APC mutations in sporadic colorectal carcinomas from The Netherlands Cohort Study

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The adenomatous polyposis coli (APC) gene is considered to be a gatekeeper in colorectal tumourigenesis. Inactivating mutations in APC have been reported in 34–70% of sporadic colorectal cancer patients, the majority of which occur in the mutation cluster region (MCR). In this study, tumour tissue from 665 incident colorectal cancer patients, who originate from 120 852 men and women (55–69 years of age at baseline) participating in The Netherlands Cohort Study, was evaluated for the occurrence and type of APC mutations with regard to age at diagnosis, gender, family history of colorectal cancer, Dukes’ stage, tumour differentiation and sub-localization. Mutation analysis of the MCR, which spans codons 1286–1513, was performed on archival adenocarcinoma samples using macrodissection, nested PCR and direct sequencing of purified PCR fragments. A large number of genetic aberrations (n = 978), including point mutations (n = 833), deletions (n = 126) and insertions (n = 19) was detected in the MCR in 72% of patients (479/665). In particular, we observed a large number of missense mutations, more than reported previously. This may indicate involvement in colorectal carcinogenesis, although their significance for APC functions is unclear. Truncating mutations were found in 37% of patients (248/665). Patients with rectosigmoid and rectum tumours relatively more frequently harbour C > T nonsense mutations and truncating frameshift mutations as compared with patients with proximal and distal colon tumours (P = 0.009 and P = 0.045, respectively). Differences in occurrence of truncating mutations with regard to tumour sub-localization suggest a different aetiology of tumourigenesis in colon and rectum.

Introduction

It is well established that sporadic colorectal cancer (CRC) arises through a gradual series of histological changes, which are accompanied by specific genetic alterations involving tumour suppressor genes (e.g. APC, DCC, SMAD4, TP53) and oncogenes (e.g. K-ras) (1,2). Adenomatous polyposis coli (APC) gene mutation is considered to be an early event in colorectal carcinogenesis.

Linkage analysis of families with the autosomal dominant inherited disease familial adenomatous polyposis coli (FAP) has led to mapping of the APC gene to 5q21 (3). This large gene with 21 exons, was subsequently cloned, identified and characterized (4). Mutations in both APC alleles were also found in most sporadic colorectal tumours (5). Whereas germ-line mutations in FAP are confined to the 5’ half of the APC gene, somatic mutations are clustered in the central region of the open reading frame, spanning codons 1286–1513 of exon 15 (5,6). Although this mutation cluster region (MCR) represents only 8% of the 8535 bp APC gene, 68–77% of somatic mutations in APC occur in this region (7,8).

The APC protein consists of 2843 aa, and comprises a number of functional domains, motifs and other signatures, as reviewed by Polakis (6). APC is capable of binding β-catenin through its 15 aa repeats, situated between aa 1020 and 1263, but also facilitate down-regulation of β-catenin through interactions with Axin and GSK3β (10,11). Through inactivating mutations in the central part of the APC gene, which often lead to complete or partial loss of function of this region, β-catenin levels are up-regulated and the Wnt signalling pathway is activated, which in turn may lead to enhanced proliferation (12). In addition to its role in the Wnt pathway, APC has other functions. Through its binding of β-catenin APC is also linked to E-cadherin and α-catenin, which in turn bind actin and actin-associated proteins, thus taking part in intercellular adhesion (13). Additionally, APC associates with the microtubule cytoskeleton directly through its C-terminus. There is also evidence that APC may play a role in the regulation of apoptosis (14).

