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Microbially mediated phenolic catabolites exert differential genoprotective activities in normal and adenocarcinoma cell lines

Brian Óg Murphy^a, Cheryl Latimer^a, Sara Dobani^a, L. Kirsty Pourshahidi^a, Massimiliano Fontana^a, Nigel G. Ternan^a, Gordon McDougall^b, Ian Rowland^c, Gema Pereira-Caro^d, Kieran M. Tuohy^e, Daniele Del Rio^f, Tahani M. Almutairi^g, Alan Crozier^{g,h}, Nenad Naumovskiⁱ and Chris I. R. Gill^a

^aNutrition Innovation Centre for Food and Health (NICHE), Ulster University, Coleraine, UK; ^bEnvironmental and Biochemical Sciences Department, The James Hutton Institute, Dundee, UK; ^cDepartment of Food and Nutritional Sciences, University of Reading, Reading, UK; ^dDepartment of Food Science and Health, IFAPA-Alameda Del Obispo, Córdoba, Spain; ^eSchool of Food Science and Nutrition, University of Leeds, Leeds, UK; ^fHuman Nutrition Unit, Department of Food and Drug, University of Parma, Parma, Italy; ^gDepartment of Chemistry, King Saud University Riyadh, Saudi Arabia; ^hSchool of Medicine, Dentistry and Nursing, University of Glasgow, Glasgow, UK; ⁱSchool of Rehabilitation and Exercise Sciences, Faculty of Health, University of Canberra, Canberra, Australia

ABSTRACT

Age-associated decline of nuclear factor erythroid 2-related factor 2 (Nrf2) activity and DNA repair efficiency leads to the accumulation of DNA damage and increased risk of cancer. Understanding the mechanisms behind increased levels of damaged DNA is crucial for developing interventions to mitigate age-related cancer risk. Associated with various health benefits, (poly)phenols and their microbially mediated phenolic catabolites represent a potential means to reduce DNA damage. Four colonic-microbiota-derived phenolic catabolites were investigated for their ability to reduce H₂O₂-induced oxidative DNA damage and modulate the Nrf2-Antioxidant Response Element (ARE) pathway, in normal (CCD 841 CoN) and adenocarcinoma (HT29) colonocyte cell lines. Each catabolite demonstrated significant ($p < .001$) genoprotective activity and modulation of key genes in the Nrf2-ARE pathway. Overall, the colon-derived phenolic metabolites, when assessed at physiologically relevant concentrations, reduced DNA damage in both normal and adenocarcinoma colonic cells in response to oxidative challenge, mediated in part *via* upregulation of the Nrf2-ARE pathway.

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Introduction

The association between ageing and tumorigenesis is well-established, with life-time accumulation of DNA damage recognised as a significant contributing factor (Soria-Valles et al. 2017; Patel et al. 2020). As individuals age, the progressive accumulation of DNA damage within tissues becomes increasingly evident, potentially triggering either DNA repair, apoptosis or cell senescence, the latter a contributing factor to the decline in tissue function observed with age (Niedernhofer et al. 2018; Schumacher et al. 2021). In addition, the efficiency of DNA repair mechanisms declines over time, leading to the persistence of DNA damage within the genome as age advances (Gupta and Heinen 2019; Rashid et al. 2019; Schumacher et al. 2021). This accumulation of DNA damage is believed to directly contribute to the increase in cancer prevalence among older individuals (Patel et al.

2020). Diet and inflammation likely play critical roles in the accumulation of genomic alterations (Gómez de Cedrón et al. 2023). Poor dietary habits, characterised by high intake of processed foods, sugars and unhealthy fats, are linked to increased chronic inflammation (Falzone et al. 2022; Rudrapal et al. 2022). These diets promote the production of pro-inflammatory cytokines such as interleukin-6 (IL-6), tumour necrosis factor-alpha (TNF- α) and C-reactive protein (CRP) and activate Toll-like receptors (TLRs) on immune cells, stimulating inflammatory pathways and generating reactive oxygen species (ROS) and reactive nitrogen species (RNS) (Falzone et al. 2022; Rudrapal et al. 2022). ROS are produced through various biochemical pathways, including mitochondrial respiration, NADPH oxidase activity and inflammatory cell activation (Krawczyk et al. 2023). Such reactive molecules can induce oxidative modifications in DNA, proteins and lipids, leading to mutations, impaired cellular

CONTACT Chris I. R. Gill  c.gill@ulster.ac.uk  Nutrition Innovation Centre for Food and Health (NICHE), Ulster University, Coleraine, UK

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functions and activation of oncogenic pathways, which contribute to the progression of diseases including cancer (Krawczyk et al. 2023).

Conversely, diets rich in fruits, vegetables and whole grains, contain greater quantities of (poly)phenols, biologically active compounds such as quercetin, epigallocatechin gallate and resveratrol, which exhibit pleiotropic effects including anti-inflammatory, anti-microbial and anti-oxidant properties (Falzone et al. 2022; Rudrapal et al. 2022). Such compounds scavenge ROS, inhibit NF- κ B activation and enhance DNA repair mechanisms, thereby reducing oxidative stress, DNA damage and inflammation, processes common to the pathogenesis of many chronic disease states (Gupta and Heinen 2019; Falzone et al. 2022; Rudrapal et al. 2022). Expanding our understanding of the mechanisms involved in age-related DNA damage accumulation could aid in the development of interventions to mitigate age-related cancer risk and improve overall health in the ageing population.

Polyphenols are a diverse group of bioactive aromatic phytochemicals with up to 10,000 different known structures, which play a role in reducing DNA damage (Durazzo et al. 2019; Di Lorenzo et al. 2021). Flavonoids, the most dietarily abundant (poly)phenols (Ahn-Jarvis et al. 2019; Khan et al. 2021; Rufino et al. 2021) are common to foods such as berries, coffee and cocoa (Del Rio et al. 2013), contributing to the estimated average European intake of 580–1780 mg of (poly)phenols per day (Zamora-Ros et al. 2016). Over the last decades, greatly improved analytical techniques have facilitated significant improvements in our understanding of both the metabolism and bioactive potential of these compounds (Gavrilas et al. 2019; Di Lorenzo et al. 2021; Dobani et al. 2021; Song et al. 2021).

