Nε-(Carboxymethyl)lysine-Receptor for Advanced Glycation End Product Axis Is a Key Modulator of Obesity-Induced Dysregulation of Adipokine Expression and Insulin Resistance


Objective—Dysregulation of inflammatory adipokines by the adipose tissue plays an important role in obesity-associated insulin resistance. Pathways leading to this dysregulation remain largely unknown. We hypothesized that the receptor for advanced glycation end products (RAGE) and the ligand Nε-(carboxymethyl)lysine (CML) are increased in adipose tissue and, moreover, that activation of the CML–RAGE axis plays an important role in obesity-associated inflammation and insulin resistance.

Approach and Results—In this study, we observed a strong CML accumulation and increased expression of RAGE in adipose tissue in obesity. We confirmed in cultured human preadipocytes that adipogenesis is associated with increased levels of CML and RAGE. Moreover, CML induced a dysregulation of inflammatory adipokines in adipocytes via a RAGE-dependent pathway. To test the role of RAGE in obesity-associated inflammation further, we constructed an obese mouse model that is deficient for RAGE (ie, RAGE+/−/Leptin−/− mice). RAGE+/−/Leptin−/− mice displayed an improved inflammatory profile and glucose homeostasis when compared with RAGE+/+/Leptin−/− mice. In addition, CML was trapped in adipose tissue in RAGE+/+/Leptin−/− mice but not in RAGE+/−/Leptin−/−. RAGE-mediated trapping in adipose tissue provides a mechanism underlying CML accumulation in adipose tissue and explaining decreased CML plasma levels in obese subjects. Decreased CML plasma levels in obese individuals were strongly associated with insulin resistance.

Conclusions—RAGE-mediated CML accumulation in adipose tissue and the activation of the CML–RAGE axis are important mechanisms involved in the dysregulation of adipokines in obesity, thereby contributing to the development of obesity-associated insulin resistance. (Arterioscler Thromb Vasc Biol. 2014;34:1199-1208.)

Key Words: advanced glycation end product ▪ inflammation ▪ Nε-(carboxymethyl)lysine ▪ obesity ▪ receptor for advanced glycation end products

Obesity is closely linked to a wide array of pathophysiological conditions, including insulin resistance.1 The adipose tissue is an important endocrine organ that produces and secretes biologically active molecules, collectively known as adipokines.2 Obesity is accompanied by a chronic, low-grade inflammation, characterized by a dysregulated production of proinflammatory adipokines, such as tumor necrosis factor-α, interleukin-6, and plasminogen activator inhibitor-1 (PAI-1), and anti-inflammatory adipokines, such as adiponectin.3-5 It has been proposed that this dysregulation is a key feature in the pathogenesis of obesity-related insulin resistance.6-8 However, mechanisms by which excessive fat accumulation leads to a dysregulation of adipokines have not yet been elucidated.

The receptor for advanced glycation end products (RAGE) is a pattern-recognition receptor and is a multiligand cell-surface molecule expressed on different cell types, such as adipocytes,
endothelial cells, and macrophages. RAGE is initially identified as the receptor for advanced glycation end products (AGEs), but, in addition to AGEs, RAGE also interacts with multiple members of the proinflammatory S100/calgranulin family and high motility group box 1 protein. Binding of these ligands to RAGE leads to activation of signaling cascade and induction of nuclear factor-κB, which can subsequently lead to the production of inflammatory mediators. Therefore, the potential role of RAGE in the regulation of inflammation suggests that RAGE might be an important mechanism contributing to obesity-associated dysregulation of adipokines and development of insulin resistance. N-(carboxymethyl)lysine (CML) is a major AGE and is an important ligand for RAGE. CML is formed on proteins by enzymatic glycation and oxidation reactions. Alternative routes for CML formation have been described, including lipid peroxidation of unsaturated fatty acids. In fact, lipid peroxidation is a more important source for CML formation than glycoxidation reactions. Because of the reaction mechanism, CML formation is increased under hyperglycemic and hyperlipidemic conditions. The adipose tissue in obese conditions is characterized by increased levels of fatty acids, lipid peroxidation, and oxidative stress. Therefore, we can deduce that obesity is also a condition in which CML formation is increased and where CML can interact with RAGE. However, the role of CML-RAGE in obesity, obesity-associated inflammation, and insulin resistance has to date not been investigated.

The aim of this study was to investigate the role of CML–RAGE axis in obesity-associated inflammation and insulin resistance. In the present study, we showed in humans, in an in vitro model of human adipocytes, and in mice lacking RAGE on a Leprdb−/− background, the importance of the CML–RAGE axis in the development of obesity-related inflammation and insulin resistance.

Materials and Methods
Materials and Methods are available in the online-only Supplement.

Results
CML Accumulation and RAGE Expression Are Increased in Human Adipose Tissue
To evaluate whether CML accumulates in human adipose tissue, we performed immunohistochemistry on biopsies of subcutaneous adipose tissue (SAT) of lean and obese subjects. Main characteristics of the lean (n=9) and obese subjects (n=10) are presented in the Table. Immunohistochemical staining for CML showed that CML was only slightly detectable in SAT of lean subjects, whereas CML was abundantly present in SAT of obese subjects (Figure 1A). Semiquantitative analysis of the CML staining demonstrated a significantly higher CML intensity in SAT of obese subjects when compared with that of lean subjects (Figure 1B). RAGE expression was also slightly higher in obese SAT versus lean SAT although not significant (P=0.189; Figure 1C). However, Western blot analysis demonstrated that RAGE protein levels were significantly higher in SAT of obese subjects versus lean controls (Figure 1D).

To analyze CML localization in adipose tissue and to study CML accumulation in different fat depots further, we also conducted immunohistochemical stainings of SAT and visceral adipose tissue (VAT) obtained from severely obese subjects (n=44; body mass index, >40 kg/m²). Main characteristics of the severely obese subjects are presented in Table I in the online-only Data Supplement. We demonstrated that CML-modified proteins were particularly evident in adipocytes, CD68-positive macrophages, and CD31-positive endothelial cells (Figure 1E). In addition, RAGE showed a similar localization as CML (Figure 1E). No differences in CML and RAGE localization were observed between SAT and VAT. However, a significant higher CML accumulation (Figure 1F) was detected in VAT when compared with SAT of severely obese subjects. In addition, RAGE gene expression levels and RAGE protein levels detected by Western blotting (Figure 1G and 1H) were significantly higher in VAT when compared with SAT of severely obese subjects.