Frequencies and specific types of somatic mutations in the APC gene have been investigated in a number of studies. Somatic mutations in APC have been found in 34–70% of sporadic tumours in CRC patients (7,8,15–21). Higher prevalences of 75–95% have been found in studies on the occurrence of somatic APC mutations in CRC cell lines (22–24). The large majority of mutations observed in different studies would lead to a truncated and therefore inactivated APC protein, either by nonsense point mutations (30%) or by frameshift mutations (68%), as reviewed by Béroud (25). Most reports, however, were based on limited numbers of (usually selected) patients. Studies on somatic APC mutations are often based on FAP patients and it has been shown that the occurrence of a second mutation in the APC gene is somehow dependent on the position of the germline mutation, thereby introducing a bias (26). Examination of APC mutations in colorectal cell lines has indicated that there may also be an interdependence of

Abbreviations: APC, adenomatous polyposis coli; CRC, colorectal cancer; FAP, familial adenomatous polyposis coli; MCR, mutation cluster region.
the two hits in APC in sporadic colorectal cancer (23). Furthermore, results from different reports are difficult to compare as different methods of detecting mutations in APC have been used and different regions of the APC gene have been studied.

In the current report, the frequency and type of APC gene mutations are assessed in a large series of unselected, incident CRC patients from The Netherlands identified in a prospective cohort study. The occurrence and type of APC gene mutations in the MCR are reported with regard to age at diagnosis, gender, family history of colorectal cancer, Dukes’ stage, tumour differentiation and sub-localization.

Materials and methods

Study population
A prospective cohort study on diet and cancer has been initiated in The Netherlands in September 1986. The study design has been described in detail elsewhere (27). Briefly, at baseline a total of 58,279 men and 62,573 women between the ages of 55 and 69 years, completed a self-administered food frequency and lifestyle questionnaire. The study population originated from 204 municipal population registries throughout the country. Incident cancer cases are identified by monitoring of the entire cohort for cancer occurrence through annual record linkage to The Netherlands Cancer Registry (NCR), nine regional cancer registries throughout The Netherlands, and to the “Pathologisch Anatomisch Landelijk Geautomatiseerd Archief” (PALGA), a nationwide database of pathology reports (28). The PALGA database was used to identify and locate tumour tissue in Dutch Pathology laboratories. The first 2.3 years of follow up were excluded due to incomplete nationwide coverage of PALGA. From 1989 until 1994, 819 incident cases with histologically confirmed CRC were identified. CRC was classified according to site as follows, 154.1, 153.1, 153.4, 153.5, 153.6); distal colon: splenic flexure through sigmoid colon (ICD-O codes 153.2, 153.3, 153.7); rectosigmoid (ICD-O code 154.0) and rectum (ICD-O code 154.1). Information about age at diagnosis, gender and family history of CRC (at baseline) was retrieved from The Netherlands Cohort Study on diet and cancer (NLCS) database. Information about tumour sub-localization, Dukes’ stage and differentiation was retrieved from the NCR database.

Table I. Fragment characteristics for the amplification and sequencing of the MCR of APC