Upon consumption, (poly)phenols undergo numerous structural changes during their transit through the gastrointestinal tract (GIT), including the production of bioactive, microbiota-derived phenolic catabolites (Carregosa et al. 2022), some of which have been reported to exert pleiotropic effects that likely contribute to reducing the risk for chronic diseases (Del Rio et al. 2013; Mena et al. 2019; Luca et al. 2020; Diotallevi et al. 2021; Rodríguez-Daza et al. 2021; Wang et al. 2022). However, the specific sites and mechanisms of action remain elusive, with multiple pathways postulated and currently under investigation. For example, the ability of (poly)phenolic-rich foods to affect aspects of the colorectal carcinogenesis pathway in gut epithelial cells has been studied *in vitro* (Brown et al. 2014; McDougall et al. 2017; Wang et al. 2022). The microbiota-derived catabolites

of dietary (poly)phenols have been reported to modulate the response of pathways involved in the cell cycle and apoptosis, by inducing variation in expression of genes such as nuclear factor erythroid 2-related factor 2 (Nrf2), phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1) or BH3-interacting domain death agonist (BID) (Jin et al. 2010; Lu et al. 2018; Zaklos-Szyda et al. 2019; Song et al. 2021). Of particular interest is Nrf2, a redox-sensitive transcription factor master regulator of oxidoreductive and immune homeostasis. Under normal conditions cytosolic Nrf2 is associated with the inhibitory protein Kelch-like ECH-associated protein 1 (Keap1), which acts as a sensor of endogenous and exogenous prooxidants (Saha et al. 2020). Under a mild increase in oxidative stress, specific cysteine residues in Keap1 allow newly synthesised Nrf2 to escape Keap1-mediated ubiquitination and to activate the transcription of Nrf2-target genes. The protein then dimerises with small Maf proteins and binds to the antioxidant response element (ARE) in the promoter region of these genes, activating their transcription and eliciting antioxidant defence and detoxification mechanisms (Gavrilas et al. 2019). Consequently, Nrf2 represents an important potential therapeutic target in human carcinogenesis (Telkoparan-Akillilar et al. 2021) as it is activated by a range of diet derived (poly)phenolics (Islam et al. 2023). Moreover, ageing is associated with a decline in Nrf2 activity and signalling, resulting in a compromised cellular response to DNA damage (Schmidlin et al. 2019). A comprehensive review by Zhou et al. (2019) highlights the importance of (poly)phenols as activators of Keap1-Nrf2 signalling pathway, with many (poly)phenolic-rich berry fractions and to a lesser degree, their colonic catabolites reported to reduce DNA damage in various cell models (Prasad and Katiyar 2015; De Santiago et al. 2019; Majidinia et al. 2019; Maleki Dana et al. 2022).

Dobani et al. (2021) recently reported an ileostomate-based *ex vivo* model in which benzoic acid (BA), 4-hydroxybenzoic acid (4HBA), 3-(3'-hydroxyphenyl)propanoic acid (3'HPPA) and 3-(phenyl)propanoic acid (3PPA) were commonly produced as colonic catabolites following ingestion of raspberries, although they are not uniquely derived from that dietary source. Consequently, we investigated the differential effects of these hydroxylated and non-hydroxylated catabolites in two contrasting colonic cell lines with greater and lesser degrees of transformation (HT29 and CCD 841 CoN cells), with respect to DNA damage and ability to modulate key genes associated with the cytoprotective Nrf2-ARE pathway.

Material and methods

Chemicals and reagents

Foetal Bovine Serum (FBS), Minimum Essential Media (MEM), Dulbecco's Modified Eagle's Medium (DMEM) and phosphate-buffered saline (PBS) were purchased from Gibco Life Technologies Ltd (Paisley, Scotland, UK). All remaining chemicals including the phenolic catabolites 4HBA, BA, 3'HPPA and 3PPA were acquired from Sigma-Aldrich (Poole, Dorset, UK) unless otherwise stated.

Cell culture

Both normal epithelial (CCD 841 CoN) and adenocarcinoma (HT29) colonic cells used for this investigation were acquired from the American Type Culture Collection (ATCC) and European Collection of Cell Cultures (ECACC), respectively. CCD 841 CoN cells were cultured in MEM supplemented with 10% FBS, 100 U/L penicillin/streptomycin, 1% sodium pyruvate, 1% non-essential amino acids. The HT29 cells were cultured in DMEM supplemented with 10% FBS and 100 U/L penicillin/streptomycin. Both cell lines were grown as monolayers in tissue culture flasks as previously reported (Brown et al. 2014; De Santiago et al. 2019).

Cell treatments

Both cell lines were incubated without treatment (control) and individually with 3'HPPA, 3PPA, 4HBA or BA at 10, 50 and 100 μ M, prepared from 5 mM stock solutions as previously detailed (Dobani et al. 2021).

Cytotoxicity assay

The 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) colorimetric assay was used to determine cell viability. Following a previously established protocol (Brown et al. 2014), cells (1.5×10^4 cells/well) were seeded in a 96 multi-well plate and incubated for

48 h (37°C, 5% CO₂) before replacement of media with 100 μ L of each treatment and incubation (37°C, 5% CO₂). After 24 h, cells were washed with PBS, treatments were replaced with an equal volume of media and 15 μ L of MTT (5 mg/mL) was added to each well. After a 4 h incubation (37°C, 5% CO₂) and addition of the solubilising solution, prepared as previously reported (Saha et al. 2020; Carregosa et al. 2022), absorbance at 570 nm was measured with a microplate-reader (VERSAmax). Experiments were carried out in triplicate and mean results expressed as a percentage (%) of cell viability normalised to untreated control. Deoxycholic acid (250 mM) was used as negative control and threshold cell viability level was set at 50%.

Genotoxicity assay

The COMET assay was used to determine each phenolic's efficacy in reducing DNA damage in CCD 841 CoN and HT29 cell lines. As outlined by De Santiago et al. (2019), both cell lines were incubated with each phenolic compound individually for 24 h at 37°C in 5% CO₂ before undergoing oxidative challenge with either 75 μ M hydrogen peroxide (H₂O₂) for HT29 cells or 25 μ M hydrogen peroxide (H₂O₂) for CCD841 CoN cells to elicit an equivalent amount of damage (~50% Tail DNA) in the untreated controls. Images were analysed using a Nikon Eclipse 600 epifluorescence microscope at 400 \times magnification, with Komet 5.0 software used to record the tail DNA (%). The genoprotective potential was assessed by comparing the effects of the phenolics against the positive (H₂O₂) control and genotoxic activity by comparing against the negative (PBS) experimental control. Experiments were carried out in triplicate and mean results expressed as a percentage Tail DNA.

Real-time PCR (qPCR)

Following the previously established method (Dobani et al. 2021), primers (Table 1) were designed for three

Table 1. Oligonucleotide primers used for PCR amplification and qPCR to assess the change in expression after treatment.

Gene	Full name	Forward primer	Sequence (5'→3')	Reverse primer	Sequence (3'→5')	Product size (bp)
Nrf2	Nuclear factor (erythroid-derived 2)-like 2	Nrf2-F	AAACCATGGGACTGCCAAC	Nrf2-R	GCACTAGGAAGACTGGGCTCTC	190
HO-1	Haem oxygenase 1	HO-1-F	ATGACACCAAGGACCAGAGC	HO-1-R	GTGTAAAGGACCCATGGCAGA	153
NQO1	NAD(P)H dehydrogenase, quinone 1	NQO1-F	AGGACCCTCCGGGAAGTAAGA	NQO1-R	AGGCTGCTTGGGAGCAAATA	279
HPRT	hypoxanthine phosphoribosyltransferase	HPRT-F	AGCTTGGCAGCTTGACCAT	HPRT-R	GACCAGTCAACAGGGGACAT	166
β -Actin	Actin, beta	β -Actin-F	GGACTTCGAGCAAGAGATGG	β -Actin-R	AGCACTGTGTGGCGTACAG	234