These data demonstrate that obesity is associated with an accumulation of CML and an increased RAGE gene expression and RAGE protein levels in adipose tissue, with higher CML accumulation and RAGE in VAT than in SAT.

CML Levels Are Increased During Adipocyte Lipid Accumulation and Induce Inflammation
To investigate the role of the CML–RAGE axis in adipose tissue, we performed an in vitro experiment with human Simpson–Golabi–Behmel syndrome (SGBS) preadipocytes and differentiated SGBS adipocytes as a model for adipogenesis. SGBS preadipocytes were differentiated to mature SGBS adipocytes, which resulted in marked lipid accumulation as detected by Oil Red O staining (Figure 2A). During the course of differentiation, CML levels were significantly increased. In addition, RAGE gene expression and protein levels also showed a significant increase during differentiation of preadipocytes to adipocytes (Figure 2A).

Table. General Characteristics of Lean and Obese Subjects

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<tr>
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<tr>
<td>Age, y</td>
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<td>Sex (men), %</td>
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<tr>
<td>BMI, kg/m²</td>
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<td>Fasting glucose, mmol/L</td>
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<tr>
<td>Fasting insulin, mmol/L</td>
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<tr>
<td>GIR, μmol×kg body weight−1×min−1</td>
<td>37.1±7.9</td>
<td>14.3±7.9*</td>
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Data are presented as mean±SD, or as percentage. BMI indicates body mass index; and GIR, glucose infusion rate (measure of insulin sensitivity).

*P<0.001, †P<0.01.
We next investigated whether the increase of the CML–RAGE axis during adipogenesis is associated with an altered inflammatory profile in preadipocytes and adipocytes. The effect of CML on adipocyte inflammation was examined by incubating SGBS preadipocytes and adipocytes with different modifications of CML-albumin (ie, control-albumin and minimally and highly modified CML-albumin). Increasing grades of CML modification of albumin were determined by UPLC-Tandem MS (ultra performance liquid chromatography-tandem mass spectrometry) and Western blotting (data not demonstrated). Long-term incubation of SGBS preadipocytes with different CML-albumin (for 72 hours) demonstrated a significant increase of RAGE, interleukin-6, and PAI-1 gene expression, whereas adiponectin expression significantly decreased. Incubation of SGBS preadipocytes during short incubation periods had no effect on RAGE, interleukin-6, PAI-1, and adiponectin gene expression (Figure I in the online-only Data Supplement). Interestingly, in SGBS adipocytes, CML increased the RAGE, interleukin-6, and PAI-1 gene expression after a short stimulation with CML, whereas adiponectin expression decreased (Figure 2B). In both SGBS preadipocytes and adipocytes, highly modified CML-albumin had a greater effect on expression levels of inflammatory markers than minimally modified CML-albumin, demonstrating a dose-dependent effect of CML.
Figure 2. (Continued)
To confirm the role of RAGE in the CML-mediated expression of inflammatory markers, preadipocytes and adipocytes were preincubated with anti-RAGE antibody or soluble RAGE (sRAGE). Inhibition of RAGE by anti-RAGE antibody and sRAGE led to the normalization of CML-induced RAGE, PAI-1, interleukin-6, and adiponectin gene expression in SGBS adipocytes (Figure 2C) and preadipocytes (Figure II in the online-only Data Supplement).

Also, the incubation of SGBS preadipocytes and adipocytes with S100 protein, which is another important ligand for RAGE, showed upregulation of RAGE, PAI-1, and interleukin-6 and downregulation of adiponectin gene expression (Figure 2D; Figure III in the online-only Data Supplement).

These experiments, therefore, demonstrate in an in vitro model of excessive lipid accumulation that adipogenesis is associated with increased levels of CML-modified proteins, increased RAGE expression, and activation of the CML–RAGE axis leading to changes in expression of adipokines, thus indicating that RAGE plays a central role in dysregulation of adipokines associated with obesity.

Obese, RAGE-Deficient Mice Are Associated With Improved Inflammation, Improved Insulin Resistance, and Increased Plasma CML Levels

To define the role of RAGE in inflammation in obesity in vivo further, we developed obese, RAGE-deficient (RAGE−/−/LeptinDb−/−) and obese, wild-type (RAGE+/−/LeptinDb−/−) mice. In the leptinDb background, no effect of RAGE on body weight was observed (39±5 and 35±5 g, respectively) at 9 weeks. RAGE−/−/LeptinDb−/− mice exhibited an improved inflammatory profile when compared with RAGE+/−/LeptinDb−/− mice (39±5 and 35±5 g, respectively) at 9 weeks. RAGE−/−/LeptinDb−/− mice had an improved glucose metabolism when compared with RAGE+/−/LeptinDb−/− mice (Figure 3B). After insulin injection, glucose did not significantly decrease in RAGE−/−/LeptinDb−/− mice (from 24.09±1.32 mmol/L at time 0 minutes to 28.3±0.99 mmol/L at time 120 minutes). In contrast, insulin injection declined blood glucose by 30% in RAGE−/−/LeptinDb−/− mice (from 26.40±2.31 mmol/L at time 0 minutes to 18.81±2.64 mmol/L at time 90 minutes; Figure 3C). These results, therefore, demonstrate that RAGE deficiency is associated with a general increase in glucose tolerance and insulin sensitivity.

Circulating CML Is Trapped in Adipose Tissue of RAGE/LeptinDb−/− Mice

Of interest, CML plasma levels were significantly higher in RAGE+/−/LeptinDb−/− mice when compared with RAGE−/−/LeptinDb−/− mice (923±114 nmol/L versus 684±78 nmol/L, P<0.05), and in RAGE−/− mice compared with wild-type mice (Figure IV in the online-only Data Supplement), indicating that RAGE also represents a mechanism for the regulation of CML plasma levels.