<table>
<thead>
<tr>
<th>Fragment</th>
<th>Nucleotide position</th>
<th>Fragment size (bp)</th>
<th>Primer sequences</th>
</tr>
</thead>
</table>
| Flank A  | 3874-4229           | 356                | Sense: 5’-GAA ATA GGA TGT AAT CAG AGC-3’
|          |                     |                    | Antisense: 5’-GA GCT GCC GAT AGA AGC ACT-3’ |
| Flank B  | 4114-4624           | 511                | Sense: 5’-GCT CAG ACA CCC AAA AGT CC-3’
|          |                     |                    | Antisense: 5’-ATT CCC ATT GAT TTC TTC C-3’ |
| Flank F1 | 3796-4092           | 297                | Sense: 5’-GAT ACT TAT GTA GAA GA-3’
|          |                     |                    | Antisense: 5’-GCG TCC TGA AGA AAA TTC AAC-3’ |
| Flank F2 | 3982-4003           | 248                | Sense: 5’-GAA GGT CCA GCA GTG TCA CAG C-3’
|          |                     |                    | Antisense: 5’-GA GCT GCC AAT CGA AGC ACT-3’ |
| Flank F3 | 4114-4383           | 270                | Sense: 5’-GCT CAG ACA CCC AAA AGT CC-3’
|          |                     |                    | Antisense: 5’-ATT TTT AGG TAC TTC TTC GTT C-3’ |
| Flank F4 | 4328-4624           | 297                | Sense: 5’-AAA ACA CCT CCA CCA CCT CC-3’
|          |                     |                    | Antisense: 5’-ATT CCC ATT GTC ATT TTC C-3’ |
| Nested S1| 3874-4092           | 219                | Sense: 5’-GAA ATA GGA TGT AAT CAG AGC-3’
|          |                     |                    | Antisense: 5’-GCC TCC TGA AGA AAA TTC AAC-3’ |
| Nested S2| 4026-4229           | 204                | Sequence primer: 5’ (Cy5)-GCC TCC TGA AGA AAA TTC AAC AGC-3’
|          |                     |                    | Sense: 5’-CTA CGT CAG GTT TCT AGT TTAG C-3’
|          |                     |                    | Antisense: 5’-GGA GCT GCC AAT CGA AGC ACT-3’ |
| Nested S3| 4179-4383           | 205                | Sequence primer: 5’ (Cy5)-GAA GCT GCC AAT CGA AGC ACT CTC-3’
|          |                     |                    | Sense: 5’-T ACT TCT GTC AGT TCA CTT GAT A-3’
|          |                     |                    | Antisense: 5’-ATT TTT AGG TAC TTC TCG G-3’ |
| Nested S4| 4328-4594           | 267                | Sequence primer: 5’ (Cy5)-TTT AGG TAC TTC TCG G-3’
|          |                     |                    | Sense: 5’-AAA ACA CCT CCA CCA CCT CC-3’
|          |                     |                    | Antisense: 5’-G CAT TAT TCT TAA TTC CAC ATC-3’ |

*Biotin-labelled primer.
semi-nested PCR consisted of 3 min pre-denaturation at 94°C, 40 s at 94°C for denaturation, 1 min at 52°C to 57°C for annealing, 1 min at 72°C for elongation and 10 min at 72°C for post-elongation. In each PCR, one round of 35 cycles was performed using a Peltier Thermal Cycler-200 (MJ Research, Biozym, Landgraaf, The Netherlands) or an i-cycler (BioRad, Veenendaal, The Netherlands). In each PCR series positive (DNA from CRC cell lines) and negative controls (no DNA) were included. The length and concentration of the PCR products were checked by electrophoresis on 2% agarose gels and visualized with ethidium bromide.

Mutation analysis was performed by direct sequencing using the Autoload SPS Sequencing Kit according to the manufacturer’s instructions (Amersham Biosciences, Roosendaal, The Netherlands). In brief, the biotinylated PCR product was captured on a sequencing comb coated with streptavidin. After removal of the non-biotinylated strands by alkaline denaturation, the remaining product was analysed on ALFexpress DNA Analysis System using ALFwin software (Amersham Biosciences, Roosendaal, The Netherlands).

Evaluation of the sequence patterns was performed by two independent observers, based on the criteria that an increase of at least 5% is observed for the mutant peak, as well as a decrease of at least 5% of the wild-type peak, relative to the wild-type pattern in the same sequence run. The reference sequence for human APC was derived from Genbank Accession Number M74088.1. Data entry was performed blindly, by two independent observers.

From 72 of the 737 patients whose tumour samples contained sufficient DNA, one or more fragments of the MCR could not be amplified and these patients were not included in this study. The 665 patients, from whom MCR mutation analysis was complete, were comparable with the 819 CRC patients initially recognized within the cohort with respect to mean age at diagnosis, gender, family history of CRC, Dukes’ stage, tumour differentiation and sub-localization.

