Disruption of the APC Gene by a Retrotransposal Insertion of L1 Sequence in a Colon Cancer

Yoshio Miki, Isamu Nishisho, Akira Horii, Yasuo Miyoshi, Joji Utsunomiya, Kenneth W. Kinzler, Bert Vogelstein, and Yusuke Nakamura

Department of Biochemistry, Cancer Institute, 1-37-1, Kami-Kasumigaoka, Setagaya-ku, Tokyo 151, Japan; Second Department of Surgery, Hyogo College of Medicine, 1-1, Mukogawa-cho, Nishinomiya, Hyogo 663, Japan; and Molecular Genetics Laboratory, The Johns Hopkins Oncology Center, Baltimore, Maryland 21231

ABSTRACT

The APC gene is responsible for familial adenomatous polyposis and is considered to be a tumor suppressor gene associated with development of sporadic colorectal tumors. Here we report the disruption of the APC gene caused by somatic insertion of a long interspersed repetitive element (LINE-1 sequence) into the last exon of the APC gene in a colon cancer. The inserted sequence was composed of a 3' portion of the LINE-1 consensus sequence and nearly 180 base pairs of polyadenylate tract. Furthermore, since an 8-base pair target site duplication was observed, retrotranscriptional insertion of an active LINE-1 sequence is suspected as the cause of this insertion event. This is the first report of the disruption of a tumor suppressor gene caused by somatic insertion of a mobile genetic element.

INTRODUCTION

The mechanism of somatic inactivation of putative tumor suppressor genes such as the RB (retinoblastoma), WT (Wilms' tumor), DCC (deleted in colorectal carcinomas), p53, and MCC (mutated in colorectal cancers) genes have thus far been detected as point mutation, chromosomal loss, intragenic deletion, and/or chromosomal rearrangement (1-6). We and others have recently identified a gene responsible for familial polyposis coli, which was designated as the APC gene (7-10). Familial polyposis coli is one of the most common autosomal-dominant diseases which lead to cancer predisposition (11). Affected patients usually develop hundreds to thousands of benign adenomatous polyps in colon, one or some of which will progress to colorectal cancer if not surgically treated. Furthermore, somatic mutations of the APC gene were also detected in sporadic colorectal cancers. Hence this gene is considered to be a tumor suppressor gene and probably plays a significant role in the initiation of sporadic colorectal tumors (8).

During our search for somatic mutations in the APC gene, we examined over 150 cases of colorectal cancers by Southern blotting using cDNA1 clones from the APC gene as probes. Here we report one case in which the APC gene was disrupted by a somatic insertion of a mobile genetic element.

MATERIALS AND METHODS

Samples. Tumors and their corresponding normal mucosal tissues were obtained at surgery from 150 patients with colorectal cancers. Immediately after removal, tissue specimens were rinsed in phosphate-buffered saline, frozen in liquid nitrogen, and stored at -70°C. Routine histopathological diagnoses were performed for all tumors.

Southern Blot Analysis. Frozen samples were ground to a very fine powder in liquid nitrogen, transferred to a 15-ml tube, and suspended in 4 ml of lysis buffer. High-molecular-weight DNAs were extracted in phenol/chloroform/isooamy alcohol as described by Sato et al. (12). DNA from each sample was digested with an appropriate restriction enzyme, electrophoresed in a 0.8% agarose gel, and transferred to a nylon membrane (Pall Biodyne, New York) with 0.1 M NaOH/0.1 M NaCl. The membrane was washed in 2× standard saline-citrate and fixed by UV cross-linking. Prehybridization was performed in 7% PEG 8000/10% sodium dodecyl sulfate at 65°C for 2 h. Hybridization was done at 65°C for 16-24 h in the same solution with a probe labeled with [32P]dCTP by the random priming method (13). After hybridization, the membrane was washed twice in 0.1× standard saline-citrate/0.1% sodium dodecyl sulfate at 65°C for 15 min and then exposed to Kodak XAR film at -70°C.

Isolation of the Fragment Containing the Insertion. A genomic phage library was constructed from colon cancer DNA. The DNA was partially digested with Sau3AI. After fractionation by sucrose density gradient centrifugation, DNA was partially filled in, and ligated with Lambda FIX vector, which was digested with XhoI and partially filled in (Stratagene, San Diego, CA). After packaging and transfection, the library was plated and screened with cDNA clones from the APC gene.

DNA Sequencing. DNA sequencing was done by a modified T7 polymerase method as described by Del Sal et al. (14).

RESULTS

Detection of Insertional Mutation in a Colon Cancer. We examined 150 cases of colorectal cancers by Southern blotting using cDNA clones from the APC gene as probes. In one case, we found a 4.1-kilobase extra BglII fragment in addition to the normal 3.4-kilobase BglII band. This 4.1-kilobase fragment was not seen in 150 normal controls (Fig. 1). DNAs from this tumor and from normal colonic tissue surrounding the tumor were further compared following digestion with other enzymes (MspI, HindIII, EcoRI or PstI) (Fig. 1). All enzymes tested showed extra bands, which were approximately 750 base pairs larger than their normal counterparts when DNA was hybridized with a probe containing APC nucleotides 4425 to 5592. These results indicated the possibility of somatic insertion of a 750-base pair fragment into the APC gene in this cancer.