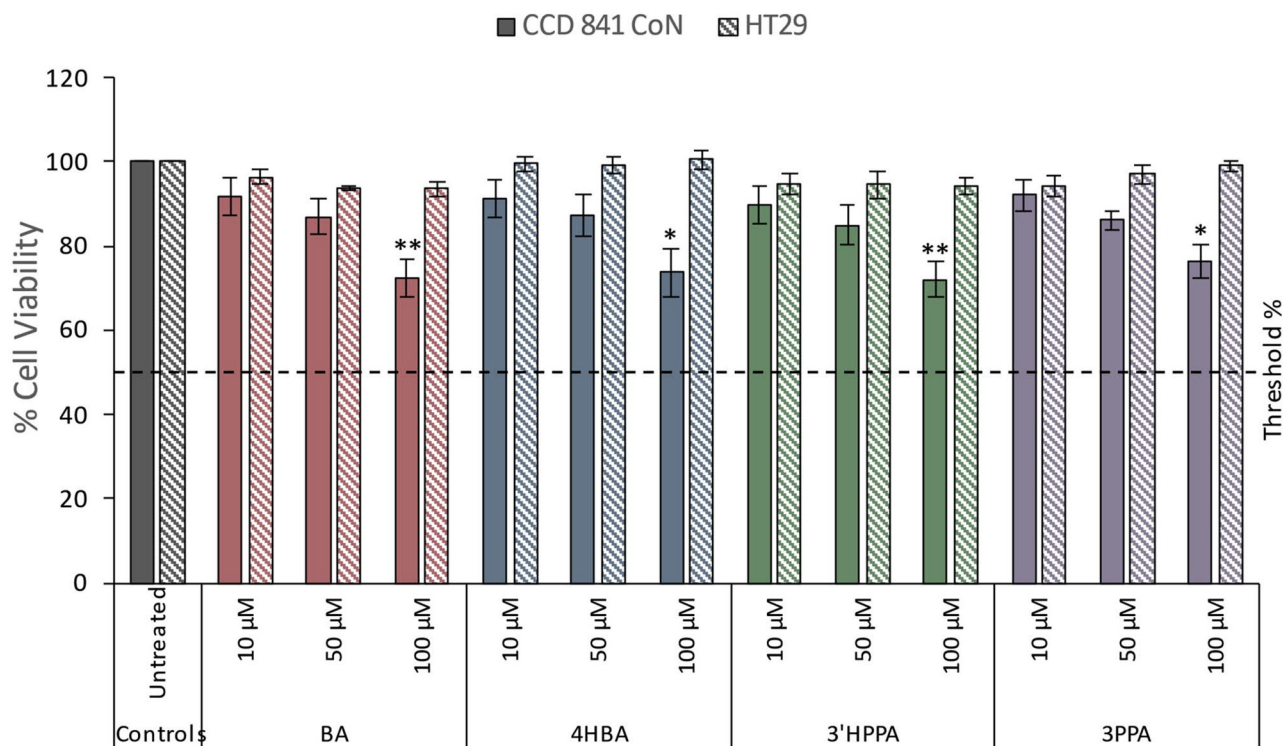


Figure 1. Cytotoxic effect of different concentrations of phenolics on CCD 841 CoN and HT29 cells. Data are presented as mean of three independent experiments \pm SEM. Significance is compared to untreated control using one-way ANOVA and Dunnett's multiple comparison test, * $p < .05$, ** $p < .01$. BA: benzoic acid; 4HBA: 4-hydroxybenzoic acid; 3'HPPA: 3-(3'-hydroxyphenyl)propanoic acid; 3PPA: 3-(phenyl)propanoic acid.

genes of interest involved in the Nrf2-ARE pathway; Nrf2, Haem oxygenase-1 (HO-1) and NAD(P)H:quinone oxidoreductase 1 (NQO1), utilising the online software tools OligoPerfect (Thermo Fisher, UK) and NCBI Primer-BLAST (Ye et al. 2012). The following cycling condition were applied; 95°C for 10 min, followed by 50 cycles of 95°C for 10 s, 57°C for 10 s and 72°C for 10 s. Expression for each target gene was normalised against two reference genes (i.e. hypoxanthine phosphoribosyltransferase (HPRT) and β -actin) and analyses were performed in triplicate and data was expressed as the logarithmic of fold change.

Statistical analysis

The results of three independent experiments were used for statistical analysis and presented as means \pm standard error of the mean (SEM) for each type of dataset. Normality of datasets was assessed with the D'Agostino and Pearson omnibus test. One-way ANOVA, with Dunnett's multiple comparison post-hoc test, was used to assessed significant differences between means ($n=3$) compared to control (untreated cells) and a Tukey's multiple comparison post-hoc test to compare concentration effects within compound for results of cytotoxicity, genoprotective activity and gene expression.

Additionally, Tukey's multiple comparisons were also used to assess significance between the different compounds at the same concentrations for both genoprotective activity and gene expression. An unpaired t-test was used to determine significance between cell lines for genotoxicity and gene expression. Significance was set at $p < .05$. Analyses were performed using Prism 9 (Version 9.5.0 for Windows).

Results

Cell viability

None of the phenolic compounds (0–100 μ M) tested significantly influenced the viability of HT29 cells (Figure 1), whereas cell viability for CCD 841 CoN cells was decreased to \sim 75% at the highest concentration tested of each phenolic. Consistent with Dobani et al. (2021), the dose range (0–100 μ M) was considered to be sub-cytotoxic for the purposes of the remaining experiments.

DNA damage reduction

All four phenolics, 3'HPPA, 3PPA, 4HBA and BA, reduced oxidative-induced DNA damage in HT29 and

CCD 841 CoN cells. In the HT29 cell line, the benzoic acids showed different patterns of effect (Figure 2(A,B)) with BA exerting a dose-dependent response with maximal effect at 100 μ M, where BA reduced DNA damage to 26.9% tail DNA ($F(4, 10) = 25.7, p < .001$), followed by 50 μ M BA (34.8%, $F(4, 10) = 25.7, p < .001$) and 10 μ M BA (43.4%, $F(4, 10) = 25.7, p < .05$) (Figure 2(A)). In contrast, 4HBA exhibited more genoprotection at the lowest concentration (10 μ M) where it produced a threshold effect, resulting in reductions in DNA damage to 29.9% ($F(4, 10) = 19.3, p < .001$) and reduced activity seen at the higher concentrations (32.2% tail DNA at 50 μ M and 31.7% tail DNA at 100 μ M) (Figure 2(B)). For the phenylpropanoic acids (3PPA and 3'HPPA; Figure 2(C,D)), the most potent effect in the HT29 cells was observed at 50 μ M with DNA damage reduced to 32.2% ($F(4, 10) = 72.2, p < .001$) and 34.4% ($F(4, 10) = 43.8, p < .001$), respectively, while higher concentrations were less genoprotective. However, it was notable that 3'HPPA caused a significant reduction in DNA

damage at 10 μ M (43.3%, $F(4, 10) = 43.8, p < .01$) and was significantly ($F(3, 8) = 10.5, p < .05$) different in comparison to 3PPA which had no observable effect (48.4%) (Figure 2(D)).