Validity and reproducibility of APC mutation analysis

In order to validate mutation analysis on paraffin-embedded tissue, 10 freshly obtained CRC specimens were each divided into two adjacent tissue blocks, one of which was fresh-frozen, and the other routinely fixed and embedded in paraffin. Two samples contained wild-type APC, three samples harboured a mutation and five samples had a polymorphism. These control specimens were obtained from patients who did not participate in the NLCS. Six CRC cell lines, i.e. HT29, Colo205, CaCo2, SW480, HCT116 and LOVO (obtained from the American Type Culture Collection, Rockville, MD) were used to check the specificity of mutation detection in the MCR of APC. The detection limit of mutation analysis was determined by mixing homozygously mutated DNA isolated from CaCo2 cells (C > T substitution at codon 1367) with increasing concentrations of the corresponding wild-type DNA sequence prepared from SW480 cells. Reproducibility of mutation analysis was established by subjecting 72 fragments, derived from 54 NLCS adenocarcinoma specimens twice to the complete mutation analysis procedure, from flank PCR of genomic DNA to sequencing of the fragments S1–S4.

Statistical analysis

The overall frequency of APC mutations as well as the type of mutation was computed for all 665 cases with respect to age at diagnosis, gender and family history of CRC. Since tumour sub-localization was unknown for 11 patients, 654 patients could be analysed for different mutation types with regard to tumour sub-localization. Differences in mean age at diagnosis were evaluated pairwise with the Mann–Whitney U test. The mean age at diagnosis of patients with an APC mutation, i.e. silent, missense or nonsense/frameshift mutations was compared with that of patients with wild-type APC. Differences in the categorical variables gender and family history of CRC, Dukes’ stage, tumour differentiation and sub-localization between patients without and with APC mutations and type of mutation were evaluated using the χ2-test. A P-value of 0.05 or less was considered to be statistically significant. All statistical procedures were performed with SPSS software (SPSS version 10.0, SPSS Chicago, IL).

Results

In the CRC cell lines HCT116, Colo205 and HT29, wild-type sequences were confirmed for the MCR of APC. Direct sequencing of the MCR of APC revealed a homozygous C > T substitution at codon 1367 in CaCo2 cells, a heterozygous C > T substitution at codon 1338 in SW480 cells and a deletion of C at codon 1430 in LOVO cells, as described previously (23). The effect of tissue processing as assessed in 10 specimens, showed that the mutation status of the MCR of APC for the paraffin-embedded block was identical to fresh unfixed tissue. The lowest level of detection was 5% mutant DNA in a background of wild-type DNA as found in three independent experiments. In 85% (61/72) of the fragments analysed for reproducibility assessment, the same APC mutation status was observed in duplicate experiments.

In 72% of tumours from CRC patients (479/665) a total of 978 mutations were observed in the MCR of the APC gene. The number of observed mutations per tumour ranged from one to eight mutations. In 215 tumours (45%) one mutation was found, in 137 tumours (29%) two mutations and in 127 tumours (27%) more than two mutations were observed. Of all mutations observed, 85% (833/978) were point mutations and 15% (145/978) were insertions and deletions (Table II). Point mutations were predominantly missense mutations (61%) and less frequently consisted of nonsense mutations (16%) or silent mutations (23%). Transitions were the most common type of point mutations (730/833), in large majority represented by C > T and G > A transitions (n = 352 and n = 286, respectively). Of C > T and G > A transitions 23% occurred at CpG dinucleotides. A polymorphism (G4497A), which does not result in an altered amino acid, was observed in 74% (493/665) of patients.

Eighty-seven per cent of frameshift mutations (126/145) were deletions (Table II). The length of the frameshift ranged from 1 to 5 bp for insertions and 1 to 49 bp for deletions. Generally, frameshift mutations would lead to serious alterations in the amino acid sequence downstream of the mutation.

