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Carboxymethylethanolamine, a Biomarker of Phospholipid Modification during the Maillard Reaction in Vivo*

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N\(^{\text{e}}\)-(Carboxymethyl)lysine (CML) is a stable chemical modification of proteins formed from both carbohydrates and lipids during autoxidation reactions. We hypothesized that carboxymethyl lysines such as carboxymethylphosphatidylethanolamine (carboxymethyl-PE) would also be formed in these reactions, and we therefore developed a gas chromatography-mass spectrometry assay for quantification of carboxymethylethanolamine (CME) following hydrolysis of phospholipids. In vitro, CME was formed during glycation of dioleoyl-PE under air and from linoleoylpalmitoyl-PE, but not from dioleoyl-PE, in the absence of glucose. In vivo, CME was detected in lipid extracts of red blood cell membranes, ~0.14 nmol of CME/mmol of ethanolamine, from control and diabetic subjects, \((n = 22, p > 0.5)\). Levels of CML in erythrocyte membrane proteins were ~0.2 nmol/mmol of lysine for both control and diabetic subjects \((p > 0.5)\). For this group of diabetic subjects there was no indication of increased oxidative modification of either lipid or protein components of red cell membranes. CME was also detected in fasting urine at 2–3 nmol/mg of creatinine in control and diabetic subjects \(p = 0.085\). CME inhibited detection of advanced glycation end product (AGE)-modified protein in a competitive enzyme-linked immunosorbent assay using an anti-AGE antibody previously shown to recognize CML, suggesting that carboxymethyl-PE may be a component of AGE lipids detected in AGE low density lipoprotein. Measurement of levels of CME in blood, tissues, and urine should be useful for assessing oxidative damage to membrane lipids during aging and in disease.

The nonenzymatic reaction of blood glucose with body proteins (glycation) followed by browning and oxidation reactions of glycated proteins leads to cumulative chemical modifications of tissue proteins throughout the body. These chemical changes, collectively termed the Maillard reaction, are considered to cause a gradual deterioration in the structure and function of tissue proteins and to contribute to the pathophysiology of normal aging (1–3). Further, the Maillard reaction is accelerated during hyperglycemia in diabetes, yielding advanced glycation end products (AGEs)\(^1\) thought to be involved in the pathogenesis of diabetic complications (4–6). Among Maillard reaction products identified thus far in tissue proteins, concentrations of pentosidine, 3,7 and \(N\text{-}(\text{carboxymethyl)lysine (CML})\) (7) are known to increase in human skin collagen with age, and age-adjusted concentrations of both are increased in skin collagen in diabetes (7). Moreover, there is a strong relationship between levels of these products in collagen and the status of diabetic complications (8–10). Both CML and pentosidine require oxidative conditions for their formation, hence their description as glycoxidation products (11). Recently we showed that CME can also be formed during the reaction of autoxidizing polyunsaturated fatty acids (PUFA) with proteins (12), so that its precise biochemical origin is uncertain. The formation of CML during both glycoxidation and lipoxidation reactions emphasizes that Maillard chemistry is a general reflection of carboxyl amine reactions, whether the carbonyl compounds are derived from carbohydrates or lipids.

Several recent reports indicate that, like proteins, aminophospholipids are also targets of Maillard reactions. Pamplona et al. (13) first showed evidence for the presence of glycated phospholipids in rat liver and found their levels increased in animals with streptozotocin-induced diabetes. Ravandi et al. (14) further documented the existence of glycated aminophospholipids in human red blood cells and plasma, although their analytical technique did not distinguish between Schiff base and Amadori compounds, both of which are formed during the initial stage of the reaction of glucose with amino groups (1). Bucala et al. (15, 16) show in vitro that glycation of phosphatidylethanolamine (PE) but not phosphatidylcholine resulted in the formation of immunologically detectable AGEs in PE. In addition, using an ELISA assay, these authors concluded that the majority of AGEs present in low density lipoprotein isolated from normal and diabetic subjects