In the CCD 841 CoN cell line, BA exhibited a dose-dependent response with maximal effect at 100 μ M, reducing DNA damage to 24.6% ($F(4, 10) = 50.7, p < .001$), followed by 50 μ M BA (35.0%, $F(4, 10) = 50.7, p < .001$) and 10 μ M BA (40.3%, $F(4, 10) = 50.7, p < .05$) (Figure 2(A)). 4HBA was most potent at the highest 100 μ M concentration (25.1%, $F(4, 10) = 32.8, p < .001$) but interestingly was similarly effective at the lowest dose 10 μ M (31.8%, $F(4, 10) = 32.8, p < .001$) (Figure 2(B)). The hydroxylated form is therefore more potent than the non-hydroxylated BA. For the phenylpropanoic acids, 3PPA and 3'HPPA (Figure 2(C,D), respectively), the most potent effect was observed at 100 μ M (reductions to 24.7% and 22.5%, respectively; $F(4, 10) = 45.1$ and 43.1 , respectively, $p < .001$), however at the lowest concentration (10 μ M) only 3'HPPA exerted a significant reduction

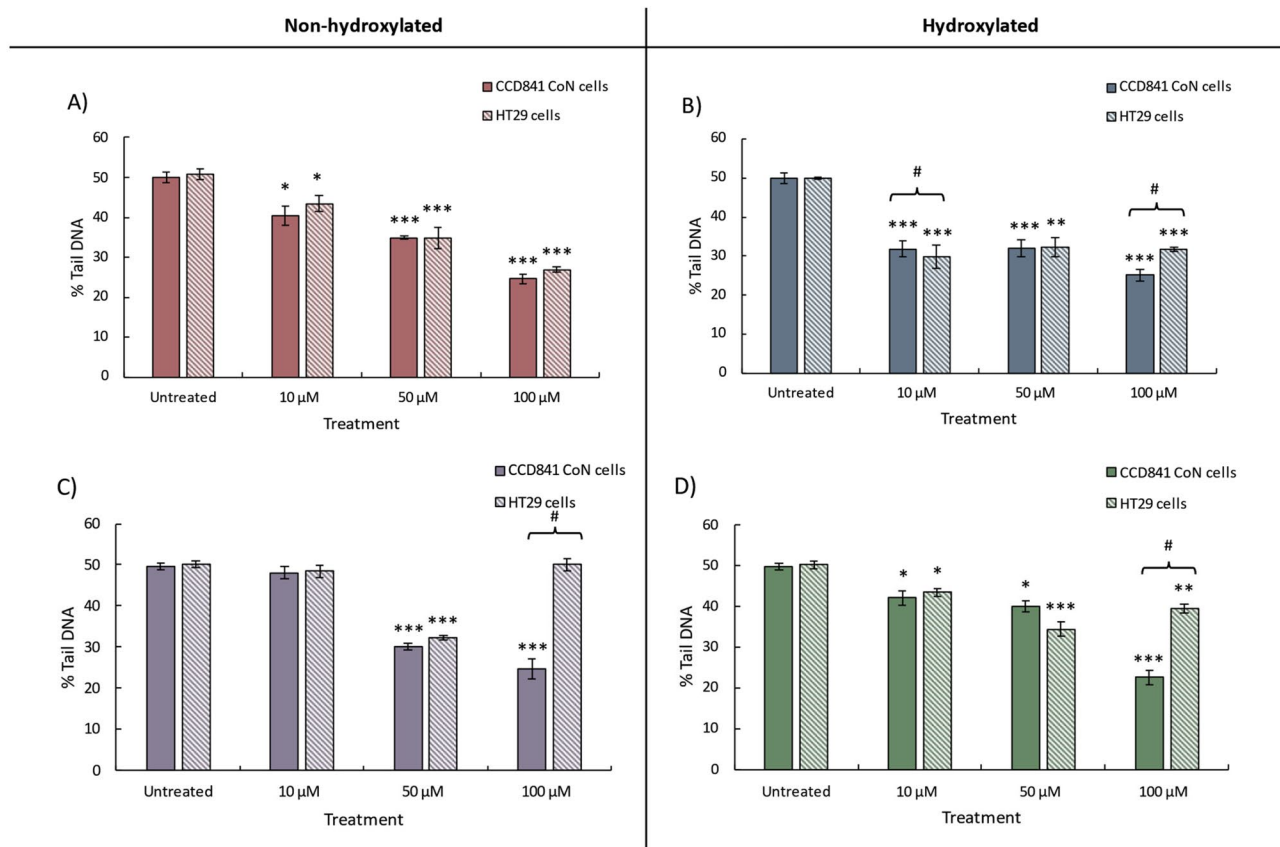


Figure 2. DNA damage reducing capacity of four individual phenolics on CCD 841 CoN and HT29 cells in response to oxidative challenge. Data for (A) benzoic acid (BA), (B) 4-hydroxybenzoic acid (4HBA), (C) 3-(phenyl)propanoic acid (3PPA) and (D) 3-(3'-hydroxyphenyl)propanoic acid (3'HPPA), at 10, 50 or 100 μ M after 24 h pre-incubation of cells at 37 $^{\circ}$ C and challenge with H_2O_2 (75 μ M – HT29 or 25 μ M – CDD 841 CoN) are presented. Data are presented as mean of three independent experiments \pm SEM. Significance is compared to untreated control using one-way ANOVA and Dunnett's multiple comparison test, * $p < .05$, ** $p < .01$, *** $p < .001$, significance compared between cell types using an independent t-test, # $p < .05$.

in DNA damage compared to control (42.0% vs 49.6%; $F(4, 10) = 43.1, p < .05$). This could indicate that 3'HPPA is the more potent compound, however, at 50 μM , 3PPA was significantly more effective in preventing DNA damage ($F(3, 8) = 6.67, p < .05$) than 3'HPPA.

The phenolic compounds under investigation did not exert significant genotoxic damage compared to the negative experimental control in either cell line (data not shown) but did significantly reduce DNA damage (% Tail DNA) in response to oxidative challenge. 4HBA was more potent than BA in both cell lines, causing significant reduction in DNA damage even at lower concentrations. The effect of hydroxylation on DNA damage reduction was less consistent for the phenylpropanoic acids as 3PPA did not significantly decrease in DNA damage at 10 μM in either cell line nor at the highest dose (100 μM) for HT29 in contrast to the pattern observed for 3'HPPA (Supplementary Table 1).

Modulation of gene expression within the Nrf2-pathway

Addition of the phenolic acids resulted in an increase in the measured expression of Nrf2 in both cell lines compared to the untreated control (Figure 3(A-D)). Changes in Nrf2 expression were generally similar between cell lines, however higher phenolic concentrations (50 and 100 μM) elicited significant increases ($F(4, 10) = 259, p < .05$) in Nrf2 expression above the controls. A dose effect was observed in HT29 cells treated with BA (maximum 2.37-fold increase, 100 μM , $p < .001$; Figure 3(A)), however an inverse correlation between dose and expression was seen for 4HBA with no significant change from the control at 100 μM (Figure 3(B)). An exception to these general observations was in HT29 adenocarcinoma cells, where the addition of 3PPA resulted in highly significant ($F(4, 10) = 521, p < .001$) decreases in Nrf2 expression at both 10 μM and 100 μM , but with a highly significant ($p < .001$) increase at 50 μM (Figure 3(C)).

