Inactivation of RAS Association Domain Family 1A Gene in Cervical Carcinomas and the Role of Human Papillomavirus Infection

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ABSTRACT

Recently, we have identified a new putative tumor suppressor gene, RASSF1A (Ras association domain family 1A gene), located at human chromosome 3p21.3, the segment that is often lost in many types of human cancers. The RASSF1A promoter was shown to be frequently hypermethylated in various epithelial tumors, including small cell lung, breast, bladder, prostate, gastric, and renal cell carcinomas. In this study, we have analyzed the methylation status of the RASSF1A gene in primary human cervical cancers and in eight cervical cancer cell lines. The RASSF1A promoter is hypermethylated in 4 of 42 (10%) of squamous cell carcinomas, in 4 of 19 (21%) of adenocarcinomas, and in 8 of 34 (24%) of cervical adenoscarcinomas. Although in adenoscarcinomas, methylation of RASSF1A and presence of human papillomavirus (HPV) type 16 or 18 sometimes coexisted, not a single case of HPV-16/18-positive squamous cell carcinomas had RASSF1A methylation. Similarly, in all eight analyzed cervical cell lines, RASSF1A inactivation and HPV infection were mutually exclusive (Fisher’s exact test; P = 0.0357): two HPV-negative cervical cancer cell lines had a methylated and silenced RASSF1A promoter (C-33A and HT-3), whereas the other six HPV-positive lines expressed RASSF1A mRNA (ME 180, MS751, SiHa, C-41, HeLa, and CaSkii). For cervical tumors and cell lines combined, the Pearson’s χ² test (χ² = 3.99; P ≤ 0.05) indicates a borderline-significant reverse correlation between inactivation of RASSF1A and the presence of high-risk HPVs. Our data imply that the presence of HPVs in cervical carcinomas alleviates the requirement for RASSF1A inactivation and suggests that these two events may engage the same tumorigenic pathway.

INTRODUCTION

Cervical cancer is the leading gynecological malignancy worldwide and is one of the most common cancers diagnosed in women in the United States (1). HPV infection is frequently detected in cervical intraepithelial neoplasia and invasive cervical carcinoma (2). It is estimated that >90% of cervical SCCs and >50% of A/Cs contain HPV DNA (3). Certain subtypes of HPV such as HPV-16 and HPV-18 are most commonly associated with cervical carcinoma. Oncogenic HPVs carry the transforming E6 and E7 genes. These genes are necessary and sufficient for malignant transformation and immortalization of cervical epithelial cells (2, 4). The E6 gene product promotes degradation of the p53 tumor suppressor protein (5), whereas the E7 protein inactivates the Rb protein and related pocket proteins (6, 7). However, the tumorigenic properties of the E6 and E7 proteins may not necessarily be limited only to the Rb and p53-related pathways (8, 9).

During malignant progression, tumor suppressor genes can be inactivated by different means. It is becoming increasingly clear that intragenic point mutations or small deletions are not the most frequent events leading to gene inactivation in cancer. Larger chromosomal deletions and promoter methylation are much more common. In cervical cancers, loss of heterozygosity has been reported for different chromosomal regions (10, 11). One of the frequently deleted chromosomal arms is the short arm of chromosome 3 (11).

Epigenetic inactivation of tumor suppressor genes through DNA methylation of promoter proximal CpG islands is an important event in tumorigenesis (12–14). In cervical cancer, aberrant methylation of the CpG islands of the p16, death-associated protein kinase, HIC-1, APC, FHIT, retinoic acid receptor β, and E-cadherin genes has been observed in 25–50% of the tumors (15–18). Other genes that are hypermethylated in their promoter regions less frequently in cervical carcinomas include the GSTP1 gene and the MLH1 gene (17).

