Expression of glutathione S-transferases (GSTs) in human colon cells and inducibility of GSTM2 by butyrate

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The glutathione S-transferases (GSTs) are a multigene family of enzymes largely involved in the detoxification of chemicals. In animals, enhanced expression is mediated by products of gut fermentation. Of these, butyrate induces GSTP1 protein expression and GST activity in the human colon tumor cell line HT29. The aim of the following investigations was to further elucidate butyrate-modulated induction of additional colonic GSTs in HT29 and to determine baseline expression in non-transformed cells, isolated from human colorectal tissue. We measured five GST protein subunits (GSTA1-2—composed of GST A1-1, A1-2 and A2-2—GSTM1, GSTM2, GSTP1, GSTT1) by western blot, GST activity using 1-chloro-2,4-dinitrobenzene as substrate and GSTM2 mRNA expression with RT–PCR. GSTP1, followed by GSTT1, were major subunits in all colon cells. Cells isolated from colon tissue were identified to be colonocytes and colon fibroblasts, both of which also expressed substantial levels of GSTM1 and GSTM2. The inter-individual variation of GST subunits in colonocytes of 15 individuals was marked, with total GST protein per 10⁶ cells differing by more than a factor of four. In HT29, butyrate significantly enhanced GSTA1/2 (3.5-fold), GSTM2 (not detectable in controls), GSTP1 (1.5-fold) and GST activity (1.4-fold), but not GSTM1 or GSTT1. GSTM2 mRNA expression was significantly induced after 24 (≈ 14-fold) and 72 h treatment (≈ 8-fold). In colon fibroblasts, butyrate (4 mM, 72 h) also induced GSTM2 protein (1.7-fold) and GST activity (1.4-fold). Colonocytes were too short lived to be used for inducibility studies. In conclusion, GSTs are expressed with high inter-individual variability in human colonocytes. This points to large differences in cellular susceptibility to xenobiotics. However, butyrate, an important luminal component produced from fermentation of dietary fibers, is an efficient inducer of GSTs and especially of GSTM2. This indicates that butyrate may act chemoprotectively by increasing detoxification capabilities in the colon mucosa.

Introduction

Susceptibility to colorectal cancer is associated with several environmental and dietary risk factors, which may be metabolized and detoxified by phase II enzymes, such as glutathione S-transferases (GSTs; EC 2.5.1.18) (1). GSTs are a multigene family of dimeric enzymes that inactivate carcinogens by catalyzing the conjugation of electrophiles to glutathione (2). They are divided into two microsomal and numerous cytosolic GST-classes (alpha, mu, kappa, pi, sigma, theta and zeta) (3). Each class consists of several isoenzymes, with only partly overlapping substrate specificities (4). Extensive deletions in GSTM1 and GSTT1 result in complete loss of enzyme function, which possibly influence colorectal cancer susceptibility (5). Therefore, a high number of studies have been performed to assess whether GSTM1-deficiency or other GST polymorphisms are associated with colorectal cancer susceptibility (6–9). The results were heterogeneous and numerous studies failed to demonstrate significant associations. One reason for this could be variations of the absolute expression levels of the GSTs. If these are large they are expected to mask differences due to null polymorphisms. Variations of GST expression in the human colon have not been investigated adequately, but on the basis of data from animal experiments it is known that the expression levels of GSTs are complex, tissue and cell specific (10–12). Moreover, it has been demonstrated in a very great number of animal experiments that they are modulated by numerous and very heterogenic dietary factors (2,13). In the colon, dietary fiber and the resulting fermentation products such as butyric acid could favorably modulate gene expression in cells of the colonic mucosa (14). Several studies have shown that an up-regulation of luminal butyrate concentrations, as a result of microbial carbohydrate fermentation, is associated with a decreased incidence of aberrant crypt foci and colon cancer in rats (15–17). Butyrate inhibits proliferation and induces apoptosis and differentiation in transformed cells, which indicates that it might play an important role in the secondary prevention of colon cancer (18,19). Additionally, butyrate could contribute to risk reduction by enhancing expression of GSTs that protect colon cells from endogenously formed oxidation products 4-hydroxy-2-nonenal (20). In this context, we have shown that butyrate increases GSTP1 expression in transformed human colon cells, which is the major isoform in the colon (21). However, in view of multidrug resistance, which may be caused in part by increased GSTP1 levels in tumor cells, the interpretation of this finding is under debate in terms of potential positive effects (22). Therefore, the aim of this paper was to examine expression profiles of additional GST isoenzymes, e.g. of the alpha, mu and theta classes, how they are affected by butyrate and whether similar effects as reported before for GSTP1 in tumor cells also occur in non-transformed cells. In particular, we determined protein expression of GSTA1/2, GSTM1, GSTM2, GSTP1 and GSTT1 as well as the overall activity of GST. First, we analyzed the