Characterization of the Inserted Sequence. To further characterize the inserted sequence, we have screened a genomic phage library constructed from the DNA of this colon cancer. Five positive clones were isolated and two of them contained a 4.1-kilobase BglII fragment presumptively containing the insertion. A 4.1-kilobase BglII fragment was subcloned into a pBluescript vector and sequenced (Figs. 2 and 3). As shown in Fig. 3a, the APC gene was disrupted at codon 1526. The inserted sequence was highly homologous to the L1 consensus sequence (15, 16). The first fifth [nucleotides 1 to 150] of the insertion was almost identical [2-base pair difference] to the L1 consensus sequence (nucleotides 5778 to 6161, more than 98% homology). The first fifth of the insertion (nucleotides 532 to 750) was composed of a polyadenylation signal and subsequent 180-base polyadenylate tract. Furthermore, dupli-
DISRUPTION OF THE APC GENE BY LI

Enzyme : Bgl II PstI MspI HindIII EcoRI

Fig. 1. Southern blot analysis of the APC gene from normal tissue (N) and colon cancer (T) of the same patient. Abscissa, restriction endonucleases used; Arrows, extra bands in colon cancer which were approximately 750 base pairs larger than those of their normal counterparts.

Fig. 2. Sequence analysis of the target site. The 4.1-kilobase BglII fragment containing the insertion was subcloned and pertinent clones were sequenced (17). A, 5' end of the insertion (AI) (arrow) and the normal counterpart (A2). B, 3' end of the insertion (arrow) (BI), preceded by polyadenylate and the normal counterpart (B2). Eight-base pair sequences in brackets (AI, BI) indicate the target site duplication.

Enzyme : Bgl II PstI MspI HindIII EcoRI

Fig. 1. Southern blot analysis of the APC gene from normal tissue (N) and colon cancer (T) of the same patient. Abscissa, restriction endonucleases used; Arrows, extra bands in colon cancer which were approximately 750 base pairs larger than those of their normal counterparts.

DISCUSSION

LI sequences are up to 7 kilobases long, flanked by target site duplications of various length. Unlike retroviral transposons, they have no terminal repeats, but have A-rich regions at their 3' ends, usually preceded by a polyadenylation signal. Many LI sequences have two long open reading frames (ORF-1, ORF-2) (17), one of which (ORF-2) contains a region which is highly homologous to retroviral reverse transcriptase and RNase H (18, 19). These features indicate that LI elements may be “nonviral retrotransposons” (16, 19), which transpose through an RNA intermediate with reverse transcriptase activity, similar to a postulated mechanism generating pseudogenes (20). However, because most LI elements are heterogeneously truncated from their 5' end [up to 95% in mammals (19)], it is extremely difficult to identify a structure or sequence which may still function as a transposon. In the case described here, the insertional sequence has a long stretch of polyadenylate, and it was therefore suspected that the functional LI sequence was transcribed and integrated into the APC gene by a retrotranscriptional mechanism. In addition, the evidence of an 8-base pair target site duplication, since this is commonly found in class II retrotransposons (16), supports this speculation.

The biological function of LI elements is unclear, but several cases indicating its mobility have been reported. For example, de novo germ line insertions of LI sequences occur in the factor VIII gene sometimes resulting in hemophilia A (21, 22). In rats, LI insertion into the Igh (immunoglobulin heavy chain) and Mtv-2 (Moloney leukemia virus integration 2) loci were also reported (23). Furthermore, the somatic insertion of an LI sequence into an intron of the myc locus in a human breast carcinoma (24) or the 5' flanking region of the c-myc gene in canine transmissible venereal tumor (25) was reported. It is interesting that somatic insertions described in the present report and Ref. 24 involved an inversion of part of the inserted LI sequences, while the germ line insertions (21, 22) had the expected colinear organization. Although the effect of the LI insertion into or upstream of the myc gene was not clear, the APC insertion described above can be expected to dramatically alter the gene product, inasmuch as it occurred in an exon in middle of the gene. It will be of interest to determine the frequency at which LI-mediated inactivation of tumor suppressor genes occurs in somatic cells and whether inherited or environmental factors influence this frequency.
Fig. 3. Comparison of the inserted sequences and L1 consensus sequences. a, nucleotide sequence comparison. The inserted sequence is shown above, and the L1 consensus sequences below, numbered as presented in Ref. 5. Lowercase letters indicate nucleotide homology. There are only 7 single base pair differences between the sequences.

b. The insertion is flanked by an 8-base pair target site duplication shown in hatched boxes. Nucleotides 1 to 150 in the insertion are similar to an inverse complement of the L1 sequence (nucleotides 5657 to 5548). The next sequences are homologous to a 3′ portion of the L1 consensus sequence (nucleotides 5778 to 6161) and are followed by a polyadenylation signal and subsequent 180-nucleotide tract of A residues.

ACKNOWLEDGMENTS

We thank Dr. Yoshiyuki Sakaki for helpful advice and Kumiko Koyama and Kiyoishi Noguchi for technical assistance.

REFERENCES


Disruption of the \textit{APC} Gene by a Retrotranspososal Insertion of L1 Sequence in a Colon Cancer

Yoshio Miki, Isamu Nishisho, Akira Horii, et al.


Updated version
Access the most recent version of this article at:
http://cancerres.aacrjournals.org/content/52/3/643

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.