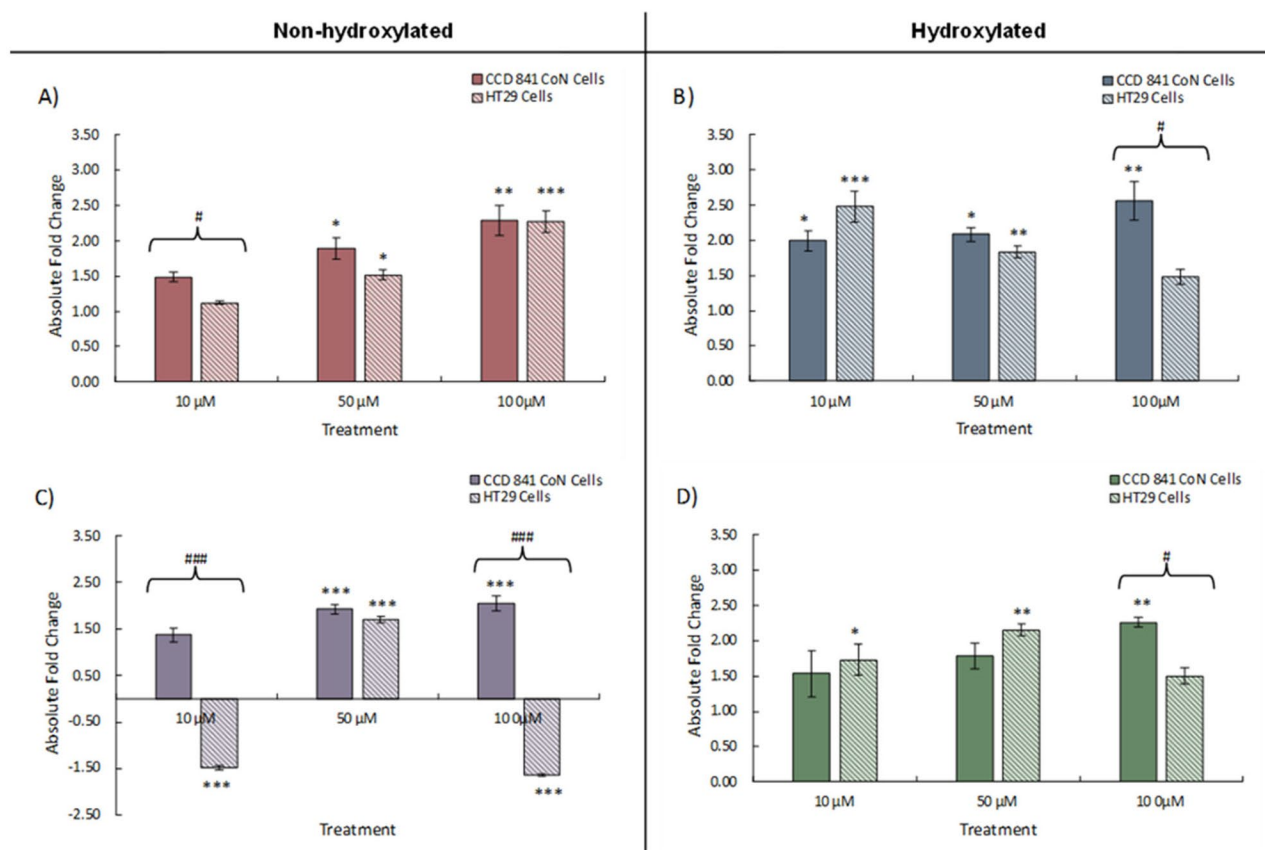


Figure 3. Change in Nrf2 expression in CCD 841 CoN and HT29 cells treated with either 10, 50 or 100 μM of individual phenolic compounds. Data for (A) benzoic acid (BA), (B) 4-hydroxybenzoic acid (4HBA), (C) 3-(phenyl)propanoic acid (3PPA) and (D) 3-(3'-hydroxyphenyl)propanoic acid (3'HPPA) are presented as mean of three independent experiments \pm SEM. Significance is compared to untreated control using one-way ANOVA and Dunnett's multiple comparison test, * $p < .05$, ** $p < .01$, *** $p < .001$, significance compared between cell types using an independent t-test, # $p < .05$, ### $p < .001$.

By comparison, the CCD 841 CoN normal cell line exhibited increases in Nrf2 expression under the same treatments and the observed difference suggests less well-regulated and/or responsive gene expression in the carcinoma cell line – in the presence of 3PPA – than normal CCD 841 CoN cells. It is known that Nrf2 binds to the ARE element upstream of target genes and increases expression of antioxidant defence/detoxification functions within the cell (Saha et al. 2020) and we therefore measured expression of NQO1 and HO-1 in the cell lines under investigation.

NQO1 scavenges ROS and is implicated in reducing DNA damage (Rashid et al. 2021) and, in our investigation, NAD(P)H:quinone oxidoreductase 1 (NQO1) expression, similar to Nrf2 expression, was increased by the addition, individually, of all four phenolic acids to both cell lines (Figure 4(A–D)). The less transformed CCD 841 CoN cells exhibited increased NQO1 expression with increasing phenolic concentration with the most pronounced dose effect observed with 3PPA (Figure 4(C)). Similar to the Nrf2 data, decreases in NQO1 expression were measured in HT29 cells in

the presence of 3PPA, possibly as a consequence of the apparently dysregulated Nrf2 expression also observed in these cells with this treatment. We also noted decreased expression (1.5-fold) of NQO1 in HT29 cells exposed to 100 μ M 4HBA, contrasting with a 1.5-fold increase in expression in CCD 841 CoN cells exposed to the same treatment (Figure 4(B)). Statistically significant differences in NQO1 expression between CCD841 and HT29 cells again mapped – broadly – to the same phenolic treatments where such differences were observed in Nrf2 expression, and the data suggests that the greatest differences in gene expression between cells occurs at both the lowest and highest phenolic concentrations.

