetic deletions or allele loss in tumors has been of paramount importance in localizing TSGs. Recently, proposals to identify the molecular pathology of human cancers by complete genomic sequencing have been formulated. The involvement of RASSFIA in papillary RCC demonstrates that such an approach will not identify all frequently inactivated TSGs and that sequence analysis of bisulfite-modified DNA may be required to identify TSGs inactivated by epigenetic silencing in regions with infrequent allele loss.

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