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Elevated Resting and Postprandial Digestive Proteolytic Activity in Peripheral Blood of Individuals With Type-2 Diabetes Mellitus, With Uncontrolled Cleavage of Insulin Receptors

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ABSTRACT
Objective: To examine resting and postprandial peripheral protease activity in healthy controls and individuals with type 2 diabetes mellitus (T2DM) and pre-T2DM.

Methods: Individuals with T2DM or pre-T2DM and healthy controls (mean age 55.8 years) were studied before and for a span of 300 minutes following a single high-calorie McDonald’s breakfast. Metalloproteases-2/-9 (MMP-2/-9), elastase, and trypsin activities were assessed in whole blood before and following the meal using a novel high-precision electrophoretic platform. Also assessed were circulating levels of inflammatory biomarkers and insulin receptor density on peripheral blood mononuclear cells (PBMCs) in relationship to protease activity.

Results: Premeal MMP-2/-9 and elastase activity levels in T2DM and in pre-T2DM participants were significantly elevated as compared to controls. The T2DM group showed a significant increase in elastase activity 15 minutes after the meal; elastase activity continued to increase to the 30-minute time point ($p < 0.01$). In control participants, MMP-2/-9, elastase, and trypsin were significantly increased at 15 minutes after the meal ($p < 0.05$) and returned to premeal values within a period of approximately 30 to 60 minutes post meal. PBMCs incubated for 1 hour with plasma from T2DM and pre-T2DM participants had significantly lower levels of insulin receptor density compared to those incubated with plasma from control participants ($p < 0.001$).

Conclusions: The results of this study suggest that individuals with T2DM and pre-T2DM have higher resting systemic protease activity than nonsymptomatic controls. A single high-calorie/high-carbohydrate meal results in further elevations of protease activity in the systemic circulation of T2DM and pre-T2DM, as well as in healthy controls. The protease activity in turn can lead to a downregulation of insulin receptor density, potentially supporting a state of insulin resistance.

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Introduction
Type 2 diabetes mellitus (T2DM) is characterized by hyperglycemia and insulin resistance (1, 2). Despite the high prevalence of T2DM, a molecular mechanism for the development of insulin resistance has not yet been fully elucidated (3).

Unchecked degrading protease activity has been shown to contribute to the development of insulin resistance. In animal models of diabetes, hypertension, and metabolic syndrome, unchecked proteolytic activity cleaves the extracellular domain of the insulin receptor, leading to deficient insulin binding and signaling, that is, insulin resistance (3, 4). In the plasma of T2DM patients, elevated levels of “soluble” insulin receptor fragments have been reported (5), and the proposed mechanism for insulin receptor cleavage is by proteases (6, 7).

As part of normal digestion, powerful pancreatic proteases reside inside the lumen of the small intestine where they degrade large volumes of macromolecules in food. Chronic overconsumption of a high-calorie diet is a major risk factor for the development of T2DM and is also associated with an increased permeability of the intestinal mucosa (8). While there is the possibility that digestive enzymes leak out of the small intestine into the central circulation, the link between nutrition and protease activity in blood remains relatively unexplored.
Based on this existing literature, we hypothesized that a high-calorie/high-carbohydrate meal would induce an increase in protease activity in the systemic circulation due to increased intestinal mucosal permeability. A key requirement to test this hypothesis was to measure protease activity in whole blood (9). Previous efforts to study proteases in T2DM have yielded conflicting results and focused on proteases in isolated plasma and with limitations in assay sensitivity (9). To overcome these limitations, we used a new electrophoretic technique that uses charge-changing fluoroscent peptides capable of detecting the activities of nanomolar concentrations of active protease in a single drop of fresh whole blood without the need for sample preparation (10–12). Furthermore, in addition to protease activity, we examined whether an elevated proteolytic activity would trigger proteolytic cleavage of the extracellular domain of the insulin receptor on peripheral blood monocytes (PBMCs).

To elucidate potential relationships between a high-calorie/high-carbohydrate meal and circulating protease activity and its potential proteolytic consequences, we therefore measured the activities of the pancreatic proteases trypsin and elastase and the metalloproteases MMP-2 and -9, and the PBMC insulin receptor density in whole blood of T2DM, pre-T2DM, and healthy controls at rest and following a single high-calorie/high-carbohydrate meal.

### Material and methods

Ten normal control (fasting glucose <100 mg/dL), 10 pre-T2DM (fasting glucose 100 mg/dL to 125 mg/dL), and 10 T2DM (fasting glucose >126 mg/dL) volunteers participated in the study. Other than T2DM and pre-T2DM, all participants were otherwise asymptomatic. Study participants fasted for a minimum of 12 hours prior to study. Anthropomorphic measurements and blood pressure were collected. The study was approved by the Institutional Review Board of the Human Research Protections Program at the University of California, San Diego. All participants provided written informed consent.

### Meal tolerance test

An intravenous catheter was placed in the antecubital vein of the nondominant arm. Blood was collected into tubes containing either lithium heparin or ethylenediaminetetraacetic acid (EDTA) (Becton Dickinson). An initial blood sample was collected to serve as the baseline. A high-calorie/high-carbohydrate McDonald’s breakfast meal consisting of the following was then served to the participants: one hot chocolate, one orange juice, two hash browns, and one Egg McMuffin (see Table 1 for estimated totals in grams for calories, proteins, fats, carbohydrates [carbs], and sodium). Subsequent blood samples were collected postprandially at 15, 30, 45, 60, 120, 180, 240, and 300 minutes. For all participants, the protocol was started between the hours of 8:00 and 9:00 a.m. Participants were told to come in a fasting state, only having ingested water the morning of testing, and to continue as usual any prescribed medications they were taking.

