Human Cancer Biology

Functional, Genetic, and Epigenetic Aspects of Base and Nucleotide Excision Repair in Colorectal Carcinomas

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Abstract

Purpose: DNA repair capacity (DRC) is a determinant not only of cancer development but also of individual response to therapy. Previously, altered base and nucleotide excision repair (BER and NER) have been described in lymphocytes of patients with sporadic colorectal cancer. We, for the first time, evaluate both excision repair capacities in human colon biopsies to study their participation in colorectal tumorigenesis.

Experimental design: Seventy pairs of tumor and adjacent healthy tissues were analyzed for BER- and NER-specific DRC by a comet repair assay. Tissue pairs were further compared for expression levels of a panel of 25 BER and NER genes complemented by their promoter methylation status.

Results: We observed a moderate increase of NER-DRC ($P = 0.019$), but not of BER-DRC in tumors. There was a strong correlation between both tissues for all investigated parameters ($P < 0.001$). However, 4 NER ($CSB$, $CCNH$, $XPA$, $XPD$) and 4 BER ($NEIL1$, $APEX1$, $OGG1$, $PARP1$) genes showed a 1.08- to 1.28-fold change difference in expression in tumors ($P < 0.05$). Individual gene expression levels did not correlate with overall DRC, and we did not detect any aberrant methylation of the investigated genes.

Conclusions: Our complex analysis showed that tumor cells are not deficient in BER and NER, but rather follow patterns characteristic for each individual and are comparable with adjacent tissue. Alteration of excision repair pathways is not a pronounced event in colorectal carcinogenesis. This study shows the feasibility of DRC evaluation in human solid tissues, representing a complex marker of multigene DNA repair processes. Clin Cancer Res; 18(21); 1–10. ©2012 AACR.

Introduction

Despite long and intensive research, colorectal cancer (CRC) has, at present, one of the highest rates of incidence and mortality worldwide (1). With the exception of KRAS mutational status for selection of biologic therapy, no predictive or prognostic biomarker has yet been validated (2, 3). Keeping in mind the importance of DNA repair in the disease development and therapy response, it seems reasonable to consider a categorization of tumors based on DNA repair characteristics. Such an approach would require a panel of functional biomarkers that can define the DNA repair status of the target tissue (4).

DNA repair is a defensive mechanism that copes with ubiquitous DNA damage occurring as a consequence of cellular metabolism or from exogenous exposure. Moreover, a large number of antineoplastic drugs impart their effect by DNA disruption. Therefore, an effective DNA damage response is essential for the maintenance of genome stability in normal cells, whereas in malignant cells, the suppression of DNA repair would, presumably, increase the effectiveness of chemotherapy through damage accumulation and consequent apoptosis. On the basis of the evidence so far, mismatch repair (MMR) defines the strongest link between DNA repair and CRC. A subset of hereditary and sporadic CRC shows genetic or epigenetic defects in MMR that are manifested by microsatellite instability. The phenomenon may also be accompanied by epigenetic instability, characterized by a high degree of aberrant methylation of CpG islands. Germline, and not somatic inactivation of base excision repair (BER) gene
Translational Relevance

DNA repair influences cancer development and sensitivity to treatment. Categorization of tumors according to their DNA repair characteristics can be relevant for personalized therapy, but functional assays to define DNA repair status of target tissue are needed. In this respect, we optimized BER- and NER-specific assays and showed their reliability and applicability to high-throughput screening of human solid tissues. The complexity of multigene DNA repair processes is comprehensively reflected by functional analysis of overall DNA repair capacity and should be recommended for DNA repair investigations.

Analysis of BER and NER with a functional, genetic, and epigenetic approach confirmed that colorectal carcinomas are only moderately altered in these repair pathways as compared with adjacent healthy tissue. Consistency of our and previously reported observations suggests that excision repair is not a factor contributing to the malignant transformation, but rather might contribute to chemoresistance and growth advantage of tumor cells.

MUTYH, causes polyposis that transforms almost always into carcinoma (5). No study has to date reported any defect in nucleotide excision repair (NER) in any form of CRC.

