

ORIGINAL ARTICLE

Plasma concentrations of advanced glycation end-products and colorectal cancer risk in the EPIC study

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Abstract

Advanced glycation end-products (AGEs) are a heterogeneous group of compounds formed by the non-enzymatic reaction between amino acids and reducing sugars, or dicarbonyls as intermediate compounds. Experimental studies suggest that AGEs may promote colorectal cancer, but prospective epidemiologic studies are inconclusive. We conducted a case-control study nested within a large European cohort. Plasma concentrations of three protein-bound AGEs—N^ε-(carboxymethyl)lysine (CML), N^ε-(carboxyethyl)lysine (CEL) and N^ε-(5-hydroxy-5-methyl-4-imidazolone-2-yl)-ornithine (MG-H1)—were measured by ultra-performance liquid chromatography–tandem mass spectrometry in baseline samples collected from 1378 incident primary colorectal cancer cases and 1378 matched controls. Multivariable-adjusted odds ratios (ORs) and 95% confidence intervals (CIs) were computed using conditional logistic regression for colorectal cancer risk associated with CML, CEL, MG-H1, total AGEs, and [CEL+MG-H1: CML] and [CEL:MG-H1] ratios. Inverse colorectal cancer risk associations were observed for CML (OR comparing highest to lowest quintile, OR_{Q5 versus Q1} = 0.40, 95% CI: 0.27–0.59), MG-H1 (OR_{Q5 versus Q1} = 0.73, 95% CI: 0.53–1.00) and total AGEs (OR_{Q5 versus Q1} = 0.52, 95% CI: 0.37–0.73), whereas no association was observed for CEL. A higher [CEL+MG-H1: CML] ratio was associated with colorectal cancer risk (OR_{Q5 versus Q1} = 1.91, 95% CI: 1.31–2.79). The associations observed did not differ by sex, or by tumour anatomical sub-site. Although individual AGEs concentrations appear to be inversely associated with colorectal cancer risk, a higher ratio of methylglyoxal-derived AGEs versus those derived from glyoxal (calculated by [CEL+MG-H1: CML] ratio) showed a strong positive risk association. Further insight on the metabolism of AGEs and their dicarbonyls precursors, and their roles in colorectal cancer development is needed.

Abbreviations

AGE	advanced glycation end-product
BMI	body mass index
CEL	N ^ε -(carboxyethyl)lysine
CI	confidence interval
CML	N ^ε -(carboxymethyl)lysine
CRC	colorectal cancer
EPIC	European Prospective Investigation into Cancer and Nutrition
GO	glyoxal
IARC	International Agency for Research on Cancer
ICD	International Classification of Diseases
MG-H1	N ^ε -(5-hydroxy-5-methyl-4-imidazolone-2-yl)-ornithine
MGO	methylglyoxal
RAGE	receptor for AGE
SD	standard deviation
UPLC-MS/MS	ultra-performance liquid chromatography–tandem mass spectrometry

Introduction

Colorectal cancer (CRC) is the third most common incident cancer and the second leading cause of cancer death globally (1). A substantial body of epidemiologic evidence, particularly from large-scale prospective cohort studies, apportions a considerable contribution of modifiable dietary and lifestyle risk factors to CRC development (2–4). Western-type diets tend to promote the formation of advanced glycation end-products (AGEs), a heterogeneous class of pro-inflammatory and pro-oxidative compounds formed irreversibly by the non-enzymatic combination of amino acids and reducing sugars (5–8). AGEs can also be formed when proteins are glycosylated by highly reactive dicarbonyls such as glyoxal (GO) and methylglyoxal (MGO) absorbed from the diet, and/or smoking or produced as sugar and lipid metabolism by-products (8,9). GO and MGO have been reported to be over 20 000 times more potent in glycosylating amino acids, compared to sugars (10,11). As a consequence, most abundant AGEs in the body are derived from GO [N^ε-(carboxymethyl)lysine (CML)] or MGO [N^ε-(carboxyethyl)lysine (CEL) and N^ε-(5-hydroxy-5-methyl-4-imidazolone-2-yl)-ornithine, (MG-H1)] (12–14).

AGEs are thought to affect CRC development by promoting a pro-inflammatory and oxidative environment, primarily via binding to the receptor for AGEs (RAGE), a transmembrane protein that belongs to the immunoglobulin superfamily (15). Immunohistochemical expression of AGEs is higher in colon cancer tumours compared to adjacent normal tissues and AGEs have been shown to enhance and promote colon cancer growth in *in vitro* models (16–18). Animal studies show that AGEs can induce sustained inflammation in the colon and promote colon cancer development (19,20). However, two case-control studies nested within prospective studies have reported inconclusive findings for the association between circulating AGEs levels and CRC. In the Women's Health Initiative (WHI) study, Chen *et al.* (21) found an inverse association between serum CML and CRC in women [odds ratio (OR) = 0.85, 95% confidence interval (CI): 0.49–1.47], while Jiao *et al.* (22) reported a positive association between circulating CML and CRC risk in male smokers (OR = 1.20, 95% CI: 0.64–2.26) in the Alpha-Tocopherol, Beta-Carotene Cancer Prevention (ATBC) study. These previous investigations focused on CML only and did not include other major AGEs or assess possible differences by sex or tumour anatomical sub-site. Furthermore, they detected AGEs by ELISA kits, which have low specificity and reproducibility (23).