<table>
<thead>
<tr>
<th>Type of mutation</th>
<th>Number of mutations</th>
<th>Silent mutationa</th>
<th>Missense mutationb</th>
<th>Mutation leading to truncationc</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mutation</td>
<td>833</td>
<td>192 (24%)</td>
<td>509(61%)</td>
<td>132 (16%)</td>
</tr>
<tr>
<td>Transition</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C &gt; T</td>
<td>352</td>
<td>63 (18%)</td>
<td>208 (59%)</td>
<td>81 (23%)</td>
</tr>
<tr>
<td>G &gt; A</td>
<td>286</td>
<td>62 (22%)</td>
<td>223 (77%)</td>
<td>1 (0%)</td>
</tr>
<tr>
<td>A &gt; G</td>
<td>63</td>
<td>24 (38%)</td>
<td>39 (62%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>T &gt; C</td>
<td>29</td>
<td>20 (69%)</td>
<td>9 (31%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Transversion</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A &gt; C</td>
<td>2</td>
<td>0 (0%)</td>
<td>2 (100%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>T &gt; G</td>
<td>5</td>
<td>0 (0%)</td>
<td>3 (60%)</td>
<td>2 (40%)</td>
</tr>
<tr>
<td>A &gt; T</td>
<td>11</td>
<td>4 (36%)</td>
<td>1 (9%)</td>
<td>6 (55%)</td>
</tr>
<tr>
<td>T &gt; A</td>
<td>20</td>
<td>16 (80%)</td>
<td>3 (15%)</td>
<td>1 (5%)</td>
</tr>
<tr>
<td>C &gt; A</td>
<td>9</td>
<td>1 (11%)</td>
<td>4 (44%)</td>
<td>4 (44%)</td>
</tr>
<tr>
<td>G &gt; T</td>
<td>38</td>
<td>1 (3%)</td>
<td>3 (8%)</td>
<td>34 (89%)</td>
</tr>
<tr>
<td>C &gt; G</td>
<td>11</td>
<td>1 (9%)</td>
<td>7 (64%)</td>
<td>3 (27%)</td>
</tr>
<tr>
<td>G &gt; C</td>
<td>7</td>
<td>0 (0%)</td>
<td>7 (100%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Insertiond</td>
<td>19</td>
<td>-</td>
<td>-</td>
<td>18 (90%)</td>
</tr>
<tr>
<td>Deletiond</td>
<td>126</td>
<td>-</td>
<td>-</td>
<td>126 (100%)</td>
</tr>
</tbody>
</table>

All 978 mutations detected in tumours from 665 sporadic CRC patients are represented.

aThe frequency of silent mutations is calculated by dividing the number of specific mutations (e.g. C > T transitions) resulting in silent mutations by the total number of that specific type of mutation.

bThe frequency of missense mutations is calculated by dividing the number of specific mutations (e.g. C > T transitions) resulting in missense mutations by the total number of that specific type of mutation.

cThe frequency of nonsense and frameshift mutations is calculated by dividing the number of specific mutations (e.g. C > T transitions) resulting in nonsense mutations by the total number of that specific type of mutation.

dOne insertion spanned 3 bp and would not result in frameshift or truncation.

eOne deletion spanned 2 bp and would result in frameshift but not truncation.
and also result in the introduction of a stop codon. However, one insertion spanned 3 bp and would not result in frameshift or truncation.

In the distribution of the truncating mutations several hotspots could be observed (Figure 1a). The frameshift mutations seem to cluster in the regions at codons 1350–1356, 1411–1419, 1465, 1485–1495 and at codon 1309, where an AAAAG deletion was detected in 26 tumours. A high frequency of nonsense point mutations was detected at codons 1294, 1306, 1328, 1367, 1378, 1406, 1429 and 1450. The large number of missense mutations was distributed rather evenly throughout the MCR of \( \text{APC} \) and did not show distinct hotspots (Figure 1b).

The 479 patients that harboured mutations were divided into different groups on the basis of having a tumour with either a wild-type or a mutant \( \text{APC} \) with various types of gene mutations (Table III). In total, 52% (248/479) of the patients with a mutation in the MCR of \( \text{APC} \), which corresponds to 37% of all patients (248/665), harboured at least one nonsense or frameshift mutation that would result in a truncated \( \text{APC} \) protein. Of patients with a truncating mutation, 59% (145/247) had more than one mutation leading to a change in the \( \text{APC} \) protein, i.e. another nonsense and frameshift mutation \((n = 27)\) or missense mutation \((n = 118)\). Forty per cent of the patients \((191/479)\) with a mutation in the MCR, corresponding to 29% of all patients \((191/665)\), harboured at least one missense mutation and no nonsense or frameshift mutations. Eighteen per cent of patients \((84/479)\) had two or more missense mutations. Of all patients, 6% \((40/665)\) had one or more silent mutations and no other type of mutation, and six of these patients had two silent mutations (Table III).