A potential role of both BER and NER in the pathogenesis of sporadic CRC is plausible. Colon epithelium is one of the most constantly regenerated tissues in the body. It therefore has increased vulnerability to a variety of mutagens present in the bowel contents or in the blood. Cigarette smoking, alcohol, overcooked red meat, or processed saturated fat have been established CRC risk factors through the generation of strong DNA-reactive compounds (6). Among other agents, benzo[a]pyrene, aromatic amines, alkylating agents, or reactive oxygen species represent substrates for excision repair. Even detoxified carcinogens can interact with mucosal DNA as carcinogen-activating enzymes have been detected in colon epithelium and in colonic bacteria (7–9). Furthermore, the well-known role of chronic inflammation in colon carcinogenesis is explained by enhanced epithelial cell turnover, accompanied by sustainable oxidative stress contributing to neoplastic transformation (10). Moreover, both pathways are plausibly expected to influence the effectiveness of anticancer therapy. The mainstays of CRC treatment are regimes based on 5-fluorouracil and/or oxaliplatin. The NER pathway is known to be essential for the removal of platinum adducts; BER, on the other hand, is involved in response to 5-fluorouracil (11, 12).

In general, there is limited information available on the mechanisms of BER and NER in sporadic CRC. No somatic genetic alteration of genes involved in either of the excision repair pathways has been identified. The investigations failed to prove any clear relationship between common genetic variants and the risk of sporadic CRC (13, 14). Aberrant promoter methylation of BER and NER genes have already been reported in other types of cancer, but not studied in CRC (15). An investigation of expression profiles of some BER and NER genes in tumor tissue did provide preliminary characterizations (16). Previous studies carried out on peripheral blood mononuclear cells (PBMC) showed suppressed BER and NER capacities in patients with CRC compared with healthy individuals (17–19). However, the validity of blood as a surrogate for cancer tissue to estimate DNA repair capacity (DRC) remains disputable.

The aim of the present study was to compare BER- and NER-DRC in different tissue specimens—colorectal adenocarcinomas, adjacent healthy mucosas, and peripheral blood cells from 70 newly diagnosed patients with CRC to investigate: (i) tissue specificity of the DNA repair processes and (ii) possible alteration of both repair pathways in colorectal carcinogenesis. DRCs analyses were carried out by comet repair assays, modified for measurement of DRC in human solid tissues. The expression levels of a panel of 8 BER and 17 NER genes were also studied and complemented by the evaluation of aberrant promoter methylation in their promoter regions.

Materials and Methods

Study patients and collection of biologic specimen

The study included seventy patients with sporadic CRC who underwent surgical resection. Patients were recruited between 2009 and 2011 at the Thomayer Hospital (Prague, Czech Republic), the General University Hospital (Prague, Czech Republic), and Teaching Hospital and Medical School of Charles University (Pilsen, Czech Republic). All patients signed informed consent. Ethics approval was granted by the appropriate committees at the 3 hospitals. The group of patients included 53 men and 17 women with a mean age of 66.2 (±10.6). The clinical stage of patients at diagnosis was classified according to the tumor–node–metastasis (TNM) system. Seven patients were diagnosed with pathologic stage I (10%), 29 as stage II (41.4%), 15 as stage III (21.4%), and 19 as stage IV (24.7%). All patients had adenocarcinomas; 44 patients had tumor localized in the colon (62.9%) and 26 in the rectum (37.1%). In 12 (17.2%) patients, tumors were of well-differentiated grade, in 47 (67.1%) moderately differentiated, and in 11 patients (15.7%) poorly differentiated. Eleven patients with rectal cancer (15.7%) received neoadjuvant therapy before surgery. Tumor tissue and adjacent healthy mucosa (5–10 cm distant from the tumor) were resected from all patients. Samples were deep frozen immediately after removal. A day before surgery, peripheral blood was also drawn from a subset of patients and was stored at 4°C no longer than 3 hours before being processed. Because of various logistical reasons, not all patients could be analyzed for all the studied parameters. Therefore, each particular analysis is further specified for actual number of cases for whom analysis was carried out.
Isolation of nucleic acids and proteins from blood and tissues