Abbreviations: GAPDH, glyceraldehyde-3-phosphate-dehydrogenase; GST, glutathione S-transferase; HBSS, Hanks balanced salt solution; PCR, polymerase chain reaction; RT–PCR, reverse transcriptase–PCR.
baseline expression levels of the GSTs in primary colon cells derived from 15 individuals to assess variability of expression levels and compared these with baseline levels in primary colon fibroblasts and in HT29 colon tumor cells. Next we incubated the cells with butyrate and determined the various GST proteins as well as GSTM2 mRNA.

Materials and methods

Cell lines

The human colon carcinoma cell line HT29 was grown in culture medium [DMEM, Gibco BRL, Karlsruhe, Germany; supplemented with 10% (v/v) fetal calf serum and 1% (v/v) penicillin/streptomycin] at 37°C in a humidified incubator (5% CO₂/95% air), as specified previously (23). Human colon fibroblasts were isolated from two different patients (see below) termed as cultures 1 and 2 and subsequently cultivated using the same conditions as described for HT29. Passages 17–46 of HT29 and 6–10 of the fibroblast cell lines were used for the experiments.

Cell treatment for analyses

HT29 and fibroblasts were incubated with 4 mM Na-butyrate (99% purity, Merck, Darmstadt, Germany) dissolved in culture medium in culture flasks. This concentration is based on concentrations found to be effective previously (20). After 48 h of incubation, the cells were trypsinized and washed in cold phosphate-buffered saline (20). Cell numbers were counted and viability was determined using trypan blue dye exclusion. The cells were frozen as pellets in liquid nitrogen and stored at −80°C prior to preparation of cytosolic fractions and isolation of RNA and DNA.

Preparation of tissue

The donors of colon tissue were admitted to the university hospital (Jena, Germany) for surgical removal of colorectal tumors, diverticulitis or colon polyps. Parts of the excised non-tumorous tissue, removed together with the tumor or other pathology samples, were used for cell isolations. The Ethical Committee of the Friedrich-Schiller-University of Jena approved the study and the patients have given their informed consent. Tissue specimens of 17 donors were studied (mean age, 60 years; range, 30–81 years). The donors were 10 males and five females. For two samples, information on gender was missing. For basal expression of GST isoforms, tissue specimens of 15 donors were examined. Six of these specimens were additionally incubated with butyrate for studies on GST induction. Two additional specimens were used only for isolation of fibroblasts.

Preparation of cytosol

The newly established procedure to isolate colon cells from surgical samples has been described in detail recently (24). Briefly, tissue was stored in Hanks balanced salt solution (HBSS) and transported on ice to the laboratory within 1 h. Sections of epithelial tissues (≈ 0.3–0.5 cm³) were separated from the underlying tissue by perfusion-supported mechanical disaggregation. The epithelial stripes were either worked up immediately (for determination of basal GST expression), or were incubated with 4, 10 and 20 mM butyrate in culture medium ± 2% (v/v) penicillin/streptomycin for 24 h at 37°C (for determination of GST induction). The cell slurries were worked up by mincing and incubation (40–60 min, 37°C) in HBSS supplemented with 1 mg/ml collagenase P (Boehringer Mannheim, Mannheim, Germany) (25). The suspensions were diluted with HBSS, centrifuged and washed with cold HBSS. Cell numbers were counted and viability was determined with trypan blue. Cells were frozen in liquid nitrogen and stored at −80°C prior to further use.