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\(^1\) The abbreviations used are: AGE, advanced glycation end product; AGE-RbsA, AGE rabbit serum albumin; CM, carboxymethyl; CML, \(N\text{-}(\text{carboxymethyl)lysine; CME, carboxymethylethanolamine; PUFAs, polyunsaturated fatty acids; PE, phosphatidylethanolamine; DO-PE, dioleyl-PE; LP-PE, linoleoylpalmitoyl-PE; ELISA, enzyme-linked immunosorbent assay; GC/MS, gas chromatography-mass spectrometry; SIM-GCMS, selected ion monitoring-GC/MS; PSR-1, anti-AGE protein antiserum; FL, fructose-lysine; TFAME, \(N\text{-}O\text{-trifluoracetyl methyl esters; BSA, bovine serum albumin.}

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were localized in the lipid phase (17). We recently identified CML as a major AGE antigen, and based on similarities in the structure of CML and CM-phospholipids such as CM-PE (Fig. 1), we proposed that AGE lipids may in fact, be immunologically cross-reactive carboxymethyl derivatives of aminophospholipids (18). Bucala et al. (15) also suggested that phospholipid glycation enhances lipid peroxidation. The interplay between glycation, glycoxidation, and lipid peroxidation may indeed be even more complex, since reaction of lipid decomposition products generated during peroxidative reactions with free amino groups of both proteins and aminophospholipids could lead to the formation of adducts chemically indistinguishable from carbohydrate-derived AGEs.

In the present study, we have developed a selected ion monitoring gas chromatography-mass spectrometry (SIM-GC/MS) assay for carboxymethylaminoholanolamine (CME), the hydrolysis product of CM-PE, and present evidence for the presence of CME in human red cell membrane lipids and as a metabolite in urine. We also compare levels of CM protein and CM lipid in the red cell membrane and present the comparative levels in red blood cell ghosts in a group of control and diabetic individuals. Further, to gain insight into the nature of AGE lipids, we monitored gas chromatography-mass spectrometry (SIM-GC/MS) and fructose-lysine (FL) were measured in the hydrolysates after derivatization as their N-O-trifluoroacetyl methyl esters (TFAME), all as described previously (19).

Analyses of Urine Samples—Second-voided fasting urine samples were obtained from all subjects and frozen at −70 °C until used. Aliquots containing ~100 μg of creatinine were mixed with 2 volumes of 0.2 M borate buffer, pH 9.2. NaBH₄ was added to a final concentration of 200 μM, and reduction was carried out overnight at room temperature. Excess borohydride was discharged by the addition of several drops of concentrated HCl, and borate was removed (19). After drying, deuterated internal standards were added, and samples were hydrolyzed in 6 N HCl for 24 h at 110 °C in screw cap test tubes that were purged with N₂. Hydrolysates were dried in vacuo and dehydrated in 1 ml of 1% trifluoroacetic acid, and brown impurities were removed using a 1-ml C-18 column as described above. The TFAME derivatives of the sample were prepared (19) and analyzed by SIM-GC/MS as described below. Creatinine was measured using a commercial kit (Sigma).

Glycoxidation and Autoxidation of PE—Incubations of PE with and without glucose were conducted in 0.2 M phosphate buffer, pH 7.4, for 2 weeks at 37 °C and were carried out under both oxidative and antioxidative conditions. For antioxidative conditions, samples in plain Vacutainer tubes were supplemented with 1 mM diethylenetriaminepentaaetic acid and 0.01% butylated hydroxytoluene, and the tubes were evacuated and flushed 3 times with nitrogen. For oxidative conditions, diethylenetriaminepentaaetic acid and butylated hydroxytoluene were omitted, and samples were opened every other day to allow entry of air. Lipids were extracted into chloroform/methanol (2:1), dried, and reduced with 50 mM NaBH₄ in 1 ml of methanol overnight at room temperature. Reduced lipids were dried in vacuo and, following the addition of deuterated internal standards, were hydrolyzed in 1 ml of 6 N HCl for 24 h at 110 °C in screw cap test tubes that were purged with N₂. Hydrolysates were dried in vacuo and dehydrated in 1 ml of 1% trifluoroacetic acid, and brown impurities were removed using a 1-ml C-18 column as described above. The TFAME derivatives of the sample were prepared (19) and analyzed by SIM-GC/MS as described below. CM-phospholipids and CME were measured by SIM-GC/MS as described below. CME was quantified by SIM-GC/MS as described below. Glyoxal was measured using a commercial kit (Sigma).