**Extraction of nucleic acids.** DNA from blood was isolated by a standard phenol/chloroform method. Before tissue processing, histologic analysis was carried out to assess the proportion of tumor cells in tumor tissues and to rule out the presence of neoplastic cells in the normal mucosal tissues. Briefly, samples were embedded in optimal cutting temperature compound (Sakura Finetek), and cut with a Leica CM 1850 cryostat. Five-micrometer thick serial sections were fixed in 90% ethanol on microscope slides and stained with 1% cresyl violet acetate (Sigma-Aldrich) and dried, and inspected using a Leica DM6000 microscope. Tissue samples were subsequently homogenized in the MagNA Lyser (Hoffmann-La Roche). AllPrep DNA/RNA mini kit (Qiagen) was used to isolate homogenized in the MagNA Lyser (Hoffmann-La Roche). AllPrep DNA/RNA mini kit (Qiagen) was used to isolate nucleic acids.

**Extraction of proteins.** PBMCs were separated on Histopaque-1077 (Sigma-Aldrich), counted, and evaluated by trypan blue exclusion. Cells were suspended in freezing medium [RPMI-1640, 20% FBS, 0.2% penicillin/streptomycin, 10% dimethyl sulfoxide (DMSO), Sigma-Aldrich] and frozen at −80°C. Tissues were weighed and ground while frozen. Furthermore, 50 μL of buffer A [45 mmol/L HEPES, 0.4 mmol/L KCl, 1 mmol/L EDTA, 0.1 mmol/L DTT, 10% glycerol, pH 7.8] was added to every 50 mg of ground tissue or 5 × 10⁶ of PBMC. Samples were vortexed, snap frozen, and thawed again, and 15 μL of 1% Triton X-100 in buffer A was added per each 50 μL. Protein concentration was measured by a fluorescamine assay (Sigma-Aldrich), with a NanoDrop 3300 (Thermo Scientific).

**In vitro DNA repair assays**

**In vitro repair assays, adopted from Langie and colleagues (20, 21),** were implemented using a 12-gel slide format (22). Briefly, protein extracts were incubated with 2 types of substrate DNA, containing artificially induced lesions known to be repaired specifically by BER or NER pathway. Levels of DNA strand breaks, generated during removal of lesions, reflect the repair activity of the extract.

**Substrate DNA.** For BER, human PBMCs were treated with 2 μmol/L Ro 19-8022 (Hoffmann-La Roche) for 5 minutes, and irradiated by a 500 W halogen lamp at a 33-cm distance to induce 8-oxoguanines. For NER, TK6 cells were irradiated with 5 J/m² of UVC (50 s at 0.1 J/m²) to generate cyclobutane pyrimidine dimers and 6–4 photoproducts. Untreated PBMCs and TK6 cells were prepared in parallel. Cells were aliquoted at 0.5 × 10⁶ in 1 mL of freezing medium (see above) and frozen. Before each experiment, cells were thawed by adding 1 mL of cold PBS, spun at 400 g for 5 minutes at 4°C, and resuspended in 1 mL of PBS. Eighty microlitres of the cell suspension was mixed with 260 μL of 1% LMP agarose to reach the desired concentration of cells. Using a multidispensing pipette, 12 gels per 5 μL agarose were plated on each microscope slide. Cells embedded in agarose underwent lysis for 1 hour in 2.5 mol/L NaCl, 100 mmol/L EDTA, 10 mmol/L Tris, 250 mmol/L NaOH, 1% Triton X-100, pH 10. Before incubation with protein extracts, slides were washed twice for 5 minutes with buffer B [45 mmol/L HEPES, 0.25 mmol/L EDTA, 0.3 mg/mL bovine serum albumin (BSA), 2% glycerol, pH 7.8], and placed in incubation chambers (Severn Biotech; ref. 22).

**Protein extracts.** Extracts were diluted into protein concentration of 3 mg/mL in buffer A in the final volume of 50 μL and mixed with 4 volumes of buffer B. For the NER-specific assay, 2.5 mmol/L of adenosine-5’-triphosphate was added. Thirty microliters of extract was pipetted per agarose gel.

**BER-specific assay.** Each extract was incubated with Ro 19-8022–treated and untreated PBMCs to determine non-specific endonuclease activity of the extract. This was used for background correction for each sample. Incubation time was 20 minutes at 37°C in a humid environment. Formamidopyrimidine DNA glycosylase was used as a positive control and, for a negative control, substrate gels were incubated with 1:4 buffer A + buffer B. Each experimental point was carried out in duplicates. A total of 5 μmol/L PARP inhibitor ABT-888 (Selleckchem) was added to the extract to test the effect of inhibition of postincision phase of BER. Reproducibility of the assay was tested by independent repeat of measurement for randomly chosen 25 samples.