A possible mechanism whereby RAGE regulates plasma CML levels is a selective uptake of circulating CML in specific tissues or organs. We first investigated the uptake of circulating CML in obesity using Leptin−/− mice. We injected Leptin−/− mice with fluorescently labeled CML-albumin (green fluorescent signal) and visualized the distribution and accumulation of the injected CML-albumin. As a control, we used a fluorescently labeled control-albumin (red fluorescent signal), which was simultaneously injected with CML-albumin in Leptin−/− mice. After injection, plasma clearance of fluorescently labeled CML-albumin was significantly faster than that of control-albumin (t50=59±5 minutes of an inflammatory marker=individual’s observed value−mean)/SD). This combined overall inflammation score was significantly lower in the RAGE−/−/LeptinDb−/− mice when compared with that in RAGE−/−/LeptinDb−/− mice (<6±0.2 versus 7±0.2; P<0.01). Moreover, RAGE deficiency in obese mice led to normalization of the inflammatory markers because the levels of inflammatory markers were comparable with those of RAGE+/−/LeptinDb−/− mice (Figure 3A). The same pattern of inflammatory cytokines emerged in RAGE deficiency mice when compared with wild-type mice (Figure IV in the online-only Data Supplement).

In addition, RAGE+/−/LeptinDb−/− mice were also associated with altered metabolic phenotype. Glucose tolerance test demonstrated significant differences in response to glucose load between RAGE+/−/LeptinDb−/− and RAGE+/−/LeptinDb−/− mice (Figure 3B). RAGE+/−/LeptinDb−/− mice had an improved glucose metabolism when compared with RAGE+/−/LeptinDb−/− mice (Figure 3B). After insulin injection, glucose did not significantly decrease in RAGE+/−/LeptinDb−/− mice (from 24.09±1.32 mmol/L at time 0 minutes to 28.3±0.99 mmol/L at time 120 minutes). In contrast, insulin injection declined blood glucose by 30% in RAGE−/−/LeptinDb−/− mice (from 26.40±2.31 mmol/L at time 0 minutes to 18.81±2.64 mmol/L at time 90 minutes; Figure 3C). These results, therefore, demonstrate that RAGE deficiency is associated with a general increase in glucose tolerance and insulin sensitivity.

Figure 2. N-[(Carboxymethyl)lysine (CML)]–receptor for advanced glycation end product (RAGE) axis is increased during adipogenesis, and activation of this pathway mediates adipokine dysregulation in human adipocytes. A, Differentiation of Simpson–Golabi–Behmel syndrome (SGBS) preadipocytes to adipocytes was evaluated by an Oil Red O staining and showed a significant lipid accumulation during adipogenesis. CML levels (determined by UPLC-Tandem MS [ultra-performance liquid chromatography-tandem mass spectrometry]), RAGE gene expression (determined by quantitative RT-PCR [real-time polymerase chain reaction]), and RAGE protein levels (determined by Western blotting) were significantly increased during the differentiation process. #P<0.05, **P<0.01 vs day 0. B, Incubation of SGBS adipocytes with minimally (dotted line) and highly modified CML-albumin (black line) increased the expression of RAGE and downstream genes plasminogen activator inhibitor (PAI)-1 and interleukin (IL)-6, and decreased adiponectin expression in a time- and concentration-dependent manner. Minimally and highly modified CML-albumin were prepared and characterized as described before.14 The expression levels of each gene are presented relative to those of the control-albumin–treated cells for each time point. #P<0.05 minimally modified CML vs control-albumin, **P<0.01 highly modified CML-albumin vs control-albumin. C, Preincubation of SGBS adipocytes with anti-RAGE antibody or soluble RAGE (sRAGE) inhibited the CML–increased expression of RAGE, PAI-1, and IL-6 and the CML–decreased expression of adiponectin. #P<0.05 and **P<0.01 CML-albumin vs control-albumin, **P<0.01 anti-RAGE antibody/sRAGE vs CML-albumin.
versus 139±13 minutes; Figure 4A). CML-albumin and control-albumin were distributed via the circulation and were visualized in the liver and kidney (Figure 4B). Importantly, both CML-albumin and control-albumin were colocalized and were restricted to the circulation of these tissues. However, a strong accumulation of CML-albumin was observed in adipose tissue of LeptrDb–/– mice, whereas control-albumin was not detectable in the adipose tissue (Figure 4B). These experiments, therefore, showed that adipose tissue itself is able to trap CML from the circulation actively and selectively, thereby contributing to local CML accumulation in adipose tissue in obesity and decreased plasma CML levels.

To study the localization of the injected CML-albumin in adipose tissue in detail, we injected only green fluorescently labeled CML-albumin in LeptrDb–/– mice and stained the adipose tissue after isolation for CD31 to visualize the endothelial cells (red fluorescently labeled anti-CD31 antibody). Adipocytes showed blue autofluorescence. Fluorescently labeled CML-albumin was present at the site of administration, namely the vasculature of the adipose tissue, but more importantly, CML-albumin was also detected in the cytosol and at the membrane of adipocytes (Figure 4C).

To investigate the role of RAGE in the trapping of CML, we repeated this CML trapping experiment in our unique mice model (ie, RAGE–/–/LeptrDb–/– and RAGE+/+/LeptrDb–/– mice). RAGE–/–/LeptrDb–/– and RAGE+/+/LeptrDb–/– mice were injected with fluorescently labeled CML-albumin (red fluorescently signal). A significant accumulation of CML-albumin was observed in adipose tissue of RAGE+/+/LeptrDb–/– mice, whereas the fluorescently labeled CML-albumin was completely absent in adipose tissue of RAGE–/–/LeptrDb–/– mice (Figure 4D). This indicates that circulating CML is trapped in the adipose tissue via a RAGE-dependent mechanism. From that observation, we can deduce that RAGE-mediated trapping of CML in adipose tissue contributes to the local accumulation of CML in adipose tissue in RAGE+/+/LeptrDb–/– mice, which is associated with a decrease of plasma CML levels.