Haem oxygenase (HO-1) is an inducible enzyme that exerts cytoprotective effects, as the products of its catabolism of haem possess antioxidative, anti-inflammatory and antiapoptotic activities (Zhang et al. 2021). For this gene, we again observed a similar response to treatment with increases in expression arising from treatment of both cell lines (Figure 5(A–D)). Divergence in HO-1 expression between CCD

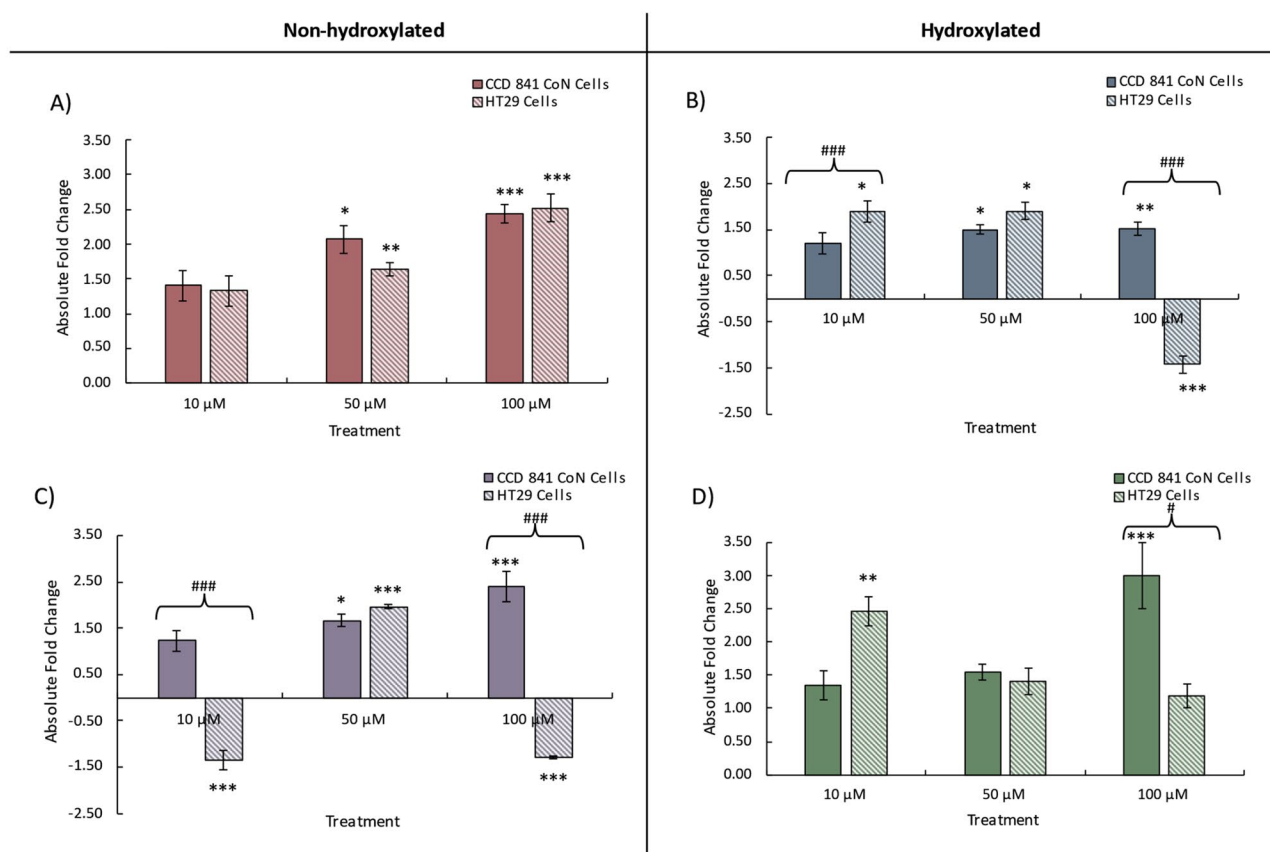


Figure 4. Change in NQO1 expression in CCD 841 CoN and HT29 cells treated with either 10, 50 or 100 μ M individual phenolics; (A) benzoic acid (BA), (B) 4-hydroxybenzoic acid (4HBA), (C) 3-(phenyl)propanoic acid (3PPA) and (D) 3-(3'-hydroxyphenyl)propanoic acid (3'HPPA). Data presented are as mean of three independent experiments \pm SEM. Significance is compared to untreated control using one-way ANOVA and Dunnett's multiple comparison test, * $p < .05$, ** $p < .01$, *** $p < .001$, significance compared between cell types using an independent t-test, # $p < .05$, ### $p < .001$.

841 CoN (increase) and HT29 cells (decrease) with 10 μ M and 100 μ M 3PPA was observed (Figure 5(C)), consistent with our observation for Nrf2 and NQO1 (Figures 3(A–D) and 4(A–D), respectively). We also noted a relatively greater maximum increase in HO-1 expression with BA (Figure 5(A)) and 4HBA (Figure 5(B)) and for 3'HPPA (Figure 5(D)), with the maximal increases – with the exception of 3PPA (50 μ M; Figure 5(C)) – observed following treatment with 100 μ M of a given phenolic. With the exception of the divergence in expression between cell lines, expressional changes following treatment with 3PPA were more modest (~1.5-fold) (Figure 5(C)) an observation made also for both Nrf2 (Figure 3(A–D)) and NQO1 (Figure 4(A–D)) expression. 3'HPPA at the lowest phenolic concentration (10 μ M) consistently exhibited no significant changes to gene expression for the normal cell line versus HT29 cells. Moreover, 3PPA and 4HBA exerted decrease in genes expression in HT29 cells whereas the normal cells were unaffected to responded with an increase in gene expression. Overall only limited differences were observed between the

hydroxylated and non-hydroxylated phenolics' ability to modulate the expression of each of the genes were evident and no discernible pattern was evident (Supplementary Table 1).

Taken together, our data indicate that each of the phenolic compounds tested reduce DNA damage in colonic cells in response to an oxidative stress challenge. This effect appears mediated, in part, by altered gene expression of Nrf2, NQO1 and HO-1 genes. Some concentration and or structure dependent effects were apparent in the response of the more and less transformed cell lines to the phenolic acids tested. For example, phenylpropanoic acid treatments (PPA and 3'HPPA) caused noticeably different patterns of response in both cell lines (except 50 μ M), while benzoic acids (BA and 4HBA) elicited similar levels of gene expression except at the highest concentration of 4HBA (Figure 3(B)).

Discussion

Reducing damage to DNA is a critical cellular defence mechanism that safeguards against mutations and