The mean age at diagnosis was lower for patients with mutation(s) in \( \text{APC} \) as compared with patients with wild-type \( \text{APC} \) (67.66 ± 4.21 versus 68.75 ± 4.32, respectively, \( P = 0.002 \)) (Table III). Detailed analysis of subgroups of mutations revealed that patients with silent mutations \((P = 0.008)\), missense mutations \((P = 0.065)\) and nonsense or frameshift mutations \((P = 0.002)\) were relatively younger when diagnosed with a colorectal tumour as compared with patients with wild-type \( \text{APC} \) (Table III). No differences were observed in the occurrence of \( \text{APC} \) mutations with respect to gender and family history of CRC \((P = 0.630)\) and tumour differentiation were observed (data not shown).

No statistically significant overall difference between patients without and with any \( \text{APC} \) mutation was observed with respect to tumour sub-localization. However, when considering specific types of mutations, patients with rectosigmoid and rectal tumours had a relatively higher frequency of

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**Fig. 1.** Distribution and frequency of 143 frameshift mutations and 132 nonsense mutations (a) and 509 missense mutations (b) observed in tumour material from 665 sporadic CRC patients. The \( x \)-axis schematically represents the codons of the \( \text{APC} \) MCR.
Characterization of most common types of truncating mutations according to sub-localization of the tumour in 654 sporadic CRC patients

<table>
<thead>
<tr>
<th>Sub-localization</th>
<th>Total CRC patients</th>
<th>Wild-type</th>
<th>Nonsense mutation</th>
<th>Frameshift</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>C &gt; T transition</td>
<td>G &gt; T transversion</td>
</tr>
<tr>
<td></td>
<td></td>
<td>(a,b,c,d)</td>
<td>(a,b,c,d)</td>
<td></td>
</tr>
<tr>
<td>Proximal colon</td>
<td>223</td>
<td>71 (32%)</td>
<td>15 (7%)</td>
<td>12 (5%)</td>
</tr>
<tr>
<td>Distal colon</td>
<td>206</td>
<td>56 (27%)</td>
<td>25 (12%)</td>
<td>7 (3%)</td>
</tr>
<tr>
<td>Rectosigmoid</td>
<td>74</td>
<td>18 (24%)</td>
<td>16 (22%)</td>
<td>8 (11%)</td>
</tr>
<tr>
<td>Rectum</td>
<td>151</td>
<td>38 (25%)</td>
<td>19 (13%)</td>
<td>6 (4%)</td>
</tr>
<tr>
<td>P-value</td>
<td></td>
<td></td>
<td>0.01</td>
<td>0.12</td>
</tr>
</tbody>
</table>

For patients with at least one nonsense or frameshift mutation. For 13 patients frameshift as well as C>T transversion were found. Patients with at least one nonsense mutation, but without any frameshift mutations. For one patient a C>T transition and a G>T transversion was found. This patient was included in both groups. For one patient a C>T transversion and a G>T transversion was found. This patient was included in both groups. P-values were calculated for pairwise comparisons of distribution of sub-localization for patients with at least one C>T transition (n = 75), patients with at least one G>T transversion (n = 33) or those with at least one frameshift mutation (n = 137) to patients with wild-type APC. P-value could not be interpreted due to lack of sufficient patients in respective groups.

Table IV.

APC mutations in sporadic colorectal carcinomas

Discussion

The occurrence and type of somatic mutations in the MCR of the APC gene was evaluated in 665 tumour samples from an unscreened, well-defined group of incident CRC patients from The Netherlands (age at diagnosis between 57 and 67 years). Seventy-two per cent of patients (479/665) harboured a total...
of 978 mutations in the APC MCR. In particular, we observed a large number (n = 508) of missense point mutations. Mutations that would lead to protein truncation were found in 37% of patients (248/665). Patients with rectosigmoid and rectum tumours relatively more frequently harboured C > T nonsense mutations and deletions and insertions that would lead to protein truncation as compared with patients with proximal and distal colon tumours.