CML Plasma Levels Are Decreased in Obesity in Humans
To investigate whether obesity is associated with decreased plasma CML in humans, CML plasma levels were measured in
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As demonstrated in Figure 5A, plasma protein-bound CML concentrations were significantly lower in obese when compared with those in lean subjects. Additional analyses demonstrated strong inverse correlations between protein-bound CML plasma concentrations and body mass index (Figure 5B). These data indicate that the CML accumulation observed in obese adipose tissue is accompanied by lower circulating protein-bound CML levels, suggesting that a CML trapping mechanism is operating in humans. This decrease of plasma protein-bound CML levels in obesity and the correlation with body mass index were confirmed in severely obese subjects (Figure V in the online-only Data Supplement).

We also evaluated the effect of weight loss on plasma CML levels. Plasma samples from severely obese subjects undergoing bariatric surgery were taken before and 6 months after surgery. During this period, they lost 16±9 kg on average. Their mean body mass index was 41.7±3.1 kg/m² before surgery and 36.3±4.4 kg/m² after 6 months. As demonstrated in Figure 5C, weight loss by bariatric surgery was associated with an increase of CML plasma levels.

CML Plasma Levels Are Associated With Insulin Resistance in Humans

The association of decreased plasma levels of CML in obesity with insulin resistance, as determined by a hyperinsulinemic-euglycemic clamp, was investigated in obese subjects (n=10) and lean controls (n=9). Obese subjects had a significantly lower insulin sensitivity when compared with lean subjects (glucose infusion rate, 16.1±9.6 versus 37.4±8.3 μmol x kg body weight⁻¹ x minutes⁻¹; P<0.001). A strong correlation was found between CML plasma concentrations and insulin sensitivity (r=0.669; P<0.01; Figure 5D), indicating that low CML plasma levels in obesity are associated with high insulin resistance.

Discussion

Here we show, for the first time, a role of the CML–RAGE axis in obesity-associated dysregulation of adipokines and in the development of obesity-related insulin resistance. First, we demonstrated in humans and in an in vitro model of adipogenesis that obesity is associated with increased CML accumulation and RAGE expression. Second, we found that the activation of this CML–RAGE axis resulted in a dysregulated expression of pro- and anti-inflammatory cytokines. We found that the RAGE–/–/LeptrDb–/– mice were characterized by improved inflammatory profile and improved insulin sensitivity. Third, we also found a RAGE-mediated trapping of CML in adipose tissue in RAGE+/+/LeptrDb–/+ mice. In line with this concept, we also found decreased CML plasma levels in obese subjects, and this decrease in CML was associated with decreased insulin sensitivity in obese subjects. Taken together, this study demonstrates a novel function of RAGE in regulating CML levels in obesity, and that the activation of the CML–RAGE axis plays a major role in the dysregulation of adipokines and the development of obesity-associated insulin resistance.

Although CML has been regarded as a traditional AGE formed from glucose, increasing numbers of reports have emphasized that CML is mainly formed from lipid peroxidation reactions and can, therefore, be considered as an advanced lipoxidation end product.14,18 The increased oxidation of fatty
Acids and formation of lipid peroxidation products in obese conditions prompted us to hypothesize that CML formation is increased in obesity. Our in vitro data confirmed that lipid accumulation during differentiation of adipocytes was associated with increased endogenous CML formation. In addition, we demonstrated in human adipose tissue that CML accumulation is higher in adipose tissue of obese subjects when compared with that in adipose tissue of lean subjects and was higher in VAT when compared with SAT of severely obese subjects. The simultaneous increase of CML and RAGE in obesity and the colocalization of RAGE and CML in the human adipose tissue support a key role for CML–RAGE axis in obesity-associated inflammation.

Only limited reports have investigated the role of AGEs in adipocyte inflammation, and no study has to date has investigated the role of CML-RAGE in human adipocyte inflammation. Unno et al. already showed that glycolaldehyde-modified albumin increased the expression of leptin in mouse adipocytes. Moreover, PAI-1 expression in rat adipocytes was upregulated on incubation with nondefined AGEs. Our data reveal that the incubation of preadipocytes and adipocytes with CML increased the expression of inflammatory markers, RAGE, PAI-1, and interleukin-6, whereas the expression of adiponectin was decreased on CML incubation. In both preadipocytes and adipocytes, we demonstrated that CML has functional consequences at the level of adipokine dysregulation. However, in adipocytes, a rapid CML-mediated upregulation of RAGE, PAI-1, interleukin-6, and downregulation of adiponectin was observed, whereas a delayed effect of CML on expression of inflammatory markers was detected in preadipocytes. Differences in basal RAGE gene expression between preadipocytes and adipocytes may underlie this effect. In preadipocytes and adipocytes, we showed that strategies to inhibit CML-RAGE interaction or to decoy CML, via administration of anti-RAGE antibody or soluble RAGE, respectively, reduced the CML-mediated inflammatory responses. Our current findings are the first to demonstrate a direct role of RAGE in human adipocyte inflammation in vitro. In addition, our data delineate that CML as ligand for RAGE plays fundamental role in RAGE-mediated adipocyte inflammation.
We further extended these in vitro observations to in vivo ones using a murine model of RAGE deficiency, obesity, and type 2 diabetes mellitus, RAGE\(^{-/-}\)/Leptin\(^{-/-}\) mice. Deletion of RAGE was protective against inflammation and was associated with greater insulin sensitivity in insulin tolerance test and improved glucose metabolism in glucose tolerance test. RAGE\(^{-/-}\) animals had slightly higher body weights then their littermate RAGE\(^{+/+}\) control mice. Because dosing for glucose tolerance test and insulin tolerance test was based on total body weight, we cannot exclude this difference in body weight and hence difference in dosing of glucose and insulin influenced the outcome of the metabolic tests. However, if anything, this would lead to an underestimation of the improved glucose tolerance in RAGE\(^{-/-}\) mice. Previous research has also demonstrated that RAGE deficiency significantly decreased the expression of pro-inflammatory mediators and lower levels of oxidative stress, whereas adiponectin levels and antioxidative defense mechanisms were higher in RAGE-deficient mice.\(^{24–28}\) In addition, the underlying mechanism.