The aim of the present study was to examine the associations between pre-diagnostic protein-bound circulating levels of CML, CEL and MG-H1 measured using ultra-performance liquid chromatography–tandem mass spectrometry (UPLC-MS/MS) and CRC risk in the European Prospective Investigation into Cancer and Nutrition (EPIC) cohort. The rationale for the selection of these three AGEs is threefold: they are considered as the most abundant in the body, they have very well-characterized chemical structures and they are derived from specific pathways of formation with CML being mainly derived from GO, whereas CEL and MG-H1 are mainly derived from MGO. For CML and CEL, lysine is the amino acid of the glycation site, whereas it is arginine for MG-H1. At the cellular level, the MGO-lysine adduct CEL is predominantly formed in the cytosol through the glycation of cytosol proteins, whereas the MGO-arginine adduct MG-H1 is equally found in cytosol, histone and mitochondria proteins (24). We hypothesized that protein-bound concentrations of these AGEs would be associated with a higher CRC risk. We also examined CRC risk associated with the ratios of

AGEs from specific dicarbonyls similar to the [CEL:MG-H1] ratio assessed in previous studies (25,26), as a potential index of the chemical origin of the AGEs. Although MGO glycate amino acids to CEL and MG-H1, both these MGO-derived AGEs have different promoting factors as they are produced from lysine and arginine, respectively. Thus, we applied the ratio of [CEL:MG-H1] as a proxy of the potential differential glycation activities of MGO in the body.

Materials and methods

Study population and data collection

We conducted a nested case-control study within the EPIC cohort, an ongoing multicentre prospective study with participants recruited from 23 centres constellated in 10 European countries (Denmark, France, Germany, Greece, Italy, the Netherlands, Norway, Spain, Sweden and the UK) (27). A total of 521 324 participants were recruited into EPIC between 1992 and 2000. Detailed data on lifestyle, dietary and socio-demographic factors were collected at baseline from all the participants. Body weight and standing height were measured by trained health professionals using standardized protocols. Lifestyle variables such as smoking, physical activity and the level of education were collected using a validated, standardized questionnaire. Information on the highest attained educational level was categorized as none, primary, technical and professional, secondary or higher (college or university). Smoking was collected as status (current, past, never), by type of products (cigarettes, cigars, pipe), intensity (number of cigarettes) and duration (in years of smoking). Information on past smoking habits and the years since quitting smoking was collected in former smokers. Physical activity was defined according to the Cambridge physical activity definitions: inactive (sedentary job plus no recreational activity), moderately inactive (sedentary job with <0.5 h recreational activity daily/or standing job with no recreational activity), moderately active (sedentary job with 0.5–1 h recreational activity daily/or standing job with 0.5 h recreational activity daily/or physical job with no recreational activity) or active (sedentary job with >1 h recreational activity daily/or standing job with >0.5 h recreational activity daily/or physical job with at least some recreational activity/or heavy manual job) (28). Blood samples were collected and are stored in liquid nitrogen (–196°C) in biobank facilities located at the International Agency for Research on Cancer (IARC), or in local biobanks in Denmark (–150°C) and Sweden (–80°C at Malmö and Umeå) until analysis. Informed consent was obtained from all the

participants. The EPIC study was approved by the IARC Ethical Committee and the local ethics committees pertaining to each participating centre.

Follow-up for CRC incidence and vital status

Vital status (98.4% complete) was ascertained on a regular basis using record linkage with centralized regional cancer registries (Denmark, Italy, the Netherlands, Norway, Spain, Sweden and UK) or via a combination of methods including use of health insurance records, connection with cancer and pathology registries and active follow-up through participants and their close relatives (France, Germany and Greece). Incident CRC cases were ascertained according to the classification by the International Classification of Diseases for Oncology (ICD-O, codes C18–C20). Colon cancer included tumours in the proximal site (C18.0–C18.5: from caecum to splenic flexure) or the distal segment (C18.6–C18.7: from descending colon down to sigmoid colon), while rectal cancer included tumours that occurred from the recto-sigmoid junction (C19) down to the rectum (C20). Tumours that arose in the anus and in the anal canal (C21) were not included in this analysis.

Nested case-control design study

A total of 1416 incident CRC cases were identified and matched on 1:1 ratio to controls by incidence density sampling from all cohort members alive and free of cancer at the time of diagnosis of the index case. Cases were selected sequentially in the order of date of diagnosis and based on sufficient biological sample availability. The following matching criteria were applied: age at blood collection (± 1 year), sex, recruiting centre, time of the day at blood collection (± 3 h), fasting status at blood collection (<3, 3–6 and >6 hours), and, additionally, among women by menopausal status (pre-menopause, peri-menopause and post-menopause) and hormone replacement therapy use at time of blood collection (yes/no). We excluded subjects within incomplete matched case sets (i.e. a case without a control or vice versa, $n = 12$), and 26 cases and their matched controls from Greece due to unforeseen data restriction issues. Thus, the final data analysis included 1378 CRC cases and their matched controls.

