Overexpression of the nonpancreatic secretory group II PLA2 messenger RNA and protein in colorectal adenomas from familial adenomatous polyposis patients

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Abstract
The synovial fluid or group II secretory phospholipase A2 (sPLA2) has been implicated in various inflammatory processes and has been shown to release arachidonic acid for prostaglandin biosynthesis. In human colorectal cancer, both arachidonic acid and eicosanoid levels are elevated. Recently, sPLA2 has been identified as a candidate gene that modifies the Apc gene in the Min mouse, a murine model for familial adenomatous polyposis (FAP). Loss of sPLA2 gene function results in susceptibility to the Min phenotype and the formation of multiple intestinal polyps, whereas mice expressing an active sPLA2 gene are resistant to polyp formation. Therefore, there are two potentially contrasting roles for sPLA2 in colon cancer; one is protection against polyp formation, and the other, the release of arachidonic acid for prostaglandin production and subsequent tumor promotion. To investigate these contrasting dual roles of sPLA2, we have examined the expression and sequence of the sPLA2 mRNA in normal mucosa and duodenal and colorectal polyps from FAP patients. In 11 of 14 patients, there was a significant increase in sPLA2 mRNA [...]
Overexpression of the Nonpancreatic Secretory Group II PLA₂ Messenger RNA and Protein in Colorectal Adenomas from Familial Adenomatous Polyposis Patients

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ABSTRACT

The synovial fluid or group II secretory phospholipase A₂ (sPLA₂) has been implicated in various inflammatory processes and has been shown to release arachidonic acid for prostaglandin biosynthesis. In human colorectal cancer, both arachidonic acid and eicosanoid levels are elevated. Recently, sPLA₂ has been identified as a candidate gene that modifies the Apc gene in the Min mouse, a murine model for familial adenomatous polyposis (FAP). Loss of sPLA₂ gene function results in susceptibility to the Min phenotype and the formation of multiple intestinal polyps, whereas mice expressing an active sPLA₂ gene are resistant to polypl formation. Therefore, there are two potentially contrasting roles for sPLA₂ in colon cancer; one is protection against polypl formation, and the other, the release of arachidonic acid for prostaglandin production and subsequent tumor promotion. To investigate these contrasting dual roles of sPLA₂, we have examined the expression and sequence of the sPLA₂ mRNA in normal mucosa and duodenal and colorectal polyps from FAP patients. In 11 of 14 patients, there was a significant increase in sPLA₂ mRNA levels in the adenoma over the normal tissue. In some cases, there was over 100-fold increase in mRNA levels in the adenoma compared with normal tissue. Analysis of multiple adenomatous polyps from individual patients revealed that not all polyps contained elevated levels of sPLA₂ mRNA. Immunoblot analysis also showed that sPLA₂ protein expression was elevated in adenoma over normal tissue in five of six FAP patients analyzed. Furthermore, sequence analysis of sPLA₂ mRNA present in these samples did not reveal mutations in the coding region. The implications of the up-regulation of sPLA₂ in FAP is not clear, but unlike the Min mouse model, it does not seem to have a significant effect on polypl formation. In contrast, the high level of sPLA₂ expression is more likely contributing to the elevated levels of arachidonic acid found in colorectal cancer and, in conjunction with the elevated expression of cyclooxygenase-2, could be another factor in tumor formation.

INTRODUCTION

sPLA₂ is a lipolytic enzyme that hydrolyzes the release of the fatty acid from the sn-2 position of glycerophospholipids (reviewed in Refs. 1–3). When this fatty acid is arachidonic acid, which is usually esterified at this position in phospholipids, it can lead to the production of various prostaglandin and leukotriene proinflammatory mediators. sPLA₂ has been shown to be involved in the release of arachidonic acid for prostaglandin production (1, 2, 4), and like Cox-2, sPLA₂ expression is induced by various inflammatory stimuli such as lipopolysaccharide, interleukin 1β, and tumor necrosis factor-α (1, 2). Recently, a new role has been proposed for sPLA₂ as a modifier of the Apc gene in the Min mouse (5). The Min mouse, which carries a nonsense mutation in the Apc gene, develops multiple intestinal adenomas and is, therefore, a murine model for FAP, an inherited human disorder that predisposes to colorectal adenomas and cancer (6–9). It was found that mouse strains with a disrupted sPLA₂ gene (5, 10) were susceptible to the Min phenotype and develop numerous intestinal polyps, whereas mouse strains with an active sPLA₂ enzyme were resistant and developed only a few polyps (5). The mechanism by which sPLA₂ promotes resistance to the Apc mutation in the mouse is unclear, but because the Min mouse is a model for FAP, one might predict that some FAP patients with a more severe phenotype may also have mutations in the sPLA₂ gene. Contrary to this is the observation that PLA₂ activity (11) and arachidonic acid levels (12) are increased in human colorectal cancer. In addition, nonsteroidal anti-inflammatory drugs, which inhibit Cox and thus prevent prostaglandin synthesis, can reduce the number and size of colorectal adenomas (13). Finally, recent evidence indicates that increased Cox-2 levels promote colorectal tumorigenesis in the mouse model for FAP (14). Therefore, there are two contrasting activities for sPLA₂ in FAP: a protective role, supposedly by reducing polypl number; and a potentially detrimental role, by contributing to elevated prostaglandin production through Cox-2, thus leading to increased cell proliferation and tumor growth. These apparently contrasting dual roles of sPLA₂ in FAP were investigated by examining the expression and sequence of the sPLA₂ mRNA in normal mucosa and adenomatous polyps from FAP patients. In agreement with recent reports (15–17), we did not find mutations in the sPLA₂ mRNA, but in nearly all cases, there was a substantial increase in sPLA₂ mRNA and protein levels in colorectal adenomas compared with normal tissue.