We observe an effect of RAGE on adiposity in the LeptrDb\(^{-/-}\) background when compared with lean subjects, and moreover, CML-RAGE accumulation was higher in VAT than compared with SAT of obese subjects. From these observations, we may deduce that in obese subjects and in VAT, there is more RAGE-mediated CML trapping present that explains the decrease of circulating CML levels.

Our human study showed, in addition to the CML accumulation in adipocytes, a strong CML staining in macrophages of obese adipose tissue. As the adipose tissue is infiltrated by inflammatory macrophages during obesity, CML accumulation in these macrophages and macrophage activation could also play an important role in adipose tissue inflammation. It has already been demonstrated that nondefined AGEs stimulate the production of tissue factor in cultured human monocytes and tumor necrosis factor-\(\alpha\) production in rat macrophages. Therefore, the role of RAGE-CML in macrophage activation, inflammation, and insulin resistance in obesity, thereby contributing to obesity-associated insulin resistance. Hence, RAGE-mediated CML trapping in adipose tissue is a potentially useful target for developing new therapies against obesity-associated dysregulation of adipokines and its complications.

Acknowledgments

We acknowledge Prof Wabitsch for providing the Simpson–Golabi–Behmel syndrome adipocytes and OleoSmithKline (the Netherlands) for providing rosiglitazone. This work is dedicated to Prof Angelika Bierhaus. She passed away on April 15, 2012. She was of inestimable value for our insights into the receptor for advanced glycation endproducts. We own her a great debt of gratitude.
Sources of Funding
This research was performed as part of the Prevention and Early Detection of Cardiovascular Complications in Type 2 diabetes mellitus (PREDICCt) projects (grant 01C-104), within the framework of the Netherlands Heart Foundation, Dutch Diabetes Research Foundation (grant 2005.00.035), and Dutch Kidney Foundation. This work was also supported in parts by grants for the Duitse Forschungsgemeinschaft (grant 2005.00.035), and Dutch Kidney Foundation. This work was also supported by grants for the Translational University Limburg and the Maag Lever Darm Stichting (WWO09-46).

Disclosures
None.

References

Significance
This study provides, for the first time, evidence that the N epsilon-(carboxymethyl)lysine-receptor for advanced glycation end product axis is a novel pathway linking obesity to inflammation and more importantly to the development of obesity-related insulin resistance. Targeting this axis may have future therapeutic potential in the management of the obesity-associated complications.
Nε-(Carboxymethyl)lysine-Receptor for Advanced Glycation End Product Axis Is a Key Modulator of Obesity-Induced Dysregulation of Adipokine Expression and Insulin Resistance


Arterioscler Thromb Vasc Biol. 2014;34:1199-1208; originally published online April 10, 2014; doi: 10.1161/ATVBAHA.113.302281

Arteriosclerosis, Thrombosis, and Vascular Biology is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
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Print ISSN: 1079-5642. Online ISSN: 1524-4636

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SUPPLEMENT:

CML-RAGE Axis is a Key Modulator of Obesity-Induced Dysregulation of Adipokine Expression and Insulin Resistance

SUPPLEMENTAL TABLE

Table I General Characteristics of Severely Obese Subjects.

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<td>BMI (kg/m(^2))</td>
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<td>HOMA-IR</td>
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Data are presented as mean ± SD, or as median [interquartile range], or as percentage. Insulin resistance was estimated using the homeostasis model assessment for insulin resistance (HOMA-IR) (http://www.dtu.ox.ac.uk).
Figure I. Activation of the CML-RAGE axis mediates dysregulation of adipokines in human preadipocytes.

To examine the potential biological effects of CML on the expression of adipokines, preadipocytes were incubated during 24h, 48h and 72h with 0.5 μM control albumin (white bars), minimally- (gray bars) and highly-modified (black bars) CML-albumin. Changes in expression of RAGE, PAI-1, IL-6 and adiponectin were examined by real time PCR. Incubation with preadipocytes during 24h and 48h did not change RAGE, PAI-1 and IL-6 gene expression, whereas incubation of preadipocytes during 72h significantly increased RAGE, PAI-1 and IL-6 gene expression compared with control albumin. *p<0.01 vs control-albumin.
Figure II. CML-induced dysregulation of adipokines is mediated via RAGE in preadipocytes.

To determine whether the effects of CML on the expression of adipokines in preadipocytes involve the activation of RAGE, CML-RAGE interaction was blocked using a RAGE antibody (5 µg/mL) or sRAGE (11.5 µg/mL). CML-induced gene expression of RAGE, IL-6 and adiponectin were significantly inhibited by RAGE antibody and sRAGE. *p<0.05 and **p<0.01 CML-albumin vs control-albumin, ##p<0.05 and ###p<0.01 anti-RAGE antibody/soluble RAGE vs CML-albumin.
Figure III. Effect of S100 protein on expression levels of adipokines in preadipocytes.

Incubation of SGBS preadipocytes with 6 and 24 µg/mL of S100 protein during 1h showed upregulation of the expression of RAGE, PAI-1 and IL-6, and downregulation of adiponectin gene expression. *p<0.01 vs control-albumin.
Figure IV. RAGE mediates CML plasma concentrations and inflammatory markers.

(A) CML plasma levels were measured by UPLC-Tandem MS in mice deficient for RAGE (RAGE^{−/−} mice) and wild-type (WT) mice (n=10 per group, 12 weeks old). Plasma CML was significantly higher in RAGE^{−/−} mice compared with WT mice. (B) Circulating levels of the pro-inflammatory markers IL-1β, IL-12, IL-6, mKC (IL-8), IFN-γ and TNF-α were decreased in RAGE^{−/−} versus WT mice, whereas the anti-inflammatory markers IL-10 and adiponectin were increased. *p-value<0.05.
Figure V. Plasma CML levels are decreased in obesity.