For isolation of fibroblasts, sections of epithelial tissue were cut into small pieces of 1 mm², which were placed in a culture flask and were allowed to dry on the bottom of the flask for 1 h in the incubator. Afterwards, culture medium [with 2% (v/v) penicillin/streptomycin] was added and fibroblasts were allowed to grow for at least 3 weeks. Then the fibroblasts were typanized and characterized using fibroblast-specific monoclonal FIB1 antibody AS02 (Dianova, Hamburg, Germany) and cultivated as described above.

Preparation of RNA

Cells were thawed in cold homogenizing buffer consisting of 250 mM sucrose, 20 mM Tris–HCl, 1 mM dithiothreitol and 1 mM Pefabloc (Roht, Karlsruhe, Germany). Homogenization of UCLA 7.4 and homogenized using ultrasound (Bandelin Electronics, Berlin, Germany). Following centrifugation (16 000 g, 60 min, 4°C), the supernatant was aliquoted and frozen at −80°C until use.

GST activity and cytosolic protein

GST activity with 1-chloro-2,4-dinitrobenzene (CDNB) as substrate was determined spectrophotometrically at 340 nm and 30°C (26). Total protein content was measured using the method by Bradford with bovine serum albumin as standard protein (27).

Western blot analysis of GST isoforms

Cytosols and GST protein standards were diluted (1:1:5) with loading buffer [125 mM Tris, 2% sodium dodecyl sulfate (SDS), 10% glycerine, 6 M urea, 324 mM diethiothreitol, 0.1% bromphenolblue] and incubated for 10 min at 65°C. Samples and standards were subjected to SDS–polyacrylamide gel electrophoresis (stacking gel, 3% w/v acrylamide; separation gel, 12% w/v acrylamide) and transferred to nitrocellulose (Schleicher & Schuell, Dassel, Germany) in a semi-drying blotting chamber (MTI, C1, Gmbh, Idstein/Taunus, Germany). For detection of GST isoforms, defined amounts of cytosolic protein were loaded (HT29: 60 μg protein for GSTA1/2, M1, M2 and 8 μg protein for GSTP1, GSTT1; fibroblasts: 10–20 μg protein and primary colon cells: 5–15 μg protein for all GSTs). The western blots were subsequently blocked with milk protein (5%) and incubated with the appropriate antibody. We used monoclonal antibodies against human GST class alpha, mu, pi (21) and theta class (LabAs, Tartu, Estonia) (28). While class pi and class theta antibodies are directed against GSTP1-1 and GSTT1-1, the class alpha antibodies recognize GSTA1-1, GSTA1-2 and GSTA2-2(20). Both protein haploids of GSTA1 and GSTA2 are detected together due to their almost identical molecular weights. The class mu antibodies react against GSTM1-1a, GSTM1-1b, GSTM1b-1b (upper band) (29) and probably against GSTM2-2 (lower band); however, because of lack of the appropriate standard protein the detection of GSTM2 is not fully proven. Specific binding of the monoclonal antibodies was detected with 3.7-diamino benzidine and hydrogen peroxide after incubation with horseradish peroxidase-conjugated rabbit anti-mouse immuno-globulins as second antibody (Dako, Hamburg, Germany). Quantitative densitometric evaluation of stained protein bands was performed with a Fluor S Multi Imager (Bio-Rad, München, Germany). Known quantities of purified GSTM1-1 (21) and GSTT1-1 (LabAs) and recombinant GSTA1-1 and GSTP1-1 (both Calbiochem, Darmstadt, Germany) were run in parallel and served as standards for calculating total amounts of the isoenzymes in the samples.