Recently, we and others (19–21) have cloned and characterized the RASSF1 gene. This gene is localized at 3p21.3, a chromosomal site where loss of genetic material is one of the most frequently observed events in many types of human solid tumors (20, 22–24). One of the two major isoforms transcribed from this locus, RASSF1A, was absent in human lung and breast tumors because of promoter methylation (19, 21, 25–27). Promoter hypermethylation, loss of heterozygosity, and even homozygous deletions are the major mechanisms inactivating the RASSF1A gene, whereas mutations are infrequent. Hypermethylation of the RASSF1A promoter region has been found in several types of primary human tumors (28), and RASSF1A is probably the most commonly inactivated gene thus far reported in human cancer. Ectopic expression of RASSF1A in cancer cells reduced colony formation, suppressed anchorage-independent growth, and inhibited tumor formation in nude mice (19, 21, 29, 30).

The precise function of the RASSF1A protein is not yet known. The homology of the RASSF1A gene with the mammalian Ras effector NORE1 suggests that the RASSF1A gene product may function in signal transduction pathways involving Ras-like proteins. It was shown that RASSF1 binds Ras in a GTP-dependent manner and that its overexpression induces apoptosis (31). However, our recent data indicate that the proapoptotic effect of RASSF1 may require heterodimerization with NORE1 and that RASSF1 itself binds to Ras only weakly (32). In addition, there is evidence for an association of both NORE1 and RASSF1A with the proapoptotic kinase MST1 and that this interaction is involved in apoptosis induced by activated Ras (33). Other investigations have uncovered a role of RASSF1A in suppression of cyclin D accumulation and cell cycle progression (34). Available data suggest that inactivation of RASSF1A may be involved in the malignant processes leading to many types of human cancers.
The frequency of RASSF1A inactivation in human tumors is generally quite high. For example, RASSF1A is shown to be methylated in >70% of small cell lung cancers (21, 26), 91% of renal cell carcinomas (29), 62% of bladder cancers (35), 71% of thyroid carcinomas (36), 84% of nasopharyngeal cancers (37), and in >70% of prostate cancers (30, 38). In a previous study of prostate cancer, it was observed that prostate cell lines immortalized by infection with HPV expressed RASSF1A mRNA, whereas spontaneously or telomerase-immortalized prostate cell lines methylated and silenced the RASSF1A gene (30). This data suggested that RASSF1A inactivation and HPV infection might be mutually exclusive.

Because HPV infection is common in cervical carcinomas, a detailed investigation of RASSF1A methylation in this type of tumor is warranted. In this study, we investigated the methylation status of RASSF1A in primary human cervical cancers and in cervical cancer cell lines to explore a possible involvement of RASSF1A as a tumor suppressor gene in cervical carcinoma and to determine its relationship with HPV infection.

MATERIALS AND METHODS

Tissue Samples. All primary frozen cervical carcinoma tissues, matching adjacent tissues, and the relevant pathological data were obtained from the tumor tissue bank of the Anatomical Pathology Department of the City of Hope National Medical Center (Duarte, CA). All tissue was collected with Institutional Review Board approval. The tissue used for the DNA extraction was examined histologically and the presence of tumor in the sample confirmed. Details of DNA extraction and estimation of tumor in the sample extracted were described previously (39). Cervical carcinoma cell lines C-33A, HT-3, ME 180, M5751, SiHa, C-41, HeLa, and CaSkii were purchased from American Type Culture Collection (Manassas, VA).

Analysis of HPV Status. The presence of HPV in the tissue was determined by PCR using M09/MY11 consensus primers and type specific primers as reported earlier (39). It is possible that our HPV detection method underestimated the frequency of HPV-positive cases. The HPV testing was done using the M09/MY11 consensus primers without microdissection of tumors as reported previously (39). MY09/MY11 are located in the LI gene, which is frequently lost in some cervical cancers during integration. Also, these primers do not detect all of the HPV types. Some tumors only retain the E6/E7 genes for which no efficient consensus primers could be designed. The presence and expression of the papillomaviral sequences in human cervical carcinoma cell lines were extensively analyzed elsewhere (40–47).