To confirm in a larger study population of obese and control subjects the association between CML plasma levels and obesity, we selected lean control subjects (n=77, BMI ≤ 25 kg/m²) and severely obese subjects (n=44, BMI > 40 kg/m²). The severely obese subjects were admitted to the Surgical Department of Maastricht University Hospital to undergo bariatric surgery. The control subjects were randomly selected from a population of subjects with normal glucose tolerance of the Cohort Study of Diabetes and Atherosclerosis Maastricht (CODAM), and from the population of spouses of familial combined hyperlipidemia patients. Details of these control subjects are described by Brouwers et al. and Jacobs et al. Plasma CML levels were measured with UPLC-Tandem MS as described in the material and methods section. In addition
to CML, plasma levels of N\(^\text{\textdegree}\)-(Carboxyethyl)lysine (CEL) were also measured in the same plasma sample and simultaneously with the CML analysis. For the CEL analysis, D4-CEL was used as internal standard. In addition to these analyses of CML and CEL in total plasma proteins, free levels of CML and CEL were also measured in these subjects. Free CML and CEL levels were measured in deproteinized plasma by UPLC-Tandem MS as described in the material and methods section. (A) CML plasma levels were significantly decreased in the severely obese subjects compared with the lean control subjects. Free CML plasma levels were also significantly decreased in the severely obese subjects compared with the lean control subjects. (B) CEL plasma levels were significantly increased in the severely obese subjects vs the lean control subjects; whereas free CEL plasma levels were not different between the groups. (C) and (D) CML plasma levels were inversely correlated with waist-to-hip ratio (C) and BMI (D), respectively. Correlation coefficient for each relationship is given.
REFERENCES


SUPPLEMENT: MATERIAL AND METHODS:

CML-RAGE Axis is a Key Modulator of Obesity-Induced Dysregulation of Adipokine Expression and Insulin Resistance


Human Study

We used 9 male lean (BMI ≤ 25 kg/m²) and 10 male obese (BMI > 25 kg/m²) subjects, which were admitted to the Maastricht University Medical Center to study in detail subcutaneous adipose tissue (SAT) function and insulin sensitivity by a hyperglycemic-euglycemic clamp. The mean glucose infusion rate during steady state (last 30 min) was used to assess insulin sensitivity. In all subjects, following plasma variables were determined after overnight fasting using standard laboratory techniques: glucose, insulin, total cholesterol, HDL- and LDL cholesterol, triglycerides and free fatty acids. Details of the study protocol are described by Goossens et al.1 In these subjects, plasma N^-{Carboxymethyl}lysine (CML) levels were measured with ultra-performance liquid chromatography-tandem mass spectrometry (UPLC-Tandem MS) and SAT biopsies were available for immunodetection and RNA isolation.

We also included severely obese subjects (n=44, BMI > 40 kg/m²) which were admitted to the Surgical Department of Maastricht University Hospital to undergo bariatric surgery.2 In all subjects, following plasma variables were determined after overnight fasting using standard laboratory techniques: glucose, insulin, total cholesterol, HDL- and LDL cholesterol, triglycerides and free fatty acids (main characteristics are presented in supplemental table S1). During bariatric surgery, SAT and visceral adipose tissue (VAT) were sampled for immunodetection and for RNA isolation.

All participants gave written informed consent for participation in the study, which was undertaken with approval from the Ethics Committee of the Maastricht University Medical Center.

Immunodetection of CML in Human Adipose Tissue

SAT of lean (n=9) and obese (n=10) male subjects were sampled during the study, fixed in 4% formalin and immediately embedded in paraffin. In addition, SAT and VAT of severely obese subjects (n=44) were sampled during bariatric surgery and embedded in paraffin after fixation in formalin. Immunohistochemistry was performed using Envision+ System-HRP (Dako, Glostrup, Denmark) to demonstrate the presence and localization of CML-modified proteins in adipose tissue. Primary antibodies that were used include: monoclonal antibody against CML-modified proteins,3 anti-CD31 antibody specific for endothelial cells (Dako), anti-CD68 antibody specific for macrophages (Dako) and antibody directed against the receptor for advanced glycation endproducts (RAGE) (R&D Systems, MN, USA).

Scoring of the CML staining of adipose tissues was performed by an investigator (HWMN) masked to the patient’s characteristics. CML-positive adipocytes were scored in three randomly selected fields and each adipocyte was given a score according to the intensity of the staining
(score 0 = no CML staining; 1 = weak CML staining; 2 = moderate CML staining; and 3 = strong CML staining). Each score was then multiplied by the number of adipocytes positive for that score, and the total CML score of an individual SAT/VAT was calculated by summing the multiplication score and dividing this sum by the total number of adipocytes.

RAGE Expression in Human Adipose Tissue

RAGE gene expression levels were measured in SAT of lean and obese subjects, and in SAT and VAT of severely obese subjects. After isolation using Tri Reagent (Sigma, MO, USA), total cellular RNA was reverse transcribed with iScript cDNA synthesis kit (Biorad). Expression of RAGE was measured quantitatively by real time PCR using SYBR Green mix (Quantace). The threshold cycle (Ct) value for every sample was measured, and mRNA expression levels of RAGE were normalized to the reference genes β-actin, cyclophilin A and β2-microglobulin. Data were analyzed by the ΔCt method.

RAGE Protein Levels in Human Adipose Tissue

Homogenates of SAT of lean controls and obese subjects, and VAT and SAT of severely obese subjects were available to analyze RAGE protein levels by Western blotting. Total proteins of VAT and SAT were randomly distributed and separated on a 12% SDS-PAGE. Proteins were blotted onto a polyvinylidene fluoride membrane (Amersham, Buckinghamshire, UK) and blocked with 3% non-fat milk/PBS. The membrane was incubated with RAGE antibody (R&D Systems), followed by incubation with goat-anti-mouse horseradish peroxidase antibody (Dako). Proteins were detected using the chemiluminescence kit (Amersham) and visualized by Chemidoc XRS (Bio-Rad). Quantification of the RAGE band was done by Quantity One (Bio-Rad) and was normalized for β-actin.