Materials and methods

Preparation of RNA

Total RNA was isolated from HT29 using the TRIzol method (Gibco BRL). Following DNA digestion (Deoxyribonuclease I, Amplification Grade, Invitrogen, Karlsruhe, Germany) cDNA equivalent to 5 μg total RNA was prepared by first-strand synthesis using oligo(dT) primer (SuperScript™ First-Strand Synthesis System, Gibco BRL). Semi-quantitative RT–PCR was used to amplify GSTM2 mRNA levels and to compare its expression in butyrate treated cells versus untreated cells. The expression of glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) served as an internal control. To avoid different cDNA concentrations between target gene (GSTM2) and control gene (GAPDH), for each sample the template (cDNA) was added to the PCR reaction mix without primers. Subsequently the mixture was aliquoted in two batches, one for GSTM2 and one for GAPDH, before adding primers, which had the following sequences for GSTM2 (sense) and GSTM2 (antisense), respectively: 5'-GGG AAT CGA AAA AGG AGC AG-3' and 5'-CAG GAG AAA GGA ACG AG-3', and for GAPDH (sense) and GAPDH (antisense), respectively: 5'-ACC ACA GTC CAT GCC ATC AC-3' and 5'-TCC ACC ACC GGT TAG TGC-3'. On the basis of the mRNA sequence (NCBI Nucleotide Sequence Database accession number NM_000848 for GSTM2 and J04038 for GAPDH) the predicted size of the GSTM2 cDNA is 508 bp, and that of GAPDH is 452 bp.

The PCR conditions were: cDNA equivalent to 0.6 μg/25 μl of RNA, 1.25 U/25 μl of Hot Star Taq DNA Polymerase (Qiagen, Heiden, Germany), either 0.25 mM of GAPDH primers or 0.5 μM of GSTM2 primers and a final MgCl₂ concentration of 1.5 mM. The cDNA was amplified by PCR, with 28 cycles for GAPDH and 41 cycles for GSTM2. After primary denaturation at 95°C for 5 min, the PCR cycles were run at 95°C for 15 s, 55°C for 30 s and 72°C for 1 min. For quantitative RT–PCR the number of PCR cycles was calibrated for GAPDH as internal control (15–41 cycles) and 41 cycles were used for GSTM2. Densitometry evaluation of the ethidium bromide bands was performed with the Quantity One 4.1 Software (Bio-Rad). The results were expressed as ratio of GSTM2 and GAPDH.

Statistical evaluation

Data were based on both the cytosolic protein content (per mg protein) and on the number of cells (per 10⁶ cells), respectively. All values given are
butyrate-mediated induction of GST subunits in primary cells from human colon tissue

In order to examine the impact of butyrate on modulating GSTs on non-transformed primary cells derived from the colon, freshly isolated epithelial cells were incubated for 24 h with 4, 10 and 20 mM butyrate and fibroblasts for 72 h with 4 mM butyrate. In epithelial cells GST proteins were not influenced after 24 h treatment, and it was not possible to assess inducibility of GSTs after 48 or 72 h in these cells as they are too short lived. However, in the colonic fibroblasts, GSTM2 protein was induced. The induction was 1.3-fold on the basis of total protein content in culture 1 (results not shown). Incubation with butyrate also increased the cellular protein content. Therefore, when evaluating the results based on the number of cells (14), a more clear-cut and significant induction of GSTM2 protein (1.7-fold) and GST activity (1.4-fold) was seen in the fibroblast cultures (results not shown).

Effect of butyrate on the GSTM2 mRNA expression in HT29

The highest butyrate-mediated induction of GST protein was observed for GSTM2. To obtain more information on the inducibility of this gene, we determined GSTM2 mRNA by semi-quantitative RT–PCR. For this, the number of PCR cycles was calibrated for GSTM2 and GAPDH (15–41 cycles). After 25 cycles GAPDH-cDNA was weakly detectable (results not shown). Based on the observed exponential increase up to 30 PCR cycles, 28 cycles were chosen for evaluation. Because of the marginal or non-detectable expression of GSTM2 mRNA in controls, induction levels were measured after 41 cycles on the basis of GSTM2-cDNA bands and background of non-apparent visible bands.

Butyrate significantly induced GSTM2 mRNA levels after 24 and 72 h (Figure 3). An example of a PCR gel is shown in Figure 4. After 24 h, mRNA was more abundant (≈14-fold) than after 72 h (≈8-fold).

Discussion

It is well known, that dietary habits and lifestyle strongly affect the development of colorectal cancer. Epidemiological data indicate, that a high intake of fibers or resistant starch producing butyrate is associated with a decreased incidence of colon cancer (34). The induction of phase-2 enzymes, such as GSTs, is one of several possible mechanisms to reduce cancer risks. The validity of this approach is uniquely being demonstrated in a study in China where the drug oltipraz was given to a group of subjects to induce GSTs in the liver (35). The enhanced exposure to the environmental liver carcinogen aflatoxin B1 was shown to enhance the deactivation of the mycotoxin (36), which is expected to result in a reduced cancer risk (37).