Expression and Methylation Analysis of RASSF1A. The methylation status of RASSF1A promoter region was determined by a bisulfite modification method (19, 48). For COBRA (49), 100 ng of bisulfite-treated DNA was PCR-amplified with primers MU379 (5'-GTTTTGTTAGTITTAAT-GAGTTTATAGTTTITTT-3') and ML730 (5'-ACCTTCCTCTCCTAACA-CAATAAAACCTAACCC-AACCTAANT-3') in a 25-μl reaction volume containing 200 μM of each deoxynucleotide triphosphate and Taq polymerase (Roche; Indianapolis, IN). The PCR conditions consisted of an initial incubation for 3 min at 95°C, followed by 25 cycles of 20 s at 95°C, 20 s at 56°C, 40 s at 73°C, and finally a 4-min extension at 74°C. One-fifth of the PCR product was used as templates for a second PCR reaction with an internal primer ML561 (5'-CCCCCA-CATCTCTCCTACCAAT-3') and primer MU379 with similar conditions as described for the preceding PCR but for 30 cycles. The PCR products were purified using a QiAquick PCR purification kit (Qiagen). Twenty to 50 ng purified PCR products were digested with 10 units of TaqI (New England Biolabs). The digested products were resolved on 2% Tris-acetate-EDTA agarose gels.

RASSF1A promoter bisulfite sequencing, COBRA, and RT-PCR quantification of the cervical cell lines were performed as described elsewhere (30). Evaluation of the RASSF1A mRNA by real-time PCR in cell lines was conducted according to standard protocols for TaqMan Gold RT-PCR kit using an ABI Prism 7900HT Sequence Detection System (Applied Biosystems, Foster City, CA). The following RASSF1A oligonucleotides were used for amplification: RASSF1A-D (5'-ACCGACACGTGTCGTC-3'); RASSF1A-R (5'-AGGGGAGGTGAACTGGA-3'); and for the probe RASSF1A-HY (5’-FAM-TGGTGCGAAGGCTCGTG-TAMRA-3’). RNA normalization and estimation were performed with standard ABI TaqMan glyceraldehyde-3-phosphate dehydrogenase control reagents and in vitro transcribed RASSF1A RNA.

RESULTS

HPV and RASSF1A Methylation Analysis of the Primary Cervical Tumors. We analyzed the methylation status of the RASSF1A gene’s 5’ CpG island and promoter region in human cervical cancer samples. We treated genomic DNA with sodium bisulfite, followed by a COBRA (49) to analyze the methylation status of this gene in 95 primary cervical cancer samples and 58 matching adjacent normal tissues. After bisulfite treatment, all unmethylated cytosines are converted to uracils and then to thymines during subsequent PCR steps. All cytosines after subsequent PCR derive solely from 5-methylcytosines, which are nonresponsive to bisulfite. With COBRA, our target sequence was a 205 bp PCR fragment, which contains 16 CpG dinucleotides (19). TaqI (5’-TCGA-3’) can digest this fragment at two CpG sites (6 and 16), only when the genomic DNA is methylated at these sites.

Genomic HeLa cell line DNA and A549 lung cancer cell line DNA have been shown to be unmethylated and methylated, respectively, in the RASSF1A promoter region in our previous work (19). These DNAs were used as negative and positive controls for methylation in our methylation analysis. We analyzed 34 cervical A/Cs, 19 A/Ss, and 42 SCCs (Fig. 1). Four of 42 (10%) of SCCs and 4 of 19 (21%) of A/Ss were methylated in the RASSF1A promoter (Fig. 1; Table 1). For cervical A/Cs, methylation frequencies were somewhat higher (8 of 34 tumors were methylated = 24%; Table 1). We analyzed 58 normal tissues in parallel with the matching tumors (Fig. 1B and data not shown). Four normal samples were partially methylated but to a much lower extent than the corresponding tumor tissue. This result might be attributable to tumor cell contamination of the normal tissue or to preexisting methylation. RASSF1A was methylated only in those normal tissues in which the cancerous counterparts also showed methylation (Fig. 1B and data not shown). The presence of a methylated RASSF1A promoter did not correlate with tumor stage or grading (data not shown). Thus, tumors with high or low grades or stage could be methylated.