MATERIALS AND METHODS

FAP patients were identified from an ongoing clinical surveillance program offered to affected polyposis kindreds through the Familial GI Cancer Registry at Mount Sinai Hospital, Toronto, Canada. Patient data and specimen collection were carried out according to a protocol approved by the Ethics Committee, University of Toronto. Samples were obtained from a panel of 25 FAP patients, consisting of histopathologically confirmed normal mucosa and matched colorectal (n = 16) or duodenal adenomas (n = 9).

Northern blot analysis was performed on total RNA prepared from 12 matched normal mucosa and colorectal adenomatous polyps and from two unmatched colorectal adenomas. RNA was prepared using Trizol (BRL) reagent as described by the manufacturer. Total RNA (8 μg) was separated on 1% agarose/formaldehyde gels and transferred to nitrocellulose (18). Prehybridization and hybridization were carried out at 42°C in 50% formamide, 5× SSPE (1× SSPE = 0.15 M NaCl, 0.01 M Na₂HPO₄, 0.001 M Na₂EDTA), 10× Denhardt’s, 2% SDS, and 100 μg/ml sheared and denatured herring sperm DNA. The probes used were human cDNAs for sPLA₂ (19), Cox-2 (20), and glyceraldehyde-3-phosphate dehydrogenase (Clontech). The cDNAs were labeled by random priming (Pharmacia), and hybridization was done using a probe concentration of 1–3 × 10⁶ cpm/ml. The blots were washed in 0.5× SSC and 0.5% SDS at 50°C and exposed to film at −70°C. Typically for sPLA₂ signals could be detected within 3–6 h, whereas for Cox-2, the film

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The abbreviations used are: sPLA₂, secretory group II phospholipase; Cox, cyclooxygenase; FAP, familial adenomatous polyposis; RT-PCR, reverse transcription-PCR; PP, forward primer; RP, reverse primer; SCSP, single-strand conformation polymorphism.
OVEREXPRESSION OF sPLA2 IN COLORECTAL ADENOMAS

Northern blotting and RT-PCR were used to investigate sPLA2 mRNA expression and sequence in both normal mucosa and adenomatous polyp tissue samples from nine FAP patients. Based on the result of the frameshift mutation in the mouse sPLA2 gene, which produces a very unstable and thus a virtually undetectable mRNA (10), it was thought that the level of sPLA2 mRNA expression in the human samples could quickly indicate whether there was any mutation in the gene. Analysis of the sPLA2 mRNA expression by Northern blot (Fig. 1) showed that sPLA2 mRNA was highly expressed in all individuals, suggesting that it was unlikely that there was a mutation in the sPLA2 gene. This was confirmed by sequencing and SSCP analysis of the RT-PCR product (see below) and in agreement with a number of recent reports that implicated in inflammation and in some cases sPLA2 and Cox-2 mRNA are overexpressed in colorectal adenomas and adenocarcinomas (24). Because sPLA2 has been implicated in inflammation and in some cases sPLA2 and Cox-2 mRNA can be coordinately induced (25), the expression of Cox-2 mRNA in some of these samples was also examined. However, due to the low levels of Cox-2 mRNA, only very weak signals were obtained for Cox-2, even after 1 week of exposure. Nevertheless, an elevated level of Cox-2 expression was detectable in the polyp samples that expressed the highest level of sPLA2 mRNA in the polyp. Multiple colorectal adenomatous polyps from three individual patients were also analyzed (Fig. 1B), and in two of the three patients, it was clearly evident that at least one of the polyps had a significant increase in sPLA2 mRNA. However, integration of the blots by laser densitometry also showed that polyp sample P1 from patient 12 (Fig. 1B) had a 3-fold increase in sPLA2 mRNA over control. Recently, it has been shown that Cox-2 mRNA is also overexpressed in colorectal adenomas and adenocarcinomas (24). Because sPLA2 has been implicated in inflammation and in some cases sPLA2 and Cox-2 mRNA can be coordinately induced (25), the expression of Cox-2 mRNA in some of these samples was also examined. However, due to the low levels of Cox-2 mRNA, only very weak signals were obtained for Cox-2, even after 1 week of exposure. Nevertheless, an elevated level of Cox-2 expression was detectable in the polyp samples that expressed the highest level of sPLA2 mRNA (data not shown). The low levels of Cox-2 mRNA in these samples were not surprising, because total RNA was used for this analysis, whereas the previous study used 5 μg of poly(A)+ and 1-week exposure to detect the Cox-2 mRNA (24). Although the polyp samples that express the highest