GC/MS Analyses—Analyses of TFAME derivatives of all samples except urine were carried out on a Hewlett-Packard model 6890 gas chromatograph equipped with a 30-m HP-5MS capillary column coupled to a Hewlett-Packard model 6890 mass selective detector (Hewlett-Packard, Palo Alto, CA). The injection port was maintained at 275 °C. The temperature program was 60 °C to 115 °C at 2 °C/min, then ramp to 240 °C at 10 °C/min and hold for 5 min. Quantitation was by internal standardization using standard curves constructed from mixtures of deuterated and nondeuterated standards. SIM of 2 ions/analyte was performed, and similar results were obtained using both ions. The ions used were ethanolamine and d₄-ethanolamine, m/z = 140, 184 and 144, 188, respectively; CME and d₄-CME, m/z = 211, 266 and 214, 270, respectively (Fig. 2). Analyses of urine samples, which contained

FIG. 1. Structures of CML and CME in protein and lipid. Enlarged portions emphasize the common features of each structure. The protein backbone is indicted by compressed wave lines and the diacylglyceride component of phospholipid is represented by relaxed wave lines.
numerous interfering substances, were carried out on a Hewlett-Packard model 5890 gas chromatograph equipped with a 30-m RTX 5 (5% phenyl) column (Restek Corp., Bellefonte, PA) coupled to a high resolution VG 70 SQ magnetic sector mass spectrometer (Fisons, Manchester, UK). The injection port was maintained at 250 °C. The temperature program was 2 min at 80 °C, ramp at 5 °C/min to 220 °C, ramp at 10 °C/min to 300 °C, and hold for 10 min. The same ions as listed above were monitored for measurement of ethanolamine and CME.

**RESULTS**

**Characterization of CME Formation on PE by Lipoxidation or Glycoxidation**—CME may be formed on PE by at least three routes (Scheme 1), including glycation of PE and oxidative cleavage of the Amadori adduct or from the reaction of glyoxal formed by autoxidation of glucose or PUFA. CME was produced during autoxidation of PL-PE in phosphate buffer (Fig. 3A, Table I) but not under antioxidative conditions. These results are consistent with the formation of glyoxal during PUFA autoxidation (12, 21, 22). CME was also formed in incubations of DO-PE with glucose (Fig. 3B, Table I) but not from DO-PE incubated in buffer only. Although the glucose levels in these incubations are clearly nonphysiological, the reaction conditions were modeled on those of Bucala et al. (15) because of the detection of AGE lipid in this system. CME was also produced, but at lower yield (10–15%), in antioxidative incubations of DO-PE with glucose (Table I). This finding was consistent in three separate experiments. Both oxidative and antioxidative incubations of DO-PE in the presence of glucose developed a brown color with time, indicating that even in the absence of PUFA, aminophospholipids are active substrates for the Maillard reaction in aqueous systems. LP-PE developed a light yellow color during 2 weeks of incubation under air.

The amounts of CME formed after 2 weeks of incubation of various reaction mixtures are summarized in Table I. Whereas the concentration of LP-PE was only 10% that of DO-PE, for reasons of economy, the amount of CME formed under oxidative conditions in LP-PE was about half that of DO-PE incubated with glucose. Thus, autoxidation of PE containing unsaturated PUFA was an efficient source of CME. The CME detected in samples prepared in vitro and from in vivo sources (Table I) was measured after reduction with NaBH₄ so that its formation as an artifact from either carbohydrate or lipid adducts during acid hydrolysis is unlikely.

**Quantification of CME, CML, and FL in Red Cell Ghosts**—As shown in Fig. 4, CME was readily detected in hydrolysates of red cell membrane lipid extracts. Levels of CME in erythrocyte membrane lipids from control subjects and diabetic patients are compared in Fig. 5. CME values were, respectively, 0.135 ± 0.054 and 0.146 ± 0.081 mmol/mol of ethanolamine; these data were calculated excluding the two high CME values shown in parentheses because they were >2 S.D. above the mean. The mean CME values were not significantly different using non-parametric, Mann-Whitney analysis. For comparison, results of analyses of CML and the Amadori compound, FL, on membrane protein fractions from these same samples are also shown in Fig. 5. CML concentrations in control and diabetic samples were 0.213 ± 0.063 and 0.184 ± 0.062 mmol/mol of lysine, respectively, and were also not significantly different.