We next investigated the relationship of RASSF1A methylation and presence of HPV DNA in the cervical tumor samples. Five of 24 (21%) of HPV-positive A/Cs carried methylated RASSF1A alleles. There were four cases of HPV-16 and one case of HPV-18 in the RASSF1A-methylated samples. Three of 10 HPV-negative A/Cs had methylated RASSF1A. Seventeen of 19 adenosquamous cancers were HPV positive, and the four methylated samples were also HPV positive (all were HPV-16). Among the SCCs, 34 of 42 (81%) were HPV positive. Two of four tumors with RASSF1A methylation were HPV negative, and two others carried HPV-45 sequences. Thus, none of the SCCs that carried high-risk HPV-16 or HPV-18 genomes contained a methylated RASSF1A gene (Table 1). In total, 25.0% (5 of 20) of HPV-negative primary tumor samples and 14.7% (11 of 75) of HPV-positive tumors were methylated in the promoter region of RASSF1A.

RASSF1A Expression and Methylation Analysis of Cervical Carcinoma Cell Lines. To further investigate the connection between HPV infection and RASSF1A methylation, we analyzed eight cervical carcinoma cell lines. In earlier studies, the cell lines were evaluated in detail for the presence and expression of HPV sequences. In C-33A and HT-3 cells, no HPV viral DNA or RNA were found (41, 43). SiHa and CaSkii cells contain HPV-16 DNA, whereas C-41 and HeLa have HPV-18 DNA (40, 41, 43). HPV-39-related virus was
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We found in ME-180 (46), and HPV-45 was reported in MS751 (47). All HPV-positive cell lines express viral RNA transcribed from the E6-E7 region (41–45).

We analyzed the methylation status of the RASSF1A promoter by COBRA. C-33A and HT-3 showed complete methylation, whereas ME-180, MS751, SiHa, C-4I, HeLa, and CaSki were not methylated (Table 2). In addition, we performed bisulfite sequencing of the RASSF1A promoter in C-33A and HT-3 cells and found complete methylation of the promoter region (data not shown).

We next quantified expression of RASSF1A mRNA in these cells. RASSF1A-specific RT-PCR was performed in the presence of different amounts of in vitro transcribed RASSF1A mRNA, producing a shorter PCR fragment (Fig. 2). RASSF1A mRNA content was calculated by comparing the intensity of both bands in each lane. RT-PCR quantification and the data on HPV status are presented in Table 2. In both HPV-negative cell lines (C-33A and HT-3), the RASSF1A transcript was not detectable (<0.0001% of total RNA). In contrast, six other cell lines, which contained HPV DNA and RNA (SiHa, HeLa, ME-180, MS751, CaSki, and C-4I), expressed RASSF1A mRNA at levels 0.01–0.05% of total RNA. These levels of expression are comparable with those found in prostate cell lines transfected with E6-E7-expressing plasmids (30). In agreement with the data obtained from primary cervical tumors, we found a somewhat lower content of E6-E7-expressing plasmids (30). In agreement with the data obtained from primary tumors (T) were digested (+) or mock digested (−) with TaqI. The digested products were resolved on 2% Tris-acetate-EDTA agarose gels and visualized by ethidium bromide staining. Unmethylated HeLa DNA and methylated AS549 cell DNA were used as controls. A, tumor samples; B, matching tumor and adjacent normal tissues. We analyzed the PCR fragments obtained from bisulfite-modified DNA by digestion with a restriction enzyme that has a CpG recognition sequence (49). TaqI (5′-TCGA-3′) will cut only previously methylated DNA after bisulfite treatment and PCR. The consensus sequence will be lost by cytosine deamination in unmethylated samples. The analyzed 205-bp fragment of RASSF1A contains two TaqI restriction sites after bisulfite conversion of CpG methylated DNA. Restriction digestion of PCR products obtained from DNA methylated at both TaqI sites results in three bands (90, 81, and 34 bp; the two larger ones migrating together and the smaller band not visible). The criteria for scoring a sample as methylation positive was the presence of an additional band migrating ~90 bp upon TaqI digestion. The data obtained with the bisulfite restriction assay were confirmed by methylation-specific PCR using primers specific for unmethylated and methylated CpGs, respectively, in the RASSF1A CpG island (data not shown).