**NER-specific assay.** Each extract was, in parallel, incubated for 30 minutes with UV-treated and untreated TK6 cells and used for background subtraction. UV substrate incubated with T4 endonuclease V was used as positive control and 1:4 buffer A + buffer B as negative control. Aphidicolin (DNA polymerase delta inhibitor; Sigma-Aldrich) at a concentration of 2.5 μmol/L was added to the extract to test the effect of DNA resynthesis inhibition. Reproducibility of the assay was tested by independently repeated measurement of randomly chosen 25 samples.

**Single-cell gel electrophoresis.** After the incubation period, the protocol followed was the same as previously described for the comet assay (23). In brief: slides were treated for 20 minutes under alkaline conditions (300 mmol/L NaOH, 1 mmol/L EDTA, pH 12) to allow DNA denaturation and subsequently electrophoresed for 20 minutes, at 25 V and 300 mA. Washing with PBS, H₂O, and ethanol followed, each for 10 minutes. Slides were stained with SybrGold (Invitrogen) and evaluated with a Nikon fluorescence microscope. Comets were scored exclusively by one person. DRC data were evaluated as tail DNA% (%T).

Gene expression profiling

**Gene selection.** A panel of BER and NER genes (Supplementary Table S1) was selected from the list of all DNA repair genes organized according to pathways, which are available online (24).

**Sample preparation.** Total RNA was measured on ASP-3700 Spectrophotometer (Avans-Biotechnology) for quantity and OD_{260/280} Fatio, which was between 1.8 and 2.0. RNA integrity number (RIN) was checked using Agilent Bioanalyzer 2100, with RNA 6000 Nano Assay (Agilent Technologies). Each pair of tumor/healthy tissue did not differ by more than ±2 RIN units. cDNA was synthesized...
from 1 μg of RNA using a RevertAid First strand cDNA synthesis kit (MBI Fermentas) using random hexamers and following the manufacturer’s instructions. All samples were tested to exclude possible inhibition of the quantitative PCR (qPCR) reaction by spiking with DNA from an extraction control kit (Primer Design). cDNA was diluted to 10 ng/μL and preamplified for 18 cycles on a Bio-Rad CFX96 Real Time PCR Instrument (Bio-Rad) with TaqMan Preamp Master Mix (Applied Biosystems) according to the manufacturer’s protocol.

High-throughput real-time PCR. qPCR was conducted using the high-throughput platform BioMark HD System (Fluidigm). Five μL of Fluidigm sample premix consisted of 1 μL of 20× diluted preamplified cDNA, 0.25 μL of 20× GE sample loading reagent (Fluidigm), 2.5 μL of TaqMan universal mastermix II without UNG (Life Technologies), and 1.25 μL of RNase/DNase-free water. Each sample premix was combined with 5 μL FAM-MGB assays (Primer Design) at a final concentration of 300 nmol/L and 2.5 μL 2× Assay loading reagent (Fluidigm). The reaction volume for a single qPCR reaction was 6.7 nL. Thermal conditions for qPCR were: 95°C for 10 minutes, 45 cycles of 95°C for 15 seconds, and 50°C for 60 seconds. TOP1 and 18S rRNA were reference genes selected from a geNorm reference genes selection kit (Primer Design) by Normfinder (GenEx Enterprise).

qPCR data processing. Data were collected from 2 GE Dynamic Arrays 96.96 (Fluidigm) and preprocessed in GenEx Enterprise software (MultiD). Interplate calibration was conducted and the technical replicates were averaged. Cut-off value for Cq was set at 25 and values higher than that were replaced by the Cq value of 25. The Cq 25 measured in BioMark system would approximately correspond to Cq 35 at the conventional qPCR cyclers (25). When more than 12% of the data were missing for each sample/gene due to a very low expression and low fluorescence signal, the particular sample/gene was removed from the dataset. Because of this selection, 6 repair genes (CSA, MMST19L, POLB, UNG, XPC, and XRCC1) were excluded from analyses. The rest of the missing data was replaced through an interpolation, that is, the missing data were replaced with values calculated from the other genes in the group of selected samples by GenEx algorithm. Data were normalized to reference genes, recalculated to relative quantities with the lowest expression set to 1, and transformed to log2 scale. This format was used for visualization of data in plots and for further statistical analysis.