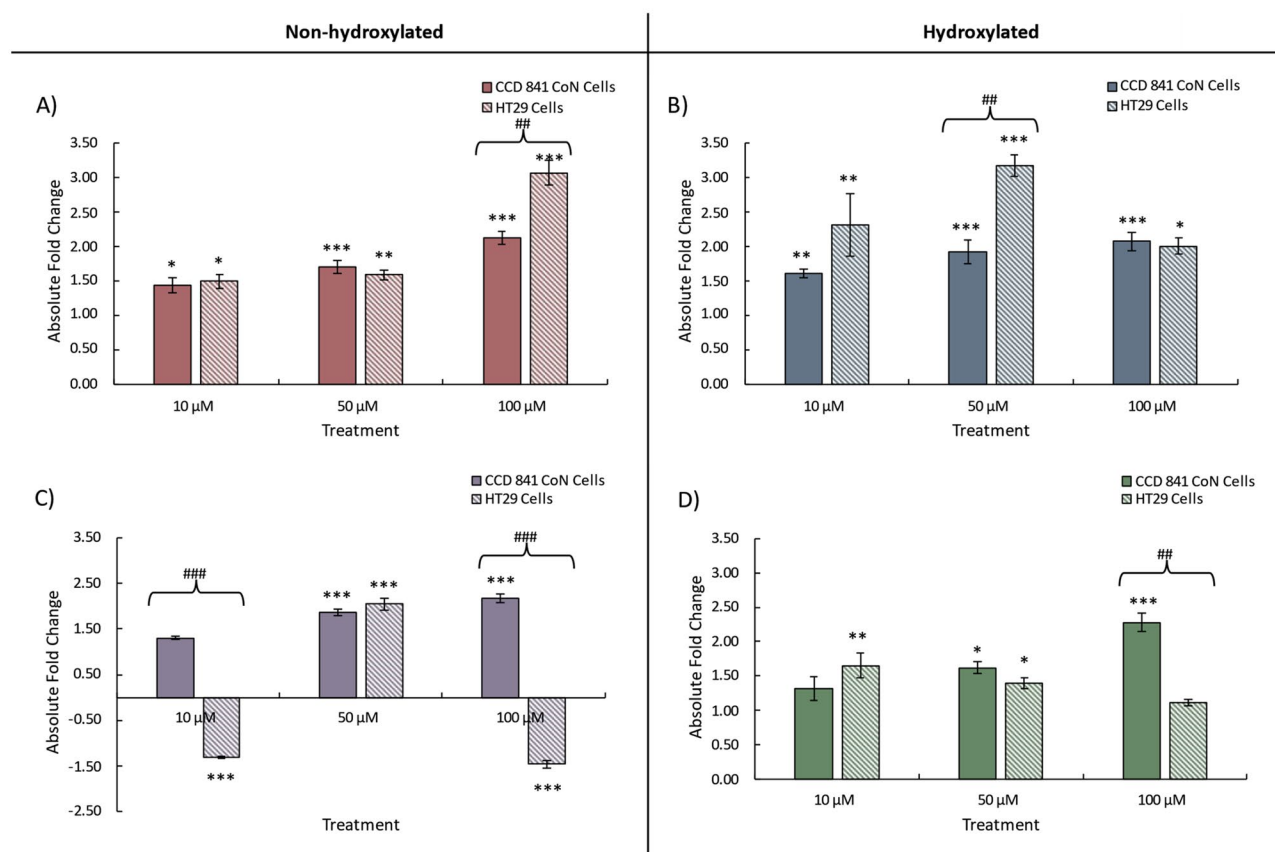


Figure 5. Change in HO-1 expression in CCD 841 CoN and HT29 cells treated with either 10, 50 or 100 μ M individual phenolics; (A) benzoic acid (BA), (B) 4-hydroxybenzoic acid (4HBA), (C) 3-(phenyl)propanoic acid (3PPA) and (D) 3-(3'-hydroxyphenyl)propanoic acid (3'HPPA). Data presented are as mean of three independent experiments \pm SEM. Significance is compared to untreated control using one-way ANOVA and Dunnett's multiple comparison test, * p < .05, ** p < .01, *** p < .001, significance compared between cell types using an independent t-test, ## p < .01, ### p < .001.

maintains normal cellular functions (Izquierdo-Vega et al. 2017). Extensive research has established that (poly)phenols could positively contribute in maintaining a healthy status by influencing this mechanism along with exerting anti-proliferative, anti-inflammatory and anti-oxidative effects (Moura et al. 2013; Coşarçâ et al. 2019; Patra et al. 2021; Pereira-Caro et al. 2023). As a result, there has been increased interest in determining the mechanism of actions of these plant-derived compounds and more recently their catabolites, at both the cellular and systemic level.

Due to their extensive biotransformation, especially in the distal gut, which alters (poly)phenol bioavailability and biological activity, it is important to test dietarily relevant phytochemicals at physiologically relevant doses and in the chemical forms encountered by different human tissues (Del Rio et al. 2013; Mena et al. 2019). Phenolic acids are present both in the food sources and as catabolites derived from their in planta parent (poly)phenols (Brown et al. 2014; McDougall et al. 2017; Mena et al. 2019; Luca et al. 2020; Diotallevi et al. 2021; Rodríguez-Daza et al. 2021; Wang et al. 2022) formed during catabolism by the intra-luminal microbiota (Carregosa et al. 2022), as well as from the putative metabolism of other compounds such as phenylalanine and catecholamines (Pereira-Caro et al. 2023). Compositional analyses of *in vivo* digestion or *in vitro* faecal fermentations can determine the physiological relevance of these compounds to the colon (Brown et al. 2012; Dobani et al. 2021). For example, Dobani et al. (2021) highlighted a clear differentiation between pre- and post-fermentation ileal fluid samples, with eight raspberry-derived phenolic acid catabolites identified as key discriminators of the fermentation process, four of which were assessed for their genoprotective potential and the ability to modulate genes in the cyto-protective Nrf2 mediated ARE pathway in normal colonocytes (CCD 841 CoN).

In the current study, the work by Dobani and colleagues on the genoprotective effects of the simple phenolics (3PPA, 3'HPPA, BA, 4'HBA) on the CCD 841 CoN cells (Dobani et al. 2021) has been expanded using the classic and more transformed colonocyte cell line HT29. This cell line exhibits rapid growth, irregular morphology and carries genetic alterations associated with colorectal adenocarcinoma (Pearce et al. 2018). In contrast, CCD 841 CoN cells are derived from normal cells, display slower growth, epithelial-like morphology and retain the genetic and phenotypic characteristics of healthy colonic epithelium (Zoetemelk et al. 2019). Heterogeneities in both physiological and biochemical response have been

report-ed between these cell lines when testing the same compound under similar conditions (Pan et al. 2021) and, in the current work, the individual phenolic acid treatments exerted greater genoprotective capacity in the CCD 841 CoN cell line, particularly at the highest concentrations of 4HBA, 3PPA and 3'HPPA. By contrast, a recent *ex vivo* study investigating strawberry enriched ileal fluid fermentates in the same cell lines, determined that a complex mixture of (poly)phenolic compounds was less effective in reducing DNA damage in CCD 841 CoN cells than HT29 cells in response to oxidative challenge (Diotallevi et al. 2021). An investigation that assessed a colonically relevant raspberry-derived triterpenoid extract elucidated that the extract exerted greater anti-genotoxic capacity in the CCD 841 CoN cells than HT29 cells, reducing DNA damage by ~55% and ~45%, respectively (McDougall et al. 2017). Overall, the data from the current investigation are generally consistent with previous work in our laboratory (Brown et al. 2012), in which HT29 cells treated with 5 µg/mL of 3'HPPA (30 µM) or 4HBA (~36 µM) exhibited a reduction in DNA damage of 30% in response to oxidative challenge (75 µM H₂O₂), similar to the magnitude of effect reported here. It has been reported that açai and blueberry extracts (2.5 mg/mL), which are also sources of simple phenolic compounds like 4HBA, in addition to other polyphenolics such as pelargonidin-3-O-glucoside, reduced DNA damage in HT29 cells by ~60% ($p < .001$) compared to the untreated control (Randah et al. 2018). What are arguably the physiologically more relevant effects were revealed when the *in vitro* digested and fermented açai extract was tested, where it significantly reduced DNA damage by ~31.5% (Alqurashi et al. 2017).