Laboratory analyses of AGEs

Plasma concentrations of protein-bound AGEs were determined with UPLC-MS/MS as previously described (29,30). In brief, protein-bound CML, CEL and MG-H1 were extracted from plasma using butanolic hydrochloric acid. The individual AGEs were quantified by calculating the area ratio of each unlabelled peak area to the corresponding internal standard. The sum of AGEs (Σ AGEs, in nmol/L) was calculated by summing up the

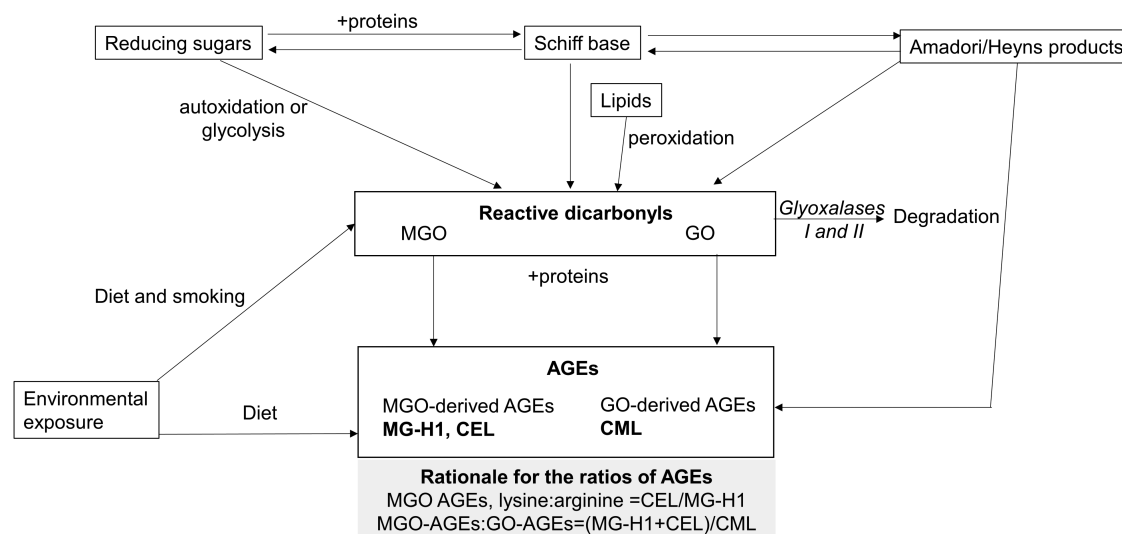


Figure 1. Schematic representation of the formation of the AGEs and the rationale for the calculation of the ratios. AGE, advanced glycation end-product; CML, N^ε-carboxy-methyllysine; CEL, N^ε-carboxy-ethyllysine; GO, glyoxal; MG-H1, N^ε-(5-hydro-5-methyl-4-imidazolone-2-yl)-ornithine; MGO, methylglyoxal. AGEs are absorbed from the diet or formed during the Maillard reactions from the Amadori or Heyns products and from the glycation actions of dicarbonyls such as MGO and GO. CML is derived from GO, whereas MG-H1 and CEL are derived from MGO.

circulating concentrations of CML, CEL and MG-H1 for each subject. We further calculated the ratios of the AGEs considering their dicarbonyl intermediates: MGO-derived:GO derived (i.e. CEL+MG-H1 divided by CML) (Figure 1). We also calculated the ratio of [(CEL+MG-H1):CML] to assess the influence of the relative abundance of lysine-sourced MGO-derived AGEs (CEL) versus arginine-sourced MGO-derived AGEs (MG-H1).

Statistical analysis

Means, standard deviations or frequencies were calculated for all variables. Multivariable conditional logistic regression was used to estimate ORs and 95% CIs for CRC risk associated with circulating levels of protein-bound CML, CEL, MG-H1, Σ AGEs as well as [(CEL+MG-H1):CML] (i.e. MGO:GO AGEs) and [(CEL+MG-H1):CML]. For each main outcome variable (measured biomarker or calculated ratio), quintile cut points were determined based on the distribution in controls. We ran two models: Model 1 was conditioned on the matching factors and Model 2 was further adjusted for body mass index (BMI, continuous), height (continuous), highest attained education level (none, primary, technical and professional, secondary, higher), physical activity (inactive, moderately inactive, moderately active, active), smoking status/duration/intensity (never, current smokers 1– ≤ 15 , 16– ≤ 25 , >26 cigarettes/day; former smokers ≤ 10 , 11– ≤ 20 , >20 years, occasional), and baseline intake levels of energy (continuous, kcal/day), alcohol, red and processed meats, dietary fibre and dairy products (all as continuous variables and as g/day). Tests for trend were run by using the median value of each quintile included in the model as continuous variables. Separate sub-group analyses were run by sex and anatomical sub-sites of CRC site (colon, rectal). The heterogeneity of the associations by sex, across anatomical sub-sites and in various sub-groups was assessed using the likelihood ratio test. We assessed the AGE-CRC association by sub-groups of type 2 diabetes (yes/no; self-reported at baseline) and obesity (defined as BMI ≥ 30 kg/m²). The potential bias of reverse causality in the AGE-CRC association was assessed by excluding cases diagnosed within the first 2 years. All the analyses were conducted using Stata 14.0 (StataCorp, College Station, TX, USA). Two-sided P-values <0.05 were statistically significant.