Promoter CpG islands methylation profiling

Methylation-specific PCR. A prediction of CpG island site within the promoter region of target genes was carried out by screening with CpG Islands Searcher (26). Genomic DNA was treated with sodium bisulfite using the Epitect Whole Bisulfiteome Kit (Qiagen). Methylation-specific PCR (MSP) analysis of bisulfate-converted (BC) DNA was conducted using the Epitect MSP kit, following the producer’s instructions. Primers specific to methylated and unmethylated BC DNA for OGG1, ERCC1, and XRCC1 genes were designed by applying MethPrimer algorithm (27) and produced by Sigma-Aldrich. Previously described primers were used for XPA, XPC, XPD, and XPG genes (28; Supplementary Table S2).

Methylation-sensitive high resolution melting. Methylation-sensitive high resolution melting (MS-HRM) was conducted to verify MSP-positive samples. Primers specific for BC DNA (Supplementary Table S3) were designed using Methyl Primer Express Software v1.0 (Applied Biosystems). Real-time PCR followed by HRM was carried out with the high-performance Eco Real-Time PCR system (Illumina). The reaction in a final volume of 10 μL consisted of 10 ng of template, 1 × EpiTect HRM Master Mix (Qiagen), and 300 nmol/L of each primer. PCR conditions were: 95°C for 5 minutes, 50 cycles at 95°C for 10 seconds, 57°C for ERCC1, 56°C for XPC, and 58°C for OGG1 for 20 seconds, and 72°C for 10 seconds. HRM thermal profile was set up according to the manufacturer’s recommendations (Qiagen).

Statistical analysis

Statistical analysis was conducted by IBM SPSS Statistics 18, GenEx Enterprise and SAS 9.2 software. All investigated parameters showed normal distribution in the study population (Kolmogorov–Smirnov test), with the exception of expression data, which were logarithmically transformed. Principal component analysis of the expression analysis indicated that data from different hospitals needed to be adjusted by the vector error correction model according to the Granger representation theorem. After processing, 2-tailed t test or ANOVA for differences between groups were used. Correlations were determined by a Pearson test. All statistical tests were conducted at a 95% confidence level; expression data were corrected for multiple testing analyses according to the method of Dunn–Bonferroni (significant P value after correction was 0.0021).

Results

BER-specific DNA repair capacity

DRCs were measured in matched pairs of tumor and adjacent healthy tissue of all 70 patients. For 28 individuals, DRC were simultaneously assessed in PBMCs. The BER-specific DRC assay (BER-DRC) showed a high degree of reproducibility, as repeated analysis in 25 samples showed Pearson’s correlation coefficient of \( R = 0.75 \). The presence of PARP inhibitor in the reaction did not influence the incision activity of the 8 analyzed extracts (with or without inhibitor: \( R = 0.92 \)).

The difference in BER-DRC between tumor and healthy tissues was not statistically significant (mean ± SD: 17.7 ± 8.3 vs. 15.7 ± 9.6%; \( P = 0.22 \)). However, we observed that PBMCs showed significantly decreased ability to repair oxidative damage compared with healthy or tumor tissues (8.4 ± 6.3 vs. 16.2 ± 10.4 and vs. 17.1 ± 8.9%; respectively, \( P = 0.001 \)). There was a strong correlation in BER-DRC between tumor and healthy epithelium (\( R = 0.57, P < 0.001 \)). Similarly, a significant correlation was observed for BER-DRC between PBMC and healthy epithelium (\( R = 0.48, P = 0.009 \)), but not between PBMC and tumor tissue.
Results for BER-DRC are presented in Fig. 1. Sex and age did not influence BER-DRC, and nor did the localization of tumors; DRC values were 18.4 ± 9.0%T for colon and 16.7 ± 9.2%T for rectum (P = 0.45). No statistical significance was observed in BER-DRC based on pathologic stage of the tumors. For TNM stage 1 and 2 combined, we observed BER-DRC of 16.2 ± 10.2%T (N = 36), whereas for diffused stages 3 and 4, it was 19.4 ± 7.4%T (N = 34), P = 0.14. Distribution of the BER-DRC in different grades of the tumors was 16.2 ± 9.3%T for grade 1, 17.7 ± 9.1%T for grade 2, and 19.6 ± 8.8%T for grade 3, P = 0.66.