The gut microbiota plays a pivotal role in the modulation of (poly)phenols and their colonic catabolites (Brown et al. 2014; McDougall et al. 2017; Luca et al. 2020). The phenolic acids used in this study are present during colonic transit at differing concentrations and in differing forms, differentiated through the presence/absence of a hydroxyl group. Hydroxylated phenolics have been reported to have higher bioavailability and bioactivity (Lee et al. 2023) and this may be corroborated by comparison of DNA damage between the hydroxylated and non-hydroxylated phenolics in each cell line. Treatment with both 4HBA and 3'HPPA resulted in greater reductions in DNA damage, particularly at lower concentrations, than either BA or 3PPA, in addition to their higher level of gene modulation, particularly in the adeno-carcinoma cells. This observation may be due to greater antioxidant activity and indeed a recent study (Chiang et al.

2016) reported that the microbially derived 3'-hydroxylated soy isoflavone derivatives, 3'-hydroxydaidzin and 3'-hydroxygenistin, exhibited higher free radical scavenging activity than their non-hydroxylated counterparts. In addition, Cao et al. (1997) reported stronger antioxidant activity in flavonoids with hydroxyl groups at both the 3' and 4' positions of the B-ring in comparison to their dehydroxylated counterparts. Our observations, therefore, may be attributable to the increased antioxidant activity seen with the hydroxylated phenolic acids, as hydroxyl groups are reported as having strong radical-scavenging and antioxidant effects (Umeno et al. 2016; Kostić et al. 2023). As both the hydroxylated and non-hydroxylated forms provide genoprotective effects *in vitro* at physiological levels, this suggests that they could provide synergistic protection following their colonic generation *via* the successive microbial degradation of intact flavonoids to the simple phenolic acids that accumulate and are excreted in the faeces.

The underlying mechanism behind the antigentotoxic effects of these compounds is not fully understood, however, accumulating evidence (Yoshimura et al. 2016; Mou et al. 2017; Bajpai et al. 2019; Silva et al. 2019; Darband et al. 2020; Moratilla-Rivera et al. 2023) suggests that the Nrf2-ARE pathway may play a role in protecting against DNA damage by activating down-stream targets such as NQO1 and HO-1, potent anti-inflammatory enzymes that alleviate oxidative stress in cells (Saha et al. 2020). The current study clearly highlights the role each phenolic acid may play in modulating the expression of Nrf2 and its target genes, NQO1 and HO-1 in both normal colonic epithelial cells (CCD 841 CoN) and carcinogenic colonic epithelial cells (HT29). The hydroxylation status of the phenolic compound tested appears to exert some differential effects on gene expression for HO1 and NQO1 but not for Nrf2. For Nrf2, no clear pattern of effect was evident, for example PPA and 3'HPPA caused noticeably different patterns (increase vs decrease) while benzoic acids elicited similar patterns and levels of gene expression in both cell lines. This is in broad agreement with the previous finding of McDougall et al. (2017) who demonstrated that a raspberry triterpenoid-rich fraction caused increased expression of Nrf2 in HT29 cells but, conversely, decreased it in CCD 841 CoN cells, while measured NQO1 (increase) and HO-1 (decrease) gene expression was similar in both cell lines. More recently, research in hepatocyte cells (HepG2) (Chen et al. 2019) demonstrated that a solvent-based raspberry extract (200 µg/mL) – albeit at physiologically questionable levels – increased Nrf2, NQO1 and HO-1

gene expression by 38.4% ($p < .01$), 18.7% ($p < .01$) and 9.4% relative to the control. (Poly)phenols, such as resveratrol, cyanidin, chlorogenic acid and luteolin also activate the Nrf2-ARE pathway and exert antigentotoxic effects (Teng et al. 2017; Kang et al. 2019). Indeed, luteolin (60 µM) reduced H₂O₂ induced ROS generation (at 24h) by 50% in a dose-dependent manner, mediated in part by significant ($p < .05$) time dependent (12, 24 and 48h) increases in Nrf2 expression (~15-, 50- and 145-fold increased mRNA levels, respectively) in HT29 cells (Kang et al. 2019).

Polyphenols also interact with intestinal microbiota modulating of composition, promoting the growth of bacteria such as *Lactobacillus*, *Akkermansia* and *Bifidobacterium* (Rodríguez-Daza et al. 2021), while suppressing pathogenic bacteria like *Escherichia coli* and *Bacteroides fragilis* (Zhao et al. 2023). Such alterations of the gut microbiota exert putative anti-cancer effects including direct tumour suppression and modulation of the immune system (Li et al. 2024; Zhao et al. 2023; Masheghati et al. 2024). For example, hydrocaffeic acid and urolithin A have been shown to exhibit anti-inflammatory and anti-cancer activities by upregulating tight junction proteins (e.g. ZO-1, occludin) through pathways like AhR and Nrf2, thereby protecting gut barrier integrity and inhibiting proinflammatory cytokines (Zhao and Jiang 2021). While a polyphenol-rich cranberry extract exerted a prebiotic effect increasing *Akkermansia muciniphila*, stimulating mucin production *via* MUC2 expression and promoting expression of tight junction proteins such as occludin and claudin, thereby improving barrier function and reducing chronic inflammation of the intestinal cells (Chelakkot et al. 2018; Yu et al. 2022; Li et al. 2024). More recently Lessard-Lord et al. (2024) demonstrated cranberry extract improving MUC2 and TJP1 although this was associated with increases bifidobacterium and the decrease of bacteroides rather than *Akkermansia*. Therefore, the current study builds upon our previous work, and that of others, albeit limited as it uses only a single cancer cell line (HT29) to contrast against the Con CD841 cell line, nonetheless, the results emphasise the role of (poly)phenols in inducing phase II detoxifying and antioxidant enzymes, regulating oxidative stress in both normal and adenocarcinoma cells. However, the effects vary depending on the compound, concentration and cell type. Future research should seek to further explore these findings, utilising multiple carcinogenic cells lines with long-term exposure to the individual phenolics. Moreover, further research is needed to evaluate the production of lactate dehydrogenase and glutathione to further elucidate the proposed protective effects.

Conclusions

This study provides evidence that microbially mediated phenolic catabolites possesses the ability to reduce DNA damage induced by oxidative challenge in two colonic epithelial models (CCD841 CoN and HT29 colonic cell lines). The protective effect is partially attributed to the upregulation of the Nrf2-ARE pathway and its downstream targets, NQO1 and HO-1. Despite this, the hydroxylation state of the phenolic acids appears to have limited impact on the bioactivity overall. Consequently, the presence of abundant amounts of low molecular weight phenolic catabolites from diets rich in (poly)phenols may exert protective effects against colonic epithelial damage *in vivo* by reducing DNA damage, a key early-stage event in colorectal carcinogenesis.

Authors contributions

C.I.R.G., G.McD., I.R. and A.C. were involved in study design. B.Ó.M. S.D., M.F. and C.L., were involved in experimental and data analysis. The manuscript was prepared by B.Ó.M., T.M.A., C.L., S.D., G.P.-C., K.M.T., N.G.T., L.K.P., D.D.R., C.L., I.R., G.McD., A.C., N.K. and C.I.R.G with contributions from all the authors.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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