RESULTS

Northern blotting and RT-PCR were used to investigate sPLA2 mRNA expression and sequence in matched normal and colorectal adenomatous polyp tissue samples from nine FAP patients. The primers used for amplification were as follows: FP, 5'-GGTGAATTTCCACAGAATGATCT-3'; RP, 5'-TTCGTGCACACGGGTGTCCTGTTGCGAGGA-3'; and segment 2 (230 bp): FP, 5'-TTGATGAGGCACAAAGGAGG-3', RP, 5'-TTGATGAGGCACAAAGGAGG-3'. Each 20-μl PCR reaction consisted of 100 ng of each primer, 70 μM of each deoxynucleotide triphosphate, 100 ng of template DNA, 0.3 unit of Taq polymerase (AmpliTag Perkin-Elmer), and 0.2 μl of (α-32P)dCTP (3000 Ci/mMol) in 1X PCR buffer [10 mM Tris (pH 8.3), 50 mM KCl, and 1.5 mM MgCl2]. The amplification conditions involved an initial denaturation step at 94°C (4 min), followed by 30 cycles each consisting of 94°C for 1 min, 55–58°C for 1 min, and 72°C for 1 min. Samples were electrophoresed under nondenaturing conditions on 6% polyacrylamide gels at 4°C with 10% glycerol in 0.5X TAE buffer. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel. The sPLA2 cDNA fragment was cut out and recovered from a low-melt agarose gel.
level of sPLA₂ mRNA also have detectable Cox-2 expression, there is a very large difference in the level of the sPLA₂ and Cox-2 mRNAs in these samples. The sPLA₂ hybridization was easily detectable after 2-3 h of exposure.

To show that the increased level of sPLA₂ mRNA expression also resulted in increased sPLA₂ enzyme levels, sPLA₂ protein in normal and tumor tissues was assayed by immunoblotting. The antibody used for the detection of sPLA₂ protein was a monoclonal antibody that recognizes the unreduced form of the enzyme. This results in the appearance of multiple sPLA₂ immunodetectable bands on SDS gels (Fig. 2) due to the different oxidized forms of the enzyme (Ref. 26; this Mr 14,000 group II sPLA₂ contains 14 cysteine residues). However, taking this into account, there was a detectable increase in the amount of immunodetectable sPLA₂ enzyme over normal tissue in 8 of 10 adenomas examined. Not all adenomas from the same patient had increased sPLA₂ protein levels, which is consistent with the result found for the mRNA expression (Fig. 1B). Therefore, the overexpressed sPLA₂ mRNA in colorectal adenomas is translated, resulting in increased levels of sPLA₂ enzyme.

The sequence of the sPLA₂ mRNA in colorectal polyps from the nine FAP patients analyzed in Fig. 1A was determined by RT-PCR (Fig. 3) and sequencing of the amplified product. SSCP analysis of an additional nine FAP duodenal adenomas (Fig. 4) was also performed, because it was hypothesized that these would be more analogous to the Min mouse small intestinal adenomas. Essentially, no significant changes in the coding sequence of sPLA₂ mRNA were detected in either the colorectal or duodenal adenomas, which is in agreement with previous results (15-17). However, in a number of samples (both normal and adenomas), an additional faster-migrating PCR product was observed (Fig. 3). Sequencing of this product revealed that it coded for a misspliced sPLA₂ cDNA that was missing exon 3. The reason for this missplicing is not clear, because it is unlikely due to mutation of the gene. It is of interest to note that the frameshift mutation in exon 3 of the mouse sPLA₂ gene also generates a similar gene product (5, 10). Exon 3-deleted sPLA₂ cDNA in both human and mouse, if translated, terminates out of frame at the exact same position in exon 4 (10).