NER-specific DNA repair capacity

We also observed high reproducibility in DRC assay for NER (N = 25, R = 0.62), and the incision activity of the extracts did not change in the presence of the DNA polymerase inhibitor (N = 8, R = 0.84).

Tumor tissues exhibited significantly higher NER-DRC than healthy epithelia (20.2 ± 11.6 vs. 15.4 ± 10.8%T, P = 0.019). The lowest NER-DRC was detected in PBMCs compared with both healthy and tumor tissues (6.1 ± 5.0 vs. 17.7 ± 14.2 vs. 24.3 ± 13.0%T, P < 0.001). Similarly to BER-DRC, a correlation between tumor and healthy tissues in NER-DRC was observed (R = 0.58, P < 0.001), and also between PBMCs and healthy tissues (R = 0.51, P = 0.006), and PBMC and tumor tissues (R = 0.47, P = 0.011). Results for NER-DRC are presented in Fig. 2. Interestingly, BER-DRC and NER-DRC showed a mutual correlation in healthy epithelium (R = 0.32, P = 0.007; Fig. 3).

Sex and age did not significantly influence NER-DRC, which was also very similar irrespective of tumor localization, with values of 20.0 ± 12.9%T in the colon and 20.5 ± 11.4%T in the rectum (P = 0.89). Tumors in noninvasive stages TNM 1 and 2 exhibited 22.0 ± 12.2%T, whereas 18.3 ± 12.3%T was detected in more diffused TNM stages 3 and
4, \( P = 0.22 \). We did not observe any apparent effect of tumor differentiation on NER-DRC. Well-differentiated tumor tissues had NER-DRC of 20.3 \( \pm \) 12.6\%T, tumors with moderate differentiation 18.9 \( \pm \) 11.2\%T, and those with poor differentiation 25.5 \( \pm \) 15.9\%T \( (P = 0.29) \).

Gene expression profiling
Successful expression analyses were conducted in 53 pairs of tumor/healthy tissue. In total, expression levels were determined for 8 BER and 17 NER genes (listed in Table 1). We observed a statistically significant correlation in expression levels of all genes between paired tumor and healthy tissues (overall \( P < 0.001 \)). We found decreased transcription levels of BER genes NEIL1 and OGG1 and NER genes CSB, CCNH, and XPA in tumor tissues compared with controls. In contrast, APEX1, PARP1 (BER), and XPD (NER) showed higher expression in tumor tissues than healthy tissues. Although differences in expression of DNA repair genes between the healthy mucosa and tumor tissue were small (1.08–1.28-fold), they were significant \( (P < 0.05) \). Individual gene \( P \) values and fold changes of transcript levels in tumors relative to healthy tissues are reported in Table 1. No correlation was detected between DRC and individual gene expression levels, either for BER or NER. Expression of studied genes was not influenced by any recorded clinic pathologic parameter. The expression pattern of excision repair genes was similar irrespectively of tumor localization in colon or rectum and no modifying effect was exerted by TNM stages and tumor differentiation.

Promoter CpG islands methylation profiling
CpG promoter methylation status of OGG1, ERCC1, XPA, XPC, XPD, XPG, and XRCC1 was evaluated in DNA from 70 tumor samples. MSP showed aberrant methylation of XPC, ERCC1, and OGG1 in 24, 56, and 51\% of tumors, respectively. However, these findings were not confirmed by MS-HRM analysis, which clearly showed only nonmethylated
cytosines in the analyzed promoter sequences for all 3 genes (Fig. 4).