Results

Selected baseline characteristics of the study participants are shown in Table 1. Compared to controls, cases had higher BMI, higher intakes of alcohol and red and processed meats, and lower intakes of fruits, vegetables and dairy products. In addition, cases tended to be less physically active compared to controls.

The associations of individual and combined AGEs, and their various ratios calculated based on pathway of AGEs derivation, are shown in Table 2. No statistically significant association was observed between CEL and CRC risk (OR comparing highest to lowest quintile, OR_{Q5 versus Q1} = 0.88, 95% CI: 0.64–1.19, P_{trend} = 0.580), whereas inverse associations for CRC were observed for both CML (OR_{Q5 versus Q1} = 0.40, 95% CI: 0.27–0.59, P_{trend} < 0.001) and MG-H1 (OR_{Q5 versus Q1} = 0.73, 95% CI: 0.53–1.00, P_{trend} = 0.016). A near 50% lower odds for developing CRC was observed for Σ AGEs (OR_{Q5 versus Q1} = 0.52, 95% CI: 0.37–0.73, P_{trend} < 0.001), mostly driven by CML and MG-H1. The ratio of [(CEL+MG-H1):CML] was associated with an increased risk of CRC (OR_{Q5 versus Q1} = 1.91, 95% CI: 1.31–2.79, P_{trend} = 0.004).

We did not observe significant heterogeneity by sex or by tumour anatomical sub-sites for individual AGEs, Σ AGEs and [(CEL+MG-H1):CML] (Table 3). Analyses stratified by baseline diabetes status and by obesity as indicated by BMI ≥ 30 kg/m² showed that [(CEL+MG-H1):CML] was associated with higher CRC risk in diabetic versus non-diabetic subjects, and in obese versus non-obese subjects (Table 4). The inverse associations observed with individual AGEs and for Σ AGEs were more prominent in obese individuals compared to non-obese ones.

Table 1. Selected baseline demographic and lifestyle characteristics of study participants by colorectal cancer status, EPIC study 1992–2012

	Cases (n = 1378)	Controls (n = 1378)
Women, %	51.7	51.5
Anthropometry, mean (SD)		
BMI, kg/m ²	26.7 \pm 4.25	26.2 \pm 3.74
Waist circumference, cm	90.4 \pm 13.0	88.3 \pm 12.1
Waist-to-hip ratio	0.88 \pm 0.10	0.87 \pm 0.10
Lifestyle variables, n (%)		
Smoking status frequency and intensity		
Never	542 (39.8)	514 (37.9)
Current, 1–15 cigarettes/day	139 (10.2)	129 (9.51)
Current, 16–25 cigarettes/day	94 (6.91)	87 (6.40)
Current, 26+ cigarettes/day	23 (1.69)	20 (1.47)
Former, quit ≤ 10 years	129 (9.48)	139 (10.3)
Former, quit 11–20 years	123 (9.04)	144 (10.6)
Former, quit 20+ years	177 (13.0)	166 (12.2)
Current, pipe/cigar/occasional	102 (7.49)	125 (9.22)
Physical activity		
Inactive	361 (25.9)	327 (23.3)
Moderately inactive	448 (32.1)	457 (32.6)
Moderately active	311 (22.3)	284 (20.3)
Active	263 (18.9)	314 (22.4)
Highest education level attained		
None	66 (4.85)	68 (5.01)
Primary school completed	490 (36.0)	453 (33.4)
Technical/professional school	343 (25.2)	324 (23.9)
Secondary school	184 (13.5)	217 (16.0)
Higher education	244 (17.9)	247 (18.2)
Dietary intake, mean (SD)		
Energy, kcal/day	2127 \pm 609	2124 \pm 620
Alcohol, g/day	17.0 \pm 22.1	15.4 \pm 19.7
Red and processed meats, g/day	87.6 \pm 53.1	85.1 \pm 52.0
Fruits and vegetables, g/day	396 \pm 233	421 \pm 248
Cereals, g/day	216 \pm 121	216 \pm 119
Dairy products, g/day	331 \pm 251	351 \pm 244
Fish and products, g/day	28.2 \pm 28.8	29.6 \pm 30.6
Sugar, cakes and confectionaries, g/day	48.7 \pm 66.6	48.7 \pm 68.9
Fats, g/day	28.3 \pm 15.6	27.9 \pm 16.0
Protein, g/day	89.3 \pm 27.9	90.3 \pm 27.5
AGEs biomarkers, mean (SD)		
CML, nmol/l	2719 \pm 1046	2855 \pm 1075
CEL, nmol/l	1475 \pm 772	1475 \pm 740
MG-H1, nmol/l	1056 \pm 259	1079 \pm 262
Σ AGEs, nmol/l	5250 \pm 1488	5411 \pm 1470
CEL:MG-H1	1.45 \pm 0.79	1.43 \pm 0.75
(CEL+MG-H1): CML	1.01 \pm 0.39	0.98 \pm 0.38

Frequencies may not add up to 100% due to missing data. AGE, advanced glycation end products; BMI, body mass index; CML, N^ε-carboxymethyllysine; CEL, N^ε-carboxyethyllysine; MG-H1, N^ε-(5-hydroxy-5-methyl-4-imidazolone-2-yl) ornithine.