Of note, the ratio of CME/ethanolamine in the lipid fraction
was similar to the ratio of CML/lysine in the protein fraction, suggesting an overall similar extent of carboxymethylation of aminophospholipids and proteins in red cell membranes. At the same time, FL values, reflecting both ambient glucose concentration and steady state level of protein glycation (1), were elevated in a statistically significant fashion in diabetic (5.27 ± 1.42 mmol/mol of lysine) versus control samples (2.13 ± 1.33 mmol/mol of lysine, *p*, 0.01). The approximately 2.5-fold increase in mean FL concentration is comparable to the approximate 2-fold increase in mean HbA1c values, and there was an overall significant correlation between FL and HbA1c values (*r* = 0.54, *p* = 0.005).

**Measurement of CME and CML in Human Urine**—As shown in Fig. 6, the mean concentrations of CM species in normal urine were 1.82 ± 0.70 nmol of CME/mg of creatinine and 5.58 ± 2.11 nmol of CML/mg of creatinine, respectively, corresponding to a CML/CME ratio of 2.6. CME is present in urine primarily in its free form, i.e. as the product of hydrolysis of CM-PE (data not shown), suggesting active catabolism of the latter compound. CME and CML concentrations in the urine of diabetic patients were 2.92 ± 1.76 nmol of CME/mg of creatinine and 8.53 ± 4.96 nmol of CML/mg of creatinine, respectively. Although the means were somewhat higher than for the control population, they did not reach statistical significance. In a previous study, using a larger number of samples, we reported a modest, though significant elevation of urinary CML in diabetes (19). In the present study there was, however, a strong correlation between urinary CME and CML (*r* = 0.737, *p* = 0.0003, *n* = 9).

**Immunochromatographic Detection of CME by Anti-AGE Protein Antibody**—We have previously shown that CML-BSA is a potent competitor for the recognition of AGE-RbSA by antiserum PSR-1, demonstrating that CML is a dominant AGE antigen (18). CML as the free amino acid is a significantly weaker competitor, about 10^3–10^4 times less efficient than CML-BSA. As shown in Fig. 7, CME was comparable to CML in inhibiting the recognition of AGE-RbSA by the PSR-1 antiserum. Ethanolamine, like lysine (not shown), was completely ineffective.

**DISCUSSION**

In this study we describe the detection and measurement of a CM lipid, CME, in human membrane lipids and urine. Based on the concentration of CME in ghost membranes, −0.14 mmol/mol of PE (Fig. 5), and the concentration of PE in red cell membranes, −1 mg/ml of packed red cells (23) (average molecular mass for PE, 800 Da), there is an estimated 0.18 nmol of CME/ml of packed erythrocytes. From the recovery of −2 nmol of CME/mg of creatinine (Fig. 6) and a mean daily excretion of 1.4 g of creatinine for a 70-kg subject, about 2.8 μmol (0.3 mg of CME) are excreted daily by a healthy human adult. Since the
average 70-kg subject has about 2 liters of packed red cells and 1% of red cells turnover/day (average red cell life span, 120 days), only about 4 nmol of the daily urinary excretion of CME can be attributed to red cell membrane degradation. This estimate emphasizes that 99% of the 2.8 $\mu\text{mol}$ of CME recovered daily in urine arises from the normal turnover of membrane phospholipids in cells other than red cells. Thus, CME represents a natural metabolite formed during glycoxidative and/or lipoxidative modification of phospholipids, and changes in these levels in urine may reflect changes in overall oxidative stress in vivo. CM-serine has also been detected in hydrolysates of ghost lipids and in urine (data not shown), indicating that carboxymethylation of both PE and phosphatidylserine occurs under physiological conditions.