Discussion

In this study, we investigated the possible involvement of BER and NER alterations in the sporadic colorectal carcinogenesis by comparing tumors with adjacent healthy tissues in 70 patients. Both repair pathways are fundamental for the removal of a vast spectrum of DNA lesions and they process DNA damage in a broadly similar way by cleaving the damaged site and leaving DNA breaks behind. These breaks reflect the excision phase of the repair process that has been recognized as the rate-limiting step (29), and is measurable by the well-established comet assay technique. To assess DRC, diversely modified comet-based assays have been developed (30). On the basis of recently published methodologic reports on BER- (20) and NER-specific assays (21), in this study, we used an in vitro repair assay, adapted for the evaluation of DRC in solid tissues. Langie and colleagues developed in vitro assays to measure DRC in animal tissues. We, for the first time, applied that approach to investigate DRC in human colon biopsies after carrying out the necessary optimization and validation experiments. Reproducibility was tested by repeating the assay on 25 duplicate samples at different times. Both BER- and NER-specific DRC assays showed high degrees of reproducibility. We also tested whether the results truly reflect the excision process of DNA repair and are not influenced by ongoing resynthesis and ligation. There was no detectable difference between DRCs of extracts with or without addition of inhibitors of polymerization; ABT-888, specific for BER, and aphidicolin for NER. To process a large number of samples, we used a medium-throughput 12-gel format (22), which proved to be efficient and gave consistent and reliable results. The assay is versatile and suitable for application in large molecular epidemiologic studies. In addition, the assay seems to be sensitive enough to detect the substantial interindividual variability of both DNA repair capacities, with yet unknown biologic relevance as this is one of a few pilot reports on this topic.

In a comparison of 70 matched sets of tumor/normal tissues, we found a significant increase of 24% in NER-DRC in tumors. The differences in BER-DRC between tumor and healthy tissues were not significant. Interestingly, we observed significant correlations of both DRCs as well as significant differences are in bold, differences significant after Dunn–Bonferroni correction ($P < 0.0021$) are underlined.

In Table 1, we observed significant correlations of both DRCs as well as yet unknown biologic relevance as this is one of a few pilot reports on this topic. In a comparison of 70 matched sets of tumor/normal tissues, we found a significant increase of 24% in NER-DRC in tumors. The differences in BER-DRC between tumor and healthy tissues were not significant. Interestingly, we observed significant differences in expression level of BER and NER genes in tumor relative to healthy epithelium.

Table 1. Fold change differences in expression level of BER and NER genes in tumor relative to healthy epithelium

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NOTE: Significant differences are in bold, differences significant after Dunn–Bonferroni correction ($P < 0.0021$) are underlined.

![Figure 3. Correlation between BER-DRC and NER-DRC in 70 healthy colorectal tissues.](image-url)
authors reported, in agreement with our findings, a strong correlation between DRCs in 2 tissues; however, NER activity in tumor tissue was increased \( (P = 0.015; \text{ref. 31}) \). Several studies have inferred higher BER or NER capacity in tumors via an indirect approach of measuring the steady-state level of DNA damage, assuming that a low damage level reflects a high repair rate. All those studies reported a significantly lower level of specific damage in DNA from tumors, presumably explained by upregulation of repair genes (32–34). No study has found evidence for deficiency of excision repair pathways in tumors. The consistency of the listed observations might lead to the conclusion that excision repair is not a factor contributing to malignant transformation, but most likely it is contributing to the growth advantage of existing tumor mass by decreasing the vulnerability to DNA damage accumulation normally followed by cell death. In this regard, Sarasin and Kauffmann hypothesized that relative genetic stability given by upregulation of DNA repair might be associated with the higher ability of cells to metastasize (35). The observed positive correlation between BER and NER in the healthy tissue, although disrupted in the tumors, is not so surprising in the light of still growing evidence of functional cross-talk between BER and NER factors. It has been documented that the XPC-HR23B complex regulates the loading and turnover of OGG1 (36). It also seems that, in the case of HR23B complex regulates the loading and turnover of NER factors. It has been documented that the XPC-HR23B complex regulates the loading and turnover of OGG1 (36). It also seems that, in the case of HR23B complex regulates the loading and turnover of OGG1 (36). It also seems that, in the case of HR23B complex regulates the loading and turnover of OGG1 (36). It also seems that, in the case of HR23B complex regulates the loading and turnover of OGG1 (36). It also seems that, in the case of HR23B complex regulates the loading and turnover of OGG1 (36). It also seems that, in the case of HR23B complex regulates the loading and turnover of OGG1 (36).