Discussion

In this study, we found that higher circulating levels of protein-bound CML, MG-H1 and Σ AGEs, but not CEL, were associated with a lower risk of CRC. We also observed that higher concentrations of MGO-derived AGEs relative to GO-derived AGEs were associated with higher CRC risk.

The inverse associations observed between the AGEs concentrations evaluated in our study and CRC risk contrast with our hypothesis that these AGEs contribute to colorectal carcinogenesis. Specifically, for CML, it is noteworthy that Jiao et al.

(22) also reported similar inverse associations as observed in our study. However, their study was based on a sub-population of male, Finnish smokers and applied an ELISA-based methodology to assess relative differences of CML between cancer cases and controls. Unfortunately, ELISA methods have limited reproducibility and do not differentiate between protein-bound and free fractions of circulating AGEs. Our initial hypothesis for positive AGEs–CRC risk association was based on evidence from experimental studies indicating that AGEs are DNA-damaging and can directly induce sustained inflammation in colon tissues through binding with RAGE (17,19,31). We chose to analyze protein-bound AGEs because these are specifically recognized by RAGE (32–34).

We assessed CML, CEL and MG-H1 because they are thought to be the most abundant AGEs in the body and although there is evidence that they have harmful pro-inflammatory and pro-oxidative effects, their relationship with the colonic mucosa may be very complicated. The colonic mucosa may be exposed to a variety of other AGEs, both exogenously from the diet and those produced endogenously within the body and colonic milieu. Similar

to endogenous AGEs, dietary AGEs may increase the body AGEs pool, interact directly with the colon mucosal and increase the risk for obesity (35). Some researchers have classified AGEs into two categories of ‘non-toxic’ and ‘toxic’ (36–38). This categorization still requires much further evidence, but it is noteworthy that we have previously shown an increased risk of rectal cancer with higher circulating levels of glycerinaldehyde-derived AGEs (39), that have been categorized as ‘toxic’ (6,36). Another speculative explanation of our observations is that circulating AGE concentration may not be reflective of their levels in colorectal tissues where they may accumulate. There is a paucity of supportive data for this assertion, and little is known about whether the concentration and actions of specific AGEs may differ between tissues. Van Heijst et al. (40) observed varying AGE levels from an immunohistochemical expression of CML and the MGO-derived AGE argpyrimidine in various human tumours (muscle, colon, breast and larynx), suggesting that separate AGEs impact tissues differently. Therefore, relevant studies focusing on the functions, effects and the interactions of CML, CEL and MG-H1 and additional AGEs within normal and cancerous colonic tissues are warranted.

Table 2. ORs and 95% CI for colorectal cancer risk associated with circulating AGEs and their ratios, EPIC study 1992–2012

	Quintile 1	Quintile 2	Quintile 3	Quintile 4	Quintile 5	P _{trend}
CML						
Range, nmol/L	<2014	2014 – <2401	2401 – <2805	2805 – <3505	≥3505	
Cases/controls	302/276	338/276	280/275	247/276	211/275	
Model 1 ^a	1.00 (ref.)	0.96 (0.75–1.23)	0.74 (0.57–0.97)	0.58 (0.44–0.78)	0.37 (0.26–0.52)	<0.001
Model 2 ^b	1.00 (ref.)	0.97 (0.75–1.26)	0.79 (0.59–1.04)	0.63 (0.46–0.86)	0.40 (0.27–0.59)	<0.001
CEL						
Range, nmol/L	<986	986 – <1234	1234 – <1478	1478 – <1807	≥1807	
Cases/controls	272/276	270/276	286/276	290/275	260/275	
Model 1 ^a	1.00 (ref.)	0.96 (0.74–1.23)	1.02 (0.78–1.33)	1.01 (0.76–1.33)	0.89 (0.66–1.19)	0.605
Model 2 ^b	1.00 (ref.)	0.98 (0.76–1.27)	1.04 (0.79–1.37)	1.04 (0.78–1.39)	0.88 (0.64–1.19)	0.580
MG-H1						
Range, nmol/L	<872	872 – <974	974 – <1082	1082 – <1248	≥1248	
Cases/controls	309/276	308/275	260/276	256/274	244/276	
Model 1 ^a	1.00 (ref.)	0.94 (0.73–1.20)	0.75 (0.58–0.97)	0.71 (0.54–0.93)	0.68 (0.50–0.91)	0.002
Model 2 ^b	1.00 (ref.)	0.97 (0.75–1.25)	0.79 (0.61–1.03)	0.77 (0.58–1.02)	0.73 (0.53–1.00)	0.016
ΣAGEs, nmol/L						
Range, nmol/L	<4284	4284 – <4848	4848 – <5414	5414 – <6306	≥6306	
Cases/controls	334/276	315/276	275/276	219/276	235/274	
Model 1 ^a	1.00 (ref.)	0.89 (0.70–1.14)	0.73 (0.56–0.95)	0.52 (0.39–0.68)	0.48 (0.35–0.65)	<0.001
Model 2 ^b	1.00 (ref.)	0.93 (0.72–1.19)	0.76 (0.58–1.00)	0.54 (0.41–0.73)	0.52 (0.37–0.73)	<0.001
CEL:MG-H1						
Range	<0.89	0.89 – <1.15	1.15 – <1.43	1.43 – <1.81	≥1.81	
Cases/controls	247/276	274/276	263/275	295/275	298/275	
Model 1 ^a	1.00 (ref.)	1.09 (0.85–1.40)	1.09 (0.83–1.42)	1.27 (0.96–1.68)	1.33 (0.98–1.80)	0.047
Model 2 ^b	1.00 (ref.)	1.13 (0.87–1.47)	1.08 (0.82–1.42)	1.27 (0.95–1.70)	1.26 (0.91–1.73)	0.139
(CEL+MG-H1): CML						
Range	<0.66	0.66 – <0.86	0.86 – <1.02	1.02 – <1.24	≥1.24	
Cases/controls	233/276	279/276	263/275	280/275	322/275	
Model 1 ^a	1.00 (ref.)	1.49 (1.12–1.99)	1.64 (1.19–2.27)	1.70 (1.21–2.39)	2.14 (1.50–3.05)	<0.001
Model 2 ^b	1.00 (ref.)	1.42 (1.05–1.90)	1.54 (1.10–2.16)	1.54 (1.08–2.19)	1.91 (1.31–2.79)	0.004