Butyrate, a major fermentation product in the gut (38), is also capable of inducing GST activity in human colon cell lines (39,40), but little is known about which GST isoenzymes in the colon are responsible for this effect. Therefore, we investigated the modulatory mechanisms of GST isoenzymes by butyrate. We used HT29 cells as we had previously used these cells to show that the consequence of the GST induction is an enhanced chemoresistance (20,40). Human colon cell lines, moreover, are models for (pre)neoplastic alterations, which occur increasingly with old age and could be present as undetected lesions in a large proportion of the aged population (41).

Results

Basal expression of GST isoenzymes in HT29, primary colon cells and colon fibroblasts

Cellular levels of GST protein expression were calculated both on the basis of the number of cells and on the cytosolic protein (Table I). Determinations were performed after cultivating HT29 and colon fibroblasts for 5 and 10 days. Values of primary colon cells were obtained from tissue specimens worked up within 3 h after surgery.

GSTP1 was the major GST subunit in all colon cells, including the fibroblasts, whereas GSTA1/2 was expressed least. GSTA1/2 was detectable in nine of 11 samples of primary colon cells, but was not found in either of the two colon fibroblast cultures. In HT29, GSTM1 and GSTM2 proteins were not detectable, although HT29 cells do not bear the null-genotype for GSTM1 (20,33). In contrast, both primary colon cells and colon fibroblasts express considerable amounts of GSTM1 and GSTM2. GSTT1 protein was detected in all cells, unless the GSTT1*0 polymorphism was identified. This was the case for one of the fibroblast cultures, whereas the other was GSTT1*0 (Table I). Figure 1 shows the variation for GST subunit expression in primary colon cells obtained from 15 different donors. Null polymorphisms were identified in several samples not expressing GSTM1 (n = 4 of 7) or GSTT1 (n = 2). Altogether, the total protein contents varied from 250 to 930 ng GST protein/10⁶ cells. Mean tertile values were 719 ± 142, 417 ± 34 and 315 ± 42 ng/10⁶ cells (or 6088 ± 1154, 3244 ± 629 and 2109 ± 331 ng/mg protein), which is equivalent to more than a 2–3-fold difference of GST expression in human colonocytes.

Butyrate-mediated induction of GST subunits in HT29

To establish optimal in vitro conditions of GST inducibility, we first determined protein expression after incubating HT29 cells with butyrate for 24, 48 and 72 h. Treatment with butyrate enhanced protein levels of GSTA1/2, GSTM2 and GSTP1 in a time-dependent manner, whereas GSTM1 and GSTT1 levels were not influenced. The increase of GSTM2 was already detectable after 24 h and of GSTA1/2 after 48 h incubation time (results not shown). Table II shows the maximal levels of induction that were apparent after 72 h with a significant increase for GSTA1/2 (3.5-fold), GSTM2, GSTP1 (1.5-fold) accompanied by 1.4-fold increase of GST activity. The calculation of induction values for GSTM2 (all time points) and GSTA1/2 (after 48 h) was not possible, as these isoenzymes were not detectable in their respective controls. Representative examples of immunoblots, detecting GSTA1/2, GSTM2, GSTP1 and GSTT1 are shown in Figure 2. This figure also demonstrates that GST inductions are already apparent for only 2 mM butyrate.

GSTA1/2 and GSTP1 levels of controls also increased with longer cultivation time. The increase of GSTP1 from 2395 ± 629 and 34 and 315 butyrate equivalent to more than a 2–3-fold difference of GST expres-

Student’s t-test (two-sided, unpaired) using the GraphPad Prism Software Version 2.01 (San Diego, USA). P < 0.05 was considered statistically significant.
Table I. Quantification of basal levels of GST subunits, GST activity and total protein content in human colon cells