**Origins of CME**—Our model reactions show that CME can be formed from either glucose or PUFA under oxidizing conditions. It is difficult to make a direct comparison of the relative efficiency of each substrate in forming CME. Thus, in *in vitro* experiments (Table I), glucose, which is resistant to autoxidation compared with PUFA, was present at a 33-fold molar excess over free amino groups, whereas the PUFA (linoleic acid) in LP-PE is present at the same concentration as the amino group. Since aminophospholipids form micelles in aqueous buffers, it is likely that reactive intermediates formed during peroxidation of PUFA in *situ* may be present at very high local concentrations. At this point we can only speculate about the metabolic origin of CM-PE. It is difficult to anticipate which of the routes, glycoxidation, glucose, or PUFA autoxidation, shown in Scheme 1 predominates in *vivo*, and thus CME, like CML, may be both a glycoxidation and lipoxidation prod-
likely that anti-AGE protein antibodies might also recognize cell. Thus, there are involved in erythrocyte turnover. That may be recognized by RAGE or other scavenger receptors present study could form part of an array of negative charge seems possible that CM lipids (and CML) measured in the present study was reported to be unreactive toward CML (17), present knowledge suggests that, given the significantly lower reactivity of free CML compared with protein-bound CML to anti-AGE protein antibody (18, Fig. 6), the amount of competing free CML used in their experiments may not have been sufficient to yield effective competition. At the same time, it should be noted that these workers reported a 4-fold increase of AGE lipids in low density lipoprotein from diabetic patients versus healthy subjects (15, 16), suggesting a greater increase in Maillard modification of aminophospholipids in diabetes than indicated by our results. The differences between our results may reflect differences in the severity of complications in the patient groups. Finally, Kume et al. (30), using a monoclonal antibody to AGE-protein, 6D12, reported the presence of AGEs in frozen sections prepared from atherosclerotic tissue of normoglycemic humans. This antibody has since been shown to recognize CML (31); however, it is possible that both CM protein and lipid may have been detected in this study.

In summary, we describe the detection of CM-PE in vivo and present quantitative data on its concentration in human red blood cell membrane lipids and on the concentration of its metabolite, CME, in urine. We also demonstrate that CME may be formed by autoxidation of carbohydrate and lipid. Measurements of CME in different tissues should prove useful for assessing the role of glycoxidation and lipid peroxidation or, more generally, carbonyl stress (32) in the pathogenesis of diabetes, its complications, and other disease processes.

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CME as an AGE Antigen—Because the terminal –CH2CH2NHCH2COOH moieties of CM-lysine and the predicted structure of CM-PE (Fig. 1) are identical, it seems likely that anti-AGE protein antibodies might also recognize CM lipids. Our results indicate that CME is an effective competitor for AGE protein binding to PSR-1, an anti-AGE protein antibody we have shown to recognize CML as a major epitope (18), emphasizing that CM phospholipids in lipoproteins may contribute to the AGE content of serum measured by ELISA. Although we do not know how much better the recognition of CM-PE in membrane or other lipoproteins may be, by analogy to the results obtained for free CML and CML-BSA, CM-PE may be an important epitope recognized by anti-AGE protein antisera. Indeed, some of the AGE lipids described in low density lipoprotein by Bucala et al. (15, 16) may be CM-aminophospholipids. Although the antibody used in their analyses was reported to be unreactive toward CML (17), present knowledge suggests that, given the significantly lower reactivity of free CML compared with protein-bound CML to anti-AGE protein antibody (18, Fig. 6), the amount of competing free CML used in their experiments may not have been sufficient to yield effective competition. At the same time, it should be noted that these workers reported a 4-fold increase of AGE lipids in low density lipoprotein from diabetic patients versus healthy subjects (15, 16), suggesting a greater increase in Maillard modification of aminophospholipids in diabetes than indicated by our results. The differences between our results may reflect differences in the severity of complications in the patient groups. Finally, Kume et al. (30), using a monoclonal antibody to AGE-protein, 6D12, reported the presence of AGEs in frozen sections prepared from atherosclerotic tissue of normoglycemic humans. This antibody has since been shown to recognize CML (31); however, it is possible that both CM protein and lipid may have been detected in this study.

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Carboxymethylation of Phospholipids