Quintiles were created based on the distribution in the control group. MG-H1 has one missing data, hence MG-H1, CEL:MG-H1 and (CEL+MG-H1): CML have 1377 cases and 1377 matched controls. AGE, advanced glycation end-product; CI, confidence interval; CML, N^ε-carboxy-methyllysine; CEL, N^ε-carboxy-ethyllysine; MG-H1, N^ε-(5-hydroxy-5-methyl-4-imidazolone-2-yl)-ornithine; OR, odds ratio.

^aModel 1 was conditioned on matching factors: age at blood collection (±1 year), sex, recruiting centre, time of the day at blood collection (±3 h), fasting status at blood collection (<3, 3–6 and >6 h), and, additionally, among women by menopausal status (pre-menopause, peri-menopause, and post-menopause) and hormone replacement therapy use at time of blood collection (yes/no).

^bModel 2 model was Model 1 adjusted for BMI (continuous), height (continuous), education (none, primary, technical and professional, secondary, higher education), physical activity (inactive, moderately inactive, moderately active, active), smoking status, duration and intensity (never, 1–15 cigarettes/day, 16–25 cigarettes/day, over 26 cigarettes/day, former smokers who quit <10 years, former smokers who quit 11–20 years, former smokers who quit >20 years, current pipe-cigar and occasional smokers), energy intake (continuous), alcohol intake (continuous), processed meat intake (continuous), fibre intake (continuous) and dairy products intake (continuous).

Table 3. ORs and 95% CI for colorectal cancer risk associated with 1 SD increase in circulating AGEs and their ratios, by sex and by tumour anatomical sub-site, EPIC study 1992–2012

	Colorectal cancer		Colon cancer		Rectal cancer		P _{heterogeneity} by tumour sub-site
	Cases/controls	OR (95% CI)	Cases/controls	OR (95% CI)	Cases/controls	OR (95% CI)	
CML, nmol/L							
All	1378/1378	0.75 (0.66–0.85)	871/871	0.69 (0.58–0.83)	503/503	0.81 (0.66–1.00)	0.073
Men	679/679	0.69 (0.57–0.83)	404/404	0.66 (0.51–0.86)	272/272	0.67 (0.49–0.92)	0.162
Women	699/699	0.81 (0.67–0.97)	467/467	0.75 (0.59–0.96)	231/231	0.90 (0.65–1.26)	0.323
P _{heterogeneity} by sex		0.197		0.223		0.622	
CEL, nmol/L							
All	1378/1378	0.98 (0.88–1.08)	871/871	0.98 (0.86–1.11)	503/503	1.00 (0.83–1.20)	0.986
Men	679/679	1.01 (0.85–1.20)	404/404	0.99 (0.77–1.25)	272/272	1.10 (0.82–1.46)	0.291
Women	699/699	0.97 (0.85–1.11)	467/467	1.00 (0.85–1.17)	231/231	0.83 (0.61–1.12)	0.298
P _{heterogeneity} by sex		0.839		0.596		0.129	
MG-H1, nmol/L							
All	1377/1377	0.88 (0.79–0.98)	871/871	0.81 (0.71–0.93)	503/503	0.99 (0.83–1.17)	0.056
Men	678/678	0.83 (0.71–0.97)	404/404	0.77 (0.62–0.95)	272/272	0.87 (0.68–1.13)	0.173
Women	699/699	0.92 (0.80–1.07)	467/467	0.87 (0.72–1.05)	231/231	1.01 (0.78–1.31)	0.346
P _{heterogeneity} by sex		0.313		0.332		0.701	
ΣAGEs, nmol/L							
All	1377/1377	0.81 (0.72–0.91)	871/871	0.76 (0.65–0.89)	503/503	0.76 (0.65–0.89)	0.144
Men	678/678	0.76 (0.64–0.91)	404/404	0.71 (0.55–0.91)	272/272	0.81 (0.61–1.07)	0.066
Women	699/699	0.85 (0.73–1.01)	467/467	0.84 (0.68–1.03)	231/231	0.85 (0.62–1.15)	0.913
P _{heterogeneity} by sex		0.233		0.083		0.747	
CEL:MG-H1							
All	1377/1377	1.03 (0.93–1.14)	871/871	1.05 (0.93–1.19)	503/503	0.99 (0.82–1.21)	0.517
Men	678/678	1.10 (0.91–1.32)	404/404	1.07 (0.83–1.37)	272/272	1.22 (0.87–1.70)	0.572
Women	699/699	1.03 (0.90–1.17)	467/467	1.08 (0.93–1.26)	231/231	0.81 (0.60–1.09)	0.175
P _{heterogeneity} for sex		0.528		0.967		0.110	
(CEL+MG-H1):CML							
All	1377/1377	1.15 (1.03–1.29)	871/871	1.15 (1.00–1.32)	503/503	1.17 (0.94–1.46)	0.630
Men	678/678	1.34 (1.10–1.64)	404/404	1.27 (0.99–1.64)	272/272	1.65 (1.12–2.44)	0.852
Women	699/699	1.10 (0.95–1.27)	467/467	1.15 (0.97–1.37)	231/231	0.89 (0.65–1.23)	0.292
P _{heterogeneity} by sex		0.084		0.292		0.065	