Similar results were obtained using a real time PCR procedure. The percentages of RASSF1A mRNA were normalized to the total RNA concentration (Table 2). In addition, RASSF1A mRNA was normalized to glyceraldehyde-3-phosphate dehydrogenase mRNA (data not shown), but this did not considerably alter the established ratios of RASSF1A expression between the cell lines.

To assess the mechanisms of RASSF1A transcriptional inactivation, we treated C-33A cells with 5-aza-2′-deoxycytidine for 1 week. RT-PCR titration of the RASSF1A indicated that its expression was not fully restored, even in the presence of high concentrations (15 μM) of the drug (data not shown). Sequencing of the RASSF1A promoter in C-33A cells did not reveal any nucleotide changes, therefore, such inactivation most likely occurs because of a lack of trans-acting factors and the promoter methylation may represent a secondary event.

DISCUSSION

HPV infection is recognized as a major contributor to the development of cervical cancer. Interestingly, RASSF1A methylation was unexpectedly low in primary cervical tumors. An earlier study had found no RASSF1A methylation in 22 cervical cancers analyzed (27). However, HPV presence was not assessed in that particular study. Our simultaneous assessment of RASSF1A inactivation and HPV presence in cervical carcinomas has revealed several interesting (albeit not statistically significant) correlations. We found that RASSF1A methylation was more common in cervical carcinomas associated with HPV16 and HPV18, but less common in HPV45-positive tumors. The highest percentage of RASSF1A methylation was observed in tumors positive for both HPV16 and HPV18.

![Fig. 1. Methylation analysis of primary cervical tumors. COBRA of primary cervical cancer samples. PCR products from bisulfite-treated DNA obtained from primary tumors (T) were digested (+) or mock digested (−) with TaqI. The digested products were resolved on 2% Tris-acetate-EDTA agarose gels and visualized by ethidium bromide staining. Unmethylated HeLa DNA and methylated AS549 cell DNA were used as controls. A, tumor samples; B, matching tumor and adjacent normal tissues.](image)

Table 1 Summary of methylation analysis and HPV status of primary human cervical cancer samples

<table>
<thead>
<tr>
<th></th>
<th>HPV16+</th>
<th>HPV18+</th>
<th>HPV45+</th>
<th>Other HPVs</th>
<th>HPV−</th>
<th>Total</th>
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<tr>
<td>SCC</td>
<td>0/26 (0)</td>
<td>0/3 (0)</td>
<td>2/3 (66)</td>
<td>0/2 (0)</td>
<td>2/8 (25)</td>
<td>4/42 (10)</td>
</tr>
<tr>
<td>A/C</td>
<td>4/15 (26)</td>
<td>1/9 (11)</td>
<td>0/0 (0)</td>
<td>0/0 (0)</td>
<td>3/10 (30)</td>
<td>8/34 (24)</td>
</tr>
<tr>
<td>A/S</td>
<td>4/8 (50)</td>
<td>0/6 (0)</td>
<td>0/1 (0)</td>
<td>0/2 (0)</td>
<td>0/2 (0)</td>
<td>4/19 (21)</td>
</tr>
<tr>
<td>Total</td>
<td>8/49 (16)</td>
<td>1/18 (5)</td>
<td>2/4 (50)</td>
<td>0/4 (0)</td>
<td>5/20 (25)</td>
<td>16/95 (17)</td>
</tr>
</tbody>
</table>

*Each value indicates the number of RASSF1A-methylated tumors (in numerator) versus the total number of tumors (in denominator). The percentage is in parentheses.