Measurements of CML levels

Protein-bound CML levels in plasma or cell homogenates were measured by UPLC-Tandem MS (Waters, UPLC/Xevo TQ MS, Etten-Leur, the Netherlands). Total proteins were reduced with 100 mM sodium borohydride in 0.2 M sodium borate buffer at pH 9.2 for 2 hours at room temperature. The proteins were then precipitated with trichloroacetic acid and hydrolyzed with 6 M HCl overnight at 110°C. HCL was evaporated at 80°C under nitrogen, and residues were resolved in 0.5 mM tridecafluoroheptanoic acid. Analysis was performed using C18 reversed phase column with a linear gradient of acetonitril. CML levels were measured using a positive ionization mode with D4-CML as internal standard.

Cell Culture of Human SGBS Adipocytes

Human SGBS (Simpson-Golabi-Behmel-Syndrome) preadipocytes were maintained in DMEM/HAM’s F12 culture medium containing 10% FCS, 1 mg/mL biotine, 1 mg/mL pantothenate and 1% penicillin/streptozotocin, and were grown to confluence. To obtain serum-free-medium (OF medium), supplementation with FCS was omitted. After reaching confluence, adipogenic differentiation was induced by incubating the preadipocytes with OF medium.
supplemented with 0.01 mg/mL human transferrin, 20 nM insulin, 100 nM cortical and 0.2 nM triiodothyronin for 12 days. For the first 6 days, this adipogenic medium was additionally supplemented with 25 nM dexamethasone, 500 µM 3-isobutyl-1-methylxanthine and 2 µM rosiglitazone (GlaxoSmithKline, London, UK). Oil Red O staining (Sigma) of SGBS cells during differentiation was performed following the manufacturer’s instructions to determine adipogenesis. In addition, homogenates of differentiating SGBS adipocytes were harvested every other day (day 0, 2, 4, 6, 8, 10 and 12) during adipogenesis to measure protein-bound CML levels by UPLC-Tandem MS (as described above), and to analyze expression levels of RAGE by real time PCR (as described above) and RAGE protein levels by Western blotting (as described above).

Effect of CML incubation of Human SGBS Pre- and Adipocytes on Inflammation

SGBS preadipocytes and mature, differentiated SGBS adipocytes were incubated for 15 min, 30 min, 1 hr, 2 hr, 4 hr (short incubation), 24 hr, 48 hr and 72 hr (long incubation) with 0.5 µM control albumin, minimally- and highly-modified CML albumin. After incubation, total cellular RNA was extracted using Tri reagent (Sigma). Total RNA was reverse-transcribed with iScript cDNA synthesis kit (Biorad) and expression of RAGE, plasminogen activator inhibitor (PAI)-1, interleukin (IL)-6 and adiponectin were measured quantitatively by real time PCR using SYBR Green mix (Quantace). The threshold cycle (C_t) value for every sample was measured, and mRNA expression levels of each gene were determined by the ΔC_t method using β-actin, cyclophilin A and β2-microglobulin as reference genes.

To determine the mechanism of CML-mediated dysregulation of inflammatory markers, SGBS preadipocytes and differentiated SGBS adipocytes were pre-incubated with anti-RAGE antibody (5 µg/mL) (R&D Systems) or soluble form of RAGE (11.5 µg/mL) (provided by Dr. M. Gebbink, Utrecht University, the Netherlands) for 1 hr to block the endogenous RAGE pathway or to block CML binding to RAGE, respectively. Cells were then incubated with 0.5 µM control-albumin or CML-modified albumin. After incubation, RNA was extracted and cDNA was synthesized as described above. Differences in gene expression of RAGE, PAI-1, IL-6 and adiponectin were determined by real time PCR.

As positive control, we incubated SGBS preadipocytes and adipocytes with S100 protein (6 and 24 µg/mL) (Merck, NJ, USA) during 1h. S100 protein is a pro-inflammatory ligand for RAGE and the effect of S100 protein incubation on RAGE, IL-6, PAI-1 and adiponectin was examined by real time PCR.

Animal experiments

Obese, RAGE deficient mice (RAGE^{+/−}/Lepr^{Db−/−}) were generated by crossing obese, non-insulin-dependent diabetic C57BLKS-Lept^{Db−/−} (Lept^{Db−/−}) (Charles River, Maastricht, the Netherlands) with RAGE^{−/−} mice (obtained from Heidelberg University) for several generations. All experiments were approved by the local ethics committee on the use of laboratory animals.

Markers of Inflammation in Mice: At 9 weeks, plasma of RAGE^{+/−}/Lept^{Db−/−} mice (n=10) and their littermate RAGE^{+/−}/Lept^{Db−/−} controls (n=10) were collected to measure circulating inflammatory markers. Mouse inflammatory panels for IL-1β, IL-12p70, interferon (IFN)-γ, tumor necrosis factor (TNF)-α, mKC (IL-8), IL-10 and adiponectin assay were purchased from Meso Scale
Discovery (MSD, MD, USA). All reagents were provided with the MSD kit, and measurements were performed according to the manufacturer’s instructions. Interassay CV were 14.9% for IL-1β, 9.0% for IL-12p70, 9.3% for IFN-γ, 12.1% for IL-6, 14.0% for TNF-α, 7.7% for mKC (IL-8), 5.8% for IL-10 and 4.0% for adiponectin. To better understand the effect of RAGE deficiency on inflammation in obesity, an overall inflammation score was calculated in RAGE+/+/LeptrDb−/− and RAGE−/−/LeptrDb−/− mice by averaging the z-scores of each of the individual inflammatory markers [z-score of an individual markers = (individual’s observed value – mean) / SD]. This score enables a more robust characterization of the overall mechanism of inflammation than that as characterized on the basis of each marker separately. In addition, this score has the advantage of reducing the influence of measurement error/biological variability.

**CML Plasma Levels in Mice:** Protein-bound CML plasma levels of RAGE−/−/LeptrDb−/− (n=10, 9 weeks) and littermate RAGE+/+/LeptrDb−/− mice (n=10, 9 weeks) were measured with UPLC-Tandem MS as described above.