MG-H1 has one missing data, hence MG-H1, CEL:MG-H1 and (CEL+MG-H1):CML have 1377 cases and 1377 matched controls. Four cases of overlapping tumours were considered as colorectal cancer cases, but not classified as colon malignant tumour or rectal one. AGE, advanced glycation end-product; CI, confidence interval; CML, N^ε-carboxy-methyllysine; CEL, N^ε-carboxy-ethyllysine; MG-H1, N^ε-(5-hydro-5-methyl-4-imidazolone-2-yl)-ornithine; OR, odds ratio.

Models were conditioned on matching factors: age at blood collection (± 1 year), sex, recruiting centre, time of the day at blood collection (± 3 h), fasting status at blood collection (<3, 3–6 and >6 h), and, additionally, among women by menopausal status (pre-menopause, peri-menopause and post-menopause) and hormone replacement therapy use at time of blood collection (yes/no) and adjusted for body mass index (continuous), height (continuous), education (none, primary, technical and professional, secondary, higher education), physical activity (inactive, moderately inactive, moderately active, active), smoking status, duration and intensity (never, 1–15 cigarettes/day, 16–25 cigarettes/day, over 26 cigarettes/day, former smokers who quit <10 years, former smokers who quit 11–20 years, former smokers who quit >20 years, current pipe-cigar and occasional smokers), energy intake (continuous), alcohol intake (continuous), processed meat intake (continuous), fibre intake (continuous) and dairy products intake (continuous).

The positive association observed with the ratio of MGO-derived AGEs:GO-derived AGEs and CRC risk suggests that the conditions that may lead to more MGO-AGEs versus GO-AGEs may be important in CRC development. This result may implicate that higher circulating MGO versus GO may be of greater importance in CRC development than AGEs. Both MGO and GO are mainly detoxified through the glyoxalase system and by other enzymes such as aldo-keto reductases and dicarbonyl and L-xylulose reductase (41,42). Compared to GO, MGO is more reactive (43) but is rapidly and efficiently detoxified, mainly in the liver (42). This may possibly explain the higher CRC risk observed with MGO-AGE-AGEs in obese individuals. Obesity is often associated with a degree of liver steatosis and decreased liver function and could possibly explain lower clearance of MGO with spillover into the circulation. It can be speculated that in the presence of a 'competition' between the production and the detoxification of dicarbonyls, MGO and its derived AGEs may be harmful to the colon tissue, and sustain systemic inflammation,

compared to GO and derived AGEs—but this requires further investigation. Diabetes has been associated with a higher risk of CRC (44). Because diabetes is associated with poor glycaemic control, hyperglycaemia and enhanced production of AGEs, one would expect that the AGE-CRC association is higher in subjects with diabetes compared to those without. Additional studies should explore whether CRC risk associated with diabetes could be partially mediated through AGEs. Likewise, future studies may also explore to which extent treatment for diabetes may mitigate endogenous AGEs production and possibly CRC risk.

It is also noteworthy that dicarbonyls and some AGEs derived from them display hormetic properties, where lower levels are associated with beneficial health outcomes while higher levels are deleterious. Hormetic effects have been reported for lower levels of MGO which have been showed to prevent tumour growth, whereas higher levels promote tumour expansion (45). Surprisingly, it has been reported that another MGO-derived AGE, MG-H3, has anti-oxidative properties comparable with those of

Table 4. ORs and 95% CI for colorectal cancer risk associated with 1 SD increase in circulating AGEs and their ratios, stratified by obesity and diabetes status, EPIC study 1992–2012