<table>
<thead>
<tr>
<th>Cells</th>
<th>GST protein (ng)</th>
<th></th>
<th>GST activity (nmol \times \text{min}^{-1})</th>
<th>Total protein (mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A1/2</td>
<td>M1</td>
<td>M2</td>
<td>P1</td>
</tr>
<tr>
<td></td>
<td>$10^{-6}$ cells</td>
<td>$\text{mg}^{-1}$ protein</td>
<td>$10^{-6}$ cells</td>
<td>$\text{mg}^{-1}$ protein</td>
</tr>
<tr>
<td>HT29 ($n = 17$)</td>
<td>1.2 ± 0.3</td>
<td>9 ± 3</td>
<td>n.d.</td>
<td>217 ± 19</td>
</tr>
<tr>
<td>Colon fibroblasts ($n = 3$)</td>
<td>n.d.</td>
<td>n.d.</td>
<td>n.d.</td>
<td>304 ± 36</td>
</tr>
<tr>
<td>Colon fibroblasts ($n = 5$)</td>
<td>n.d.</td>
<td>n.d.</td>
<td>GSTMI&lt;sup&gt;0&lt;/sup&gt;</td>
<td>GSTMI&lt;sup&gt;0&lt;/sup&gt;</td>
</tr>
<tr>
<td>Primary colon cells ($n = 11–15$)</td>
<td>17 ± 15</td>
<td>92 ± 74</td>
<td>62 ± 31</td>
<td>682 ± 371</td>
</tr>
<tr>
<td></td>
<td>48 ± 28</td>
<td>427 ± 270</td>
<td>194 ± 90</td>
<td>1885 ± 1167</td>
</tr>
<tr>
<td></td>
<td>541 ± 235</td>
<td>159 ± 76</td>
<td>133 ± 74</td>
<td>159 ± 76</td>
</tr>
</tbody>
</table>

Values are given as mean ± SD. n.d., not detectable. GSTM1<sup>0</sup> and GSTT1<sup>0</sup>, null-polymorphism genotyping.
Our data show a time-dependent up-regulation of GSTA1/2, GSTM2 and GSTP1 protein by butyrate, but no change of GSTT1 in the human colon tumor cell line HT29. It would be a matter of perception to describe the increase of GSTP1 as a marker of chemoprevention, as it is also discussed as being a tumor marker due to its over-expression in colon carcinoma (42). However, the increases of GSTA1/2 and GSTM2, which are down-regulated in tumor cells (21), could very well be interpreted as contributing to the differentiation of the transformed cells. The inducibility of GSTP1 was relatively small compared with the degree of induction for GSTA1/2 and GSTM2, which can be explained by the already high basal expression of this isoenzyme. Despite the remarkable induction of GSTA1/2 and GSTM2 protein, the absolute amounts of these isoenzymes still represented < 1% of detected GSTP1 protein. Therefore, the induction of overall GST activity was probably mainly due to the increase of GSTP1 levels. The increase of GST protein with cultivation time that we observed for GSTA1/2 and GSTP1 corresponds to earlier results with the human colon carcinoma cell line Caco-2 (43).

The butyrate-mediated enhancement of GSTM2 mRNA confirms the western blot data on induced GSTM2 protein levels. Possible explanations are that butyrate could either enhance the transcripational activity of the gene or improve the stability of GSTM2 mRNA. In any case, this is the first time that a butyrate-mediated increase of GSTM2 has been demonstrated in human colon cells. An induction of this isoenzyme by the green tea polyphenol epigallocatechin gallate was recently found in rat liver, where it also enhanced overall GST activity (44). GSTM2 has a high specific activity toward CDNB, the standard substrate of activity measurement (3,26). In vivo GSTM2 is known to efficiently detoxicate o-quinones (e.g. aminochrome), the oxidation products of catecholamines, which may be involved in the development of the Parkinson’s disease (45). Furthermore, noticeable activities of hepatic rat GSTM2 towards 4-hydroxy-2-nonenal were found (46), which may be of importance for carcinogenesis (47,48). However, it is not clear which putative colon risk factors are specifically detoxified by GSTM2. Moreover, it is also not known how the induction of GSTM2 mRNA levels occur on a molecular level.

The murine GSTM2 promoter region does not contain a TATA-box and activation of the gene is based on an SP-1 binding sites (49). The binding sites for transcription factors of the human GSTM2 gene have not been characterized yet.