**DISCUSSION**

The results presented here show that sPLA₂ mRNA and protein can be overexpressed to very high levels in FAP adenomas. In the Min mouse model of adenomatous polyposis coli, sPLA₂ expression appears to confer resistance to the Apc⁵⁸⁷⁶ phenotype (5, 27), thus suggesting that the increased sPLA₂ gene expression in FAP may be a protective response to reduce polyp formation. Previous reports have shown that PLA₂ activity (11) and arachidonic acid levels (12) are increased in human colorectal cancer. It is also well-documented that sPLA₂ is involved in the inflammatory response and can provide arachidonic acid for eicosanoid production. Therefore, the increased PLA₂ activity and arachidonic acid levels in colorectal adenomas could be due to the overexpression of sPLA₂. Nonsteroidal anti-inflammatory drugs, which inhibit prostaglandin synthesis, have been reported to reduce poly size and number (13, 14), as well as colon cancer cell growth (28). Furthermore, Cox-2 mRNA (24) and protein (29) are also induced in colorectal cancer and inhibition of Cox-2, either by gene knock-out or by a selective Cox-2 inhibitor, suppresses intestinal polyposis in Apc⁵⁸⁷⁶ mutant mice (14). Therefore, it is possible that this supposedly protective response of sPLA₂ overexpression in FAP could inadvertently be contributing substrate to the Cox-2 pathway for the increased production of prostaglandins. In this regard, the increased expression of sPLA₂ in adenomas is more likely contributing to tumor promotion. Overexpression of sPLA₂ has been observed in other cancers. For example, sPLA₂ overexpression in breast cancer has been correlated with increased malignant potential (30, 31). There is also increased sPLA₂ expression in gastric cancer (32), hepatocellular carcinomas (33), and in large bowel neoplasms of rats treated with carcinogen (34). Thus, the increased sPLA₂ expression in FAP could be contributing to tumor progression and not preventing polyp formation as appears to be the case in the Min mouse (5, 27). The absence of sPLA₂ gene mutations in sporadic and FAP colorectal neoplasms as observed by us and others (15-17) is also not consistent with sPLA₂ being a modifier.
of APC mutations in humans. Therefore, it is somewhat difficult to reconcile the difference between the Min mouse model and FAP. There are a few possibilities that may account for this difference. Mouse physiology is different than that of humans; for example, APC mutations in the mouse produce numerous intestinal adenomas, whereas in humans, polypos occur primarily in the colon and duodenum. The modifiers of APC mutations in humans are different than in the mouse, and the genetic backgrounds of humans are much more diverse than that of inbred mouse strains.

The expression of sPLA₂ mRNA in the Min mouse and in FAP patients have in common the presence of a misspliced sPLA₂ mRNA that has exon 3 deleted. The C57BL/6 mouse strain in which the Min phenotype was established (6) carries a frameshift mutation in exon 3 of the sPLA₂ gene (5, 10). This mutation is thought to be responsible for the exon skipping, because similar exonic mutations in several other genes have been shown to result in aberrant mRNA splicing (10). The FAP patients' colorectal or duodenal adenomas are unlikely to have mutations in the sPLA₂ gene, because no mutations were observed in the sPLA₂ CDNA, and the mRNA is expressed at very high levels. Furthermore, the misspliced transcript is found in both normal and adenoma samples of FAP patients. In the mouse, it was only detected in the intestine mRNA of sPLA₂-deficient mouse strains and not in the wild-type sPLA₂ strains. Therefore, how and why this alternatively spliced sPLA₂ mRNA is produced in these samples is not known. It is unlikely to be a PCR artifact because exon 3 is specifically deleted. The fact that the mRNA is expressed at such high levels may contribute to missplicing. It is of interest to note that the mouse and human exon 3-deleted sPLA₂ mRNA, if translated, terminate out of frame in exon 4 at the exact same position. The translated product, if produced, would contain 13 amino acids from the sPLA₂ signal peptide sequence and a new 22-amino acid sequence. Whether this product has some fortuitous function remains to be determined.

In conclusion, the results presented here are in agreement with previous results that showed the absence of sPLA₂ gene mutations in FAP adenomas. However, the high level of sPLA₂ mRNA expression in adenomas could account for the elevated levels of arachidonic acid in colorectal cancer, thus providing substrate for Cox-2 and leading to increased prostaglandin production and tumor promotion.

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REFERENCES

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