	Diabetes ^a			Obese ^b		
	Yes (n = 61)	No (n = 1099)	P for heterogeneity	Yes (n = 247)	No (n = 1131)	P for heterogeneity
CML	0.56 (0.25–1.25)	0.74 (0.64–0.85)	0.486	0.30 (0.19–0.47)	0.85 (0.74–0.97)	<0.001
CEL	2.07 (0.89–4.82)	0.99 (0.88–1.10)	0.088	1.01 (0.68–1.50)	1.01 (0.90–1.12)	0.999
MG-H1	1.20 (0.55–2.61)	0.87 (0.78–0.98)	0.443	0.46 (0.32–0.67)	0.96 (0.86–1.07)	<0.001
ΣAGEs	1.07 (0.48–2.40)	0.81 (0.72–0.92)	0.499	0.38 (0.25–0.57)	0.90 (0.80–1.02)	<0.001
CEL:MG-H1	1.73 (0.78–3.84)	1.05 (0.94–1.17)	0.228	1.59 (1.11–2.27)	1.02 (0.92–1.14)	0.019
(CEL+MG-H1):CML	2.94 (1.21–7.15)	1.19 (1.05–1.35)	0.046	2.36 (1.60–3.47)	1.10 (0.98–1.24)	<0.001

AGE, advanced glycation end-product; CI, confidence interval; CML, N^ε-carboxy-methyllysine; CEL, N^ε-carboxy-ethyllysine; MG-H1, N^ε-(5-hydroxy-5-methyl-4-imidazolone-2-yl)-ornithine; OR, odds ratio.

Models were conditioned on matching factors: age at blood collection (± 1 year), sex, recruiting centre, time of the day at blood collection (± 3 h), fasting status at blood collection (<3, 3–6 and >6 hours), and, additionally, among women by menopausal status (pre-menopause, peri-menopause and post-menopause), and hormone replacement therapy use at time of blood collection (yes/no) and adjusted for height (continuous), education (none, primary, technical and professional, secondary, higher education), physical activity (inactive, moderately inactive, moderately active, active), smoking status, duration and intensity (never, 1–15 cigarettes/day, 16–25 cigarettes/day, over 26 cigarettes/day, former smokers who quit <10 years, former smokers who quit 11–20 years, former smokers who quit >20 years, current pipe-cigar and occasional smokers), energy intake (continuous), alcohol intake (continuous), processed meat intake (continuous), fibre intake (continuous) and dairy products intake (continuous).

^aSelf-reported history of diabetes at baseline (n missing = 218).

^bObesity was defined depending on body mass index (BMI). Obese: BMI ≥ 30 kg/m² and non-obese: BMI < 30 kg/m².

ascorbic acid (46). There is substantial evidence showing that the deleterious effects of AGEs are dependent upon the level of RAGE activity. In RAGE knockout mice, cancer development is greatly reduced, suggesting that the cancer-promotive and pro-inflammatory effects of AGEs are necessarily expressed in the presence of RAGE (47,48). Interestingly, there is mounting evidence showing that soluble RAGE, a free circulating isoform of RAGE, is inversely associated with CRC (21,49). The knowledge of AGEs metabolism and CRC need to be expanded, and additional studies are needed to better understand the role of dicarbonyls, and derived AGEs in the aetiology of CRC.

This study has several strengths, including the quantitative measurement of CEL, CML and MG-H1 by a state-of-the-art UPLC-MS/MS instrumental method. UPLC-MS/MS could be considered the gold standard method for the analysis of AGEs in plasma. UPLC-MS/MS could be used to accurately and precisely measure specific AGEs in both free and protein-bound forms. The major known drawback of using UPLC-MS/MS is its relatively higher cost and the necessity for trained personnel (23,50). Additional strengths include the prospective design, the large sample size and the ability to conduct analyses stratified by sex, and by anatomical sub-site (colon versus rectum). A limitation to our study is that we lack information on other AGEs produced from MGO including other MGO-derived hydroimidazolone (MG-Hs) such as MG-H2, MG-H3 and MG-H4, N^ε-(4-carboxy-4,6-dimethyl-5,6-dihydroxy-1,4,5,6-tetrahydropyrimidin-2-yl)-ornithine, argpyrimidine and cross-linking dimer methylglyoxal-lysine dimer (8), which may all have roles in CRC development. Another limitation is the use of plasma AGEs levels which are dependent on kidney and liver functions; hence they may not represent tissue levels. Further research is required to determine how circulating AGE measures in the same individual may relate to levels in colon tumour and normal colon tissues. Therefore, our assessment of AGEs in CRC development is far from complete, even though we analysed three major AGEs compounds. Also, our findings show that circulating measures of AGEs are likely to have differential associations with CRC, indicating that their posited detrimental properties may not be equivalent or that they vary in their pro-inflammatory capacity. More study is required on the individual and interactive roles of AGEs in the development of cancers and other chronic diseases.

A deeper assessment of the qualitative pathways of AGEs production and their cumulative roles in cancer development may shed more insight into this fascinating topic. An additional limitation of this nested case-control study is the fact that blood samples and lifestyle factors were collected at baseline and may not necessarily reflect changes over time.

In conclusion, in this large, comprehensive prospective study, CML and MG-H1 are inversely associated with CRC risk, contrary to our initial hypothesis. However, we observed a significantly higher CRC risk with higher ratio of MGO-derived:GO-derived AGEs. Our observations highlight the complexity of the proposed roles of AGEs in CRC development and suggest that AGEs levels may not be interpreted alone, but in consideration of their chemical origins. Additional studies examining toxic dicarbonyl AGE precursor compounds in CRC development and assessing the role of AGEs in the colonic milieu and within normal and tumorigenic colonic tissues are required. In addition, the development of laboratory instrumental methodologies for the assessment of a larger number of AGEs would aid greatly in better defining the roles of this diverse family of compounds in health and disease.

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