In primary colon cells GSTs are expressed differently than in the tumor cell line HT29. Thus, primary colon cells expressed GSTM1 and GSTM2 protein in considerable amounts, provided that no null-deletion for GSTM1 was present. Also, the GSTA1/A2 levels on the average were several times higher than in HT29 cells (21). The relatively high levels of these GSTA are interesting in terms of colon cancer risk, as several putative colon carcinogens can be specifically deactivated by these enzymes, such as N-acetoxy-2-amino-1-methyl-6-phenylimidazo
[4,5-b]pyridine (N-acetoxy-PhIP) by GSTA1-1 (50). Total GSTs are also expressed with a marked intraindividual variability—some of the samples containing 2–4-fold higher GST protein levels than others. In at least three of the investigated tissues (from donors 7, 12 and 13), not even GSTP1 was available in abundant quantities (<100 ng/10⁶ cells). Another interesting find was that cells with the GSTM1-null genotypes do not necessarily compensate their deficiency by higher expression levels of the other GST enzymes, a finding which confirms previous reports (51–53). On the basis of our present knowledge, these findings mean that a considerable number of subjects could be at higher risk on account of low GST expression levels. Whereas many studies have been published on associations of polymorphisms and colon cancer risk, hardly any are available on the associations of expression levels and cancer risks, probably due to technical limitations. Technical limitations were also the reason why we could not study an additional butyrate-mediated GST-protein-induction in the primary colon epithelial cells, as they do not survive long enough. Adult colon epithelial cells can be considered as models for the actual target cells of cancer, which are the stem cells and their migrating daughter cells localized in the lower crypt segments (54). It is not known to which percentage stem cells and their immediate daughter cells are contained in our mixed cellular suspensions as they cannot easily be identified, but their proportion is probably variable and rather low (55). On the other hand, the expression levels in the adult colonocytes are probably also very important for protecting the stem cells from genotoxic insults. Luminal genotoxins could be warded off, by first being detoxified in the more mature cells of the upper crypt of the mucosal epithelium. Moreover, the colon epithelium consists not only of enterocytes and seam cells—but is also surrounded by connective tissue containing fibroblasts. Fibroblasts can be involved in the human body’s defence by adaptive gene expression (56) and by detoxifying xenobiotics through enhanced GST expression (57). Thus, the enzyme pattern of fibroblasts in the colon could be adapted to the surrounding colon tissue and together with the colon tissue protect the stem cells from genotoxic insults. Butyrate treatment of two non-transformed fibroblast cultures (4 mM; 72 h) increased the already strongly expressed GSTM1 and GSTM2 protein levels.

On the basis of these results, we suggest that butyrate modulates GST expression in colon cells, especially GSTM2, and that this enhanced expression in adult colonocytes and in fibroblasts can protect not only the cells themselves, but also the actual target cells of cancer, which are located in the bottom portions of the colon crypts. An enhancement of GSTP1 by resistant starch (14) or GSTA1/2 by wheat bran (58) has been reported and attributed to increased luminal butyrate concentrations. In spite of the extensive literature on the various mechanisms by which butyrate could act as a chemopreventive compound, its in vivo potentials of protective activities are hardly elucidated. Butyrate-mediated induction of cellular protein content, as we found, indicates an up-regulation of a large number of genes (59), possibly due to the modification of histone acetylation (60). Also, we have shown that butyrate activates ERK1/2 (20), but further studies...
are needed to clarify how GSTM2 or GSTP1-gene activation is caused at the molecular level.

In conclusion, our study shows that primary human colon cells express different GST proteins with large inter-individual variability. The expression patterns are also highly different from transformed HT29 colon tumor cells, particularly in that GSTM2 is more abundant. The luminal factor butyrate specifically induces GSTM2 in two types of colon cell cultures and could thus be the source of enhanced GSTM2 levels in adult colonocytes. It is an isoenzyme with specificity for substrates that arise from oxidative stress. Therefore, it may well be possible, that dietary-mediated butyrate formation in the gut will modulate GSTs of the colon mucosa in a favorable manner, leading to a reduced impact of certain genotoxic colon cancer risk factors and thus enhancing lifelong protection in the general population.

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