**Glucose and Insulin Tolerance Tests in Mice:** Glucose tolerance tests (GTT) were performed in 12 weeks old RAGE−/−/LeptrDb−/− (n=8) and littermate RAGE+/+/LeptrDb−/− (n=10) mice. Following a 16 hr overnight fasting period, a small tail cut was made and whole blood glucose was measured by a glucometer (Contour) (Bayer, Mijdrecht, the Netherlands) from the second drop of blood expressed at time 0 and at time 30, 60, 90 and 120 min following intraperitoneal injection of glucose (2 g/kg bodyweight in filtered saline solution) (Sigma). Insulin tolerance tests (ITT) were performed in the same RAGE−/−/LeptrDb−/− and RAGE+/+/LeptrDb−/− at 13 weeks of age. Food was removed 6 hr prior to insulin treatment (0.75 U/kg bodyweight, intraperitoneal injection) (Actrapid Penfill, Novo Nordisk, Bagsvaerd, Denmark), which was administered at time 0, following measurements of bodyweight and baseline glucose. A small tail cut was made for glucose measuring at 0, 30, 60, 90 and 120 min.

**CML Trapping in Mice:** Trapping of CML in obesity was first investigated in a murine model of obesity and type 2 diabetes, i.e. LeptrDb−/− mice (Charles River). LeptrDb−/− mice (n=6, 6-8 weeks) were intravenously injected with fluorescently-labeled CML-albumin and fluorescently-labeled control-albumin to visualize distribution/accumulation of circulating CML among different organs. To produce fluorescently-labeled CML-albumin and fluorescently-labeled control-albumin, Alexa-labeled albumin 488 (green fluorescent signal) and 555 (red fluorescent signal) (Invitrogen, CA, USA) were incubated overnight with or without 100 mM glyoxal, respectively, to induce CML-modification in albumin. Glycation and grade of modification of the fluorescently-labeled CML-albumin and control-albumin was confirmed by UPLC-Tandem MS and Western blotting (data not demonstrated). Fluorescently-labeled CML-albumin and control-albumin (3.5 mg/kg bodyweight) were simultaneously injected intravenously into the tail vein of these LeprDb−/− mice. Blood samples were collected before and at different time points after injection from the tip of the tail using a heparin-coated microcapillary (Microvette CB 300 LH, Sarstedt, Nümbrecht, Germany) and centrifuged. Plasma fluorescence was measured at 515 and 565nm with the NanoDrop 3300 Fluorospectrometer (Thermo Fisher Scientific, Wilmington, Delaware, USA) to study the clearance of fluorescently labeled CML-albumin and unmodified-albumin from the circulation. Four hrs after injection, mice were sacrificed and adipose tissue, liver and kidney were sampled, washed in 0.9% NaCl and then embedded in 1% agarose (Biorad). These intact tissues were immediately, and without further processing, analyzed by two-photon microscopy to detect trapping of the injected fluorescently-labeled CML-albumin. Two-photon laser scanning microscopy (TPLSM) images were recorded with a Leica DM6000 CFS upright microscope incorporated in a Multiphoton optical imaging system (Leica TCSPC SP5, Leica Microsystems, Mannheim, Germany). Fluorophores and autofluorescence of the tissues were excited by a mode-locked Coherent Chameleon Ti:Sapphire laser (Coherent, Santa Clara, CA, USA) with an
880 nm central wavelength and a 120 fs pulse width at the focal plane. Datasets were acquired using a 20× water-dipping objective lens (Leica, WD 3 mm) with a 1.00 numerical aperture and subsequent optical zoom. Fluorescence in LeptinDb-/ mice was detected in the direct detector system with emission filters IF525/50 and IF585/40 and color-coded in green (CML-albumin) and red (unmodified albumin), respectively. Autofluorescence of adipocytes was also detected with the green filter replaced by a BP460/50 filter, color-coded in blue. The chosen combination of emission filters minimized leak-through, while simultaneously optimizing sensitivity. All images shown have a pixel field of 512×512 pixels and are imaged with a line frequency of 400 Hz, resulting in a pixel dwell time of 4.9 μs and an image frame time of 1.28 s.

Next, we repeated this CML trapping experiment in RAGE+/LeptinDb-/- and littermate RAGE+/+LeptinDb-/- mice (n=10 in both groups, 9 weeks) to investigate the role of RAGE in the distribution and accumulation of circulating CML among different organs. Because of the presence of an EGFP/RAGE construct in RAGE+/LeptinDb-/- mice, mice were injected with red fluorescently-labeled CML-albumin (Alexa-labeled albumin 555). Production of fluorescently-labeled CML-albumin and trapping experiments was performed as described above. Processing and analysis of the tissues by two-photon microscopy was performed as described above. Fluorescence in RAGE+/LeptinDb-/- and RAGE+/+LeptinDb-/- mice was detected in the direct detector system with emission filters 397-451 nm, 500-450 nm and 550-661 nm and color-coded in blue (collagen), green (EGFP/RAGE construct) and red (CML-albumin), respectively.

Statistics

All analyses were performed with the Statistical Package for Social Sciences (SPSS) version 15.0 for Windows (SPSS Inc, Chicago, Illinois, USA). Variables with a skewed distribution were log transformed prior to further analyses. Differences in CML immunostaining, RAGE gene expression levels and RAGE protein levels between SAT of lean and obese subjects, and between SAT and VAT of severely obese subjects were analyzed by unpaired or paired Student’s t-test, respectively. Differences in gene expression levels of RAGE, PAI-1, IL-6 and Adiponectin after incubation of SGBS adipocytes with CML were investigated using a Student’s t-test. In addition, changes of CML concentration, RAGE gene expression levels and RAGE protein levels during differentiation of SGBS preadipocytes to adipocytes were also investigated using a Student’s t-test. In mice, differences in circulating levels of inflammatory markers and CML plasma levels were also investigated using a Student’s t-test. A Two Way ANOVA with Bonferroni correction was used to analyze the results of GTT and ITT. Comparisons of characteristics between lean and obese subjects were performed with a Student’s t-test or Chi-square test. Associations between CML plasma levels, BMI and glucose infusion rate were determined by partial correlation and were adjusted for age and sex. P-values less than 0.05 were considered statistically significant. All data are presented as mean ± SD.
REFERENCES