In this study, DNA from archival tumour tissue was used. As this formalin-fixed, paraffin-embedded tissue contains highly fragmented genomic DNA, gene analysis can be difficult. The analysis of APC mutations is based on nested amplification and direct sequencing of purified PCR fragments, a highly sensitive and specific detection method. Using this method on archival tissue yields valid results, as shown in the identical mutations status of fresh tissue and paraffin-embedded tissue. Moreover, most mutations leading to truncation of the APC protein observed in this study were also reported in an APC database (http://www.umd.necker.fr:2008/).

As a result of fragmentation of DNA from archival sources, a protein truncation test or similar methods are not feasible, as these techniques require fully intact DNA strands. In other studies, protein truncation test (7), in vitro synthesized protein/in vitro transcription and translation assay (19,24) were used, thereby selectively identifying truncating mutations. Although these methods provide conclusive information on the functional aberrations in APC, i.e. truncating mutations, these do not yield information on the occurrence of other than truncating mutations. Indeed, the large number of mutations detected in our study is mainly due to the high prevalence of other than truncating mutations.

Techniques used for mutation screening such as single-strand conformational polymorphism (8,16-18,21,31), RNase protection assay (7) or denaturing gradient gel electrophoresis (31) show differences in sensitivity and/or specificity of mutation detection. In particular, the interpretation of single-strand conformational polymorphism assays is difficult and its sensitivity is relatively low (32). Omission of a screening assay prior to sequence analysis may therefore partially explain the large number of mutations found in this study.

We observed multiple mutations in 55% of adenocarcinomas, ranging from two to eight mutations per tumour. Possibly, this reflects the occurrence of mutations in both alleles of the APC locus. Since APC is a tumour suppressor gene, more than one inactivating mutation would be necessary to result in loss of APC function in the cell. However, we are unable to distinguish different alleles in our analyses. Another explanation for multiple mutations within a tumour may be that it is a reflection of tumour heterogeneity. In a recent study of advanced colorectal tumours, heterogeneity in the mutational status of p53 and K-ras within the same tumour was demonstrated (33). We performed macrodissection on the samples that were analysed, as a result of which we may have included different subclones of a tumour that possibly harbour different mutations.

Another plausible cause of multiple mutations is a defect in the DNA repair systems. Inherited variants of the base excision repair gene MYH were found to give rise to G > T and C > A transversions in a family that is affected with multiple colorectal adenomas and carcinoma (34). Recently, these inherited variants of MYH have also been observed in a population-based series of CRC patients (35), suggesting that a proportion of the 46 patients that harboured a G > T or C > A transversion in our study may be due to inherited MYH mutations. Defects in the mismatch repair genes hMLH1 and hMSH2, resulting in mismatch repair deficiency is found in hereditary non-polyposis coli and is also found in ~15% of sporadic colorectal tumours. However, reported results are inconsistent as to whether mismatch repair deficiency is an alternative pathway in colorectal tumours with intact APC function (36,37) or that it independently gives rise to an increased frequency of APC mutations (38-40).

The majority of observed mutations were point mutations, 61% of which give rise to substitution of one amino acid. The relevance of missense mutations in APC is not yet understood. It is unclear which of these changes would affect the structure and function of the APC protein and whether such an alteration would lead to selective advantage of tumour cells and tumour growth. Intriguingly, 52% of patients with truncating mutations also had one or more concurrent missense mutation(s). If the occurrence of these missense mutations is the reflection of a biallelic event, this may indicate involvement of APC missense mutations in colorectal tumourigenesis.