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titrated in cell lines, we never found RASSF1A. The correlation does not reach statistical significance in RASSF1A HPV/HPV-positive cases in primary tumors (see our HPV detection method could underestimate the number of normal cells and lower quality of the extracted RNA. In addition, it is difficult to quantify in primary tumors because of the presence of infections in the same samples. Unfortunately, RASSF1A primary cervical tumors alone (Fisher’s exact test; P = 0.24), even after these difficult-to-score HPV-45-positive samples were excluded (P = 0.11). However, when only SCC tumors are considered (excluding three HPV-45-infected samples), this correlation was quite significant (Fisher’s test; P = 0.038). For all cervical tumors and cell lines combined, both Pearson’s (χ² = 3.99; P ≤ 0.05) and Fisher’s (P = 0.05) tests indicate a borderline-significant reverse correlation between inactivation of RASSF1A and the presence of high-risk papillomaviruses.

Moreover, the RASSF1A gene was expressed in all six HPV-positive cervical lines and completely silenced in two HPV-negative lines, indicating statistically significant reverse correlation (Fisher’s exact test; P = 0.0357).

In the same panel of eight cervical cell lines, a similar correlation was established earlier in connection with the Rb and p53 mutations. Only HPV-negative cells contained mutated Rb and p53 genes, whereas the wild-type genes were retained in all six HPV-positive cell lines (7), implying that the wild-type Rb and p53 proteins were inactivated by the viral oncoproteins E6 and E7.

Recently, the absence of RASSF1A methylation in HPV-immortalized prostate cell lines has been reported (30). The expression of the RASSF1A gene was tested in four prostate carcinoma cell lines, adapted to grow in cell culture by transfection with DNA, which encodes E6/E7-transforming proteins of HPV serotype 16 or 18. All four tested HPV-transformed cell lines expressed normal levels of RASSF1A mRNA. All four tested HPV-transformed cell lines expressed normal levels of RASSF1A mRNA. In total, using the same semiquantitative RT-PCR analysis, we measured RASSF1A mRNA expression in 17 cervical and prostate carcinoma cell lines with known HPV status.

In all 7 HPV-negative lines, the RASSF1A gene was silenced, whereas it was expressed in the other 10 HPV-positive lines. These data also points to a possible correlation between HPV infection and RASSF1A expression (Fisher’s exact test P = 0.00005). This correlation could reflect a functional interaction between the cellular RASSF1A and the viral E6/E7 proteins, which may play important roles in both neoplastic transformation and immortalization of certain epithelial cells.

Evidence for a causal association between HPV and a subset of head and neck cancers has also been reported (50). Therefore, a similar reverse correlation between HPV infection and RASSF1A methylation may exist for this type of cancer but this has not yet been investigated. It is of note, however, that the methylation frequency of RASSF1A in primary head and neck tumors is quite low (5–15%; Refs. 28, 51). However, RASSF1A is frequently methylated in nasopharyngeal tumors, which may not be related to HPV infection (37).

The reverse correlation between RASSF1A inactivation and presence of HPV-transforming gene products is intriguing but is presently unexplained. The presence of HPV-16 or HPV-18 in cervical carcinomas may alleviate the requirement for RASSF1A inactivation. There is not enough information available regarding the exact biological function of the RASSF1 proteins. One piece of evidence points to an inhibitory effect of RASSF1A on cyclin D protein levels (34). Cyclin D-dependent phosphorylation negatively regulates Rb. Because the...
E7 protein of high-risk papillomaviruses can inactivate the Rb protein, both RASSF1A and E7 may interact in the same pathway. However, other evidence suggests that it is unlikely that RASSF1A functions in the Rb pathway. The Rb pathway appears to be inactivated in the majority of human cancers by ways that do not seem to depend on RASSF1. For example, the Rb protein is inactivated in the majority of small cell lung cancers (52), and yet RASSF1A is inactivated in ~80% of these tumors (19, 21, 26, 27). Cyclin D1 overexpression and Rb inactivation can coexist in small cell lung cancer (53). Other evidence also argues against a placement of RASSF1A into the known p16/Rb pathway. Ninety percent of thyroid tumors with p16 inactivation were also silenced for RASSF1A expression (36). Thus, the precise mechanistic connection between HPV infection and RASSF1A inactivation remains to be determined. Our data suggest that E6 and E7 proteins may target not only the Rb- and p53-related tumor suppressing mechanisms, but also some other essential pathways, most likely involving Ras signaling.

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