In our previous case-control study, we reported a reduced NER-DRC in PBMCs of incident patients with CRC with no family history of this disease as compared with a healthy population (19). This is consistent with many other investigations on various cancers. But are PBMCs a valid cell type to study in relation to CRC? There is a belief that PBMCs may represent the general condition of the organism and specifically reflect individual DRC. Accordingly, in the current study, we attempted to test that hypothesis by comparing DRC in PBMCs, tumor, and normal colon epithelium. To ensure the validity of the comparison, we assayed all studied tissues at equal protein concentration. For both excision repair pathways, PBMCs exhibited on average approximately 3-fold lower DRC than either healthy or tumor tissue. This finding is somehow understandable considering that PBMCs, if unstimulated, do not divide and therefore do not require the pool of repair proteins in contrast to the constantly reproducing cells, such as colon epithelial cells (38). Furthermore, in nonreplicating cells, NER is carried out predominantly by transcription-coupled repair with suppressed global genome repair (39). Interestingly, despite the difference in repair capacities between colorectal epithelial cells and blood cells, there was a clear positive correlation between their repair capacities. This shows that DRC measured in blood cells does indeed reflect the repair potential of the cancer target tissue (40). PBMCs, technically easy to obtain, might thus provide a useful index of individual DRC in comparative population studies.

Expression levels of the analyzed genes correlated positively between the normal and tumor tissues. Although some genes within both pathways were observed to be up- or downregulated in tumors, this difference was relatively modest, never exceeding 1.3-fold. It is questionable whether these nuances in gene expressions might have any fundamental functional consequences. In fact, many potential biomarkers have failed because they showed only a slight change in expression in cancer compared with normal tissue or their cognate protein levels did not correlate with transcript levels (41). In our study, the transcript level of the major BER player, OGG1, was observed to be significantly lower in tumors compared with normal tissues. However, a 1.2-fold change in expression did not cause any difference in its activity (BER-DRC, measured with substrate DNA presenting 8-oxoguanines, reflects predominantly the activity of OGG1 protein). Moreover, no correlation between mRNA level of OGG1 and its enzymatic activity was observed. On the other hand, overall NER-DRC comprises the joint performance of many genes. In this case, the repair process relies on the formation of protein complexes that assemble at the site of the DNA lesions and facilitate their removal in a coordinated fashion. The expression level of none of the NER genes showed any correlation with NER-DRC. Moreover, according to the expression profiling, there were several genes up or downregulated in tumor cells while the final repair ability was enhanced. Thus, individual gene expression levels did not prove to be sufficiently informative about the overall DRC, and measurement of enzymatic activity can presumably give more relevant and interpretable information than can individual transcript measurement. In this respect, several other studies have...
reported an inconsistency between transcript level and respective protein quantity (42), or actual protein/pathway activity (19, 43–45).

In CRC, epigenetic alteration of gene expression, the so-called CpG island methylator phenotype, is known to affect several DNA repair genes (MLH1, MSH2, MGMT; ref. 46). DNA hypermethylation is often observed as a targeted event in tumor cells, resulting in loss of gene expression. BER and NER genes have been described to be aberrantly methylated in a variety of cancers, such as OGG1 in thyroid, XPC in bladder, XPG in ovarian, or ERCC1 in glioma, as well as in some CRC cell lines (15). In the present study, we investigated the CpG island methylation status of core BER and NER genes in colorectal carcinomas. Neither BER genes (OGG1 and XRCC1) nor NER genes (XPA, XPC, XPD, XPG, and ERCC1) were hypermethylated in tumor cells. In the light of gene expression data that showed fairly similar levels of gene transcripts between tumor and healthy tissues, these findings are coherent. Nevertheless, we have observed a relatively high frequency of false-positive signals provided by MSP analysis that have not been confirmed by subsequent verification by MS-HRM. Inaccuracy of MSP outcome might be for various reasons, such as an incomplete bisulfide conversion, which might result in an overestimation of DNA methylation (47). Another possible source of discrepancies may be allelic dropout or semiallelic methylation (48). Therefore, MSP does not seem to be reliable enough for methylation studies and a subsequent verification by MS-HRM. Inaccuracy of MSP of this work.

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Functional, Genetic, and Epigenetic Aspects of Base and Nucleotide Excision Repair in Colorectal Carcinomas

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