Twenty-three per cent of the point mutations would not lead to protein truncation or an altered amino acid. In addition, a polymorphism (G4497A), which does not result in an altered amino acid was observed in 74% (493/665) of patients. This polymorphism has also been described recently in a series of adenoma samples from Dutch patients (31), which suggests that this polymorphism represents a wild-type DNA sequence in APC in the Dutch population.

Considering all mutations that are detected in the MCR, only 28% (276/978) would lead to a truncated APC protein, half of which are represented by point mutations. This is in contrast with previous reports that up to 98% of mutations would lead to a truncated APC protein, and only one-third of these are caused by point mutations (25).

Only 37% of patients (247/665) harboured mutations that would lead to a truncated APC protein. Considering the general idea that most colorectal tumours follow a molecular pathway involving APC, our observed frequency seems low. It is, however, in keeping with the frequency of 34% truncating mutations found in the MCR in another Dutch population-based case-control study (21). The MCR spans several 20 aa repeats, which form the β-catenin binding sites and therefore the MCR represents a functionally important domain of the APC gene. According to several reports 68-77% of the somatic mutations in APC are found in the MCR, which represents <10% of the APC coding region (5,7,8). We are unable to make any predictions of the occurrence of mutations in the complete APC gene, since our mutation analysis was restricted to the MCR of APC.

Other explanations for the relatively low frequency of truncating mutations of APC in the colorectal tumours observed here, are that these tumours may have arisen through other genetic or epi-genetic events. APC is a key player in the Wnt pathway. Inactivating mutations that cause loss of β-catenin binding and degradation sites on the APC protein, would lead to increased levels of intra-nuclear β-catenin (9,22). However, it has also been shown that activating mutations in the CTNNB1 gene can lead to stabilization and accumulation of the β-catenin protein (41,42), thereby circumventing the necessity for mutations in APC to activate the Wnt pathway. Hypermethylation of the promotor region of APC constitutes an alternative mechanism for gene inactivation. This was found to occur in 18% of primary sporadic colorectal carcinomas (43), and in 39% of a sample of 122 CRC patients from...
our study, although these cases were selected on high and low methyl donor intake (44).

FAP tumours generally arise at a young age through a germ-line mutation in the APC gene. Our APC gene mutation analysis is based on a relatively large series of unselected, incident CRC patients, who were between 55 and 69 years of age at baseline and have developed a first colorectal tumour since. This strongly suggests that the mutations observed in this study are acquired and therefore of somatic nature. Moreover, no significant differences in family history of CRC between patients without and with APC mutations were observed, which also argues against germline mutations. The observation that there were no statistically significant differences in occurrence and type of APC mutations with respect to Dukes’ stage and tumour differentiation support the hypothesis that APC gene mutation is an early event in colorectal tumourigenesis.

The differences in the occurrence of specific types of mutations in colon versus rectosigmoid and rectum cancer shown here, suggests a different aetiology of tumourigenesis in the different sub-localizations and it may also reflect the exogenous origin of mutations. This is supported by a recent report of K-ras mutations in CRC tissue of patients from our study, in which mutations in K-ras were also more frequently observed in rectum tumours as compared with rectosigmoid and colon tumours (29). The data with respect to the rectosigmoid have to be regarded with some caution as the rectosigmoid is a more clinically applied term rather than an anatomically defined transitional zone between colon and rectum (29). When rectosigmoid tumours were excluded from the analyses, both frameshift and C > T mutations that would result in protein truncation occurred relatively more frequently in the rectum as compared with proximal and distal colon. However, the asymmetry of C > T nonsense mutations with regard to tumour sub-localization was less pronounced.

In conclusion, a large number of mutations was found in the MCR of the APC gene, in particular, we observed many missense point mutations, more than reported previously. Missense mutations need further exploring with regard to their role in APC function and colorectal tumourigenesis. Patients with a rectosigmoid or rectum tumour relatively more frequently have a truncating C > T transition or frameshift mutation as compared with patients with a proximal or distal colon tumour. The pattern of APC mutations observed in the different sub-localizations of the colorectal tract suggests a different aetiology for tumour site within the large bowel.

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