### Protease activity measurements: charge-changing fluorescent peptide substrates

Samples were collected into lithium heparin tubes and immediately stored at 4°C. Protease activity was determined within 2 hours. Activities of MMP-2 and -9, elastase, and trypsin were measured using charge-changing protease

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**Table 1. McDonald’s Breakfast Meal Composition (Estimates in Grams).**

<table>
<thead>
<tr>
<th></th>
<th>Calories</th>
<th>Protein</th>
<th>Total fat</th>
<th>Saturated fat</th>
<th>Trans fat</th>
<th>Carbohydrates</th>
<th>Sodium</th>
</tr>
</thead>
<tbody>
<tr>
<td>One Egg McMuffin</td>
<td>280</td>
<td>17</td>
<td>12</td>
<td>6</td>
<td>0</td>
<td>29</td>
<td>777</td>
</tr>
<tr>
<td>Two hash browns</td>
<td>300</td>
<td>2</td>
<td>18</td>
<td>3</td>
<td>0</td>
<td>32</td>
<td>640</td>
</tr>
<tr>
<td>One orange juice</td>
<td>150</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>34</td>
<td>0</td>
</tr>
<tr>
<td>One McCafe hot chocolate</td>
<td>380</td>
<td>11</td>
<td>15</td>
<td>9</td>
<td>0.1</td>
<td>53</td>
<td>170</td>
</tr>
<tr>
<td>Totals</td>
<td>1,110</td>
<td>32</td>
<td>45</td>
<td>18</td>
<td>0.1</td>
<td>148</td>
<td>1,587</td>
</tr>
</tbody>
</table>

**Table 2. Baseline Characteristics of Study Participants (Mean ± SEM).**

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Control</th>
<th>pre-T2DM</th>
<th>T2DM</th>
<th>Control Fasting</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample size</td>
<td>7</td>
<td>10</td>
<td>10</td>
<td>3</td>
</tr>
<tr>
<td>Age (years)</td>
<td>53.0 ± 5.6</td>
<td>57.4 ± 4.0</td>
<td>57 ± 4.4</td>
<td>44 ± 2.6</td>
</tr>
<tr>
<td>Females (#)</td>
<td>5 (0.71)</td>
<td>6 (0.6)</td>
<td>6 (0.6)</td>
<td>1</td>
</tr>
<tr>
<td>Weight (kg)</td>
<td>78.5 ± 6.8*</td>
<td>86.6 ± 6.7</td>
<td>99.6 ± 7.4</td>
<td>56.3 ± 1.3** ,A</td>
</tr>
<tr>
<td>Waist (cm)</td>
<td>98.9 ± 6.0</td>
<td>102 ± 5.5</td>
<td>112.2 ± 5.2</td>
<td>81.9 ± 3.2**</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>29.1 ± 2.5</td>
<td>31.7 ± 2.5</td>
<td>33.4 ± 2.8</td>
<td>21.5 ± 0.6**</td>
</tr>
<tr>
<td>Fasting glucose (mg/dL)</td>
<td>77.6 ± 3.4**</td>
<td>114.1 ± 1.8**</td>
<td>147.9 ± 5.4</td>
<td>73.9 ± 4.8**</td>
</tr>
<tr>
<td>SBP (mm Hg)</td>
<td>118.0 ± 4.7*</td>
<td>129.0 ± 1.25</td>
<td>133.0 ± 2.9</td>
<td>108.0 ± 0.9**</td>
</tr>
<tr>
<td>DBP (mm Hg)</td>
<td>69.4 ± 1.5</td>
<td>71.3 ± 4.6</td>
<td>73.7 ± 3.0</td>
<td>73.3 ± 1.1</td>
</tr>
<tr>
<td>Race and ethnicity</td>
<td>Non-Hispanic White</td>
<td>6 (0.9)</td>
<td>9 (0.9)</td>
<td>10 (1)</td>
</tr>
<tr>
<td></td>
<td>Hispanic</td>
<td>1 (0.09)</td>
<td>1 (0.1)</td>
<td>0 (0)</td>
</tr>
</tbody>
</table>

* p < 0.05 when compared to T2DM.
** p < 0.001 when compared to T2DM.
* p < 0.05 when compared to pre-T2DM.
** p < 0.001 when compared to pre-T2DM.

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substrates and an electrophoretic method (10–12). This method uses synthetic fluorescent peptides that are specifically cleaved by a protease. The peptides are originally negatively or neutrally charged, but upon cleavage by the protease of interest two fragments are produced: a negative one and a fluorescently labeled positive one. This allows for electrophoretic separation and detection in the whole blood without sample preparation. The substrate Ac-NGDVPVLTAGAGKNH₂ was used for MMP-2 and MMP-9; the substrate Ac-NDGDAGRAAGK-NH₂ was used for trypsin; and the substrate Ac-DAGSVAGAGK-NH₂ was used for elastase. Substrates were tagged with a fluorophore (Bodipy-FL-SE, Invitrogen, Carlsbad, CA) via the peptide’s diaminoethyl-amine group. Stock solutions of the substrates with concentrations of 1.2 mg/mL were prepared using 1× phosphate-buffered saline (1× PBS; pH 7.8).

Whole blood (4.0 μL) was mixed with the substrate (4.0 μL) to a final concentration of the substrate in the reaction of 0.6 mg/mL. As negative control, 1× PBS was combined with the substrate. Positive controls consisted of a combination of known concentrations of enzyme (1000, 100, and 10 nM) and the fluorescent substrates. Reactions were allowed to proceed for 30 minutes and then 6-μL aliquots of the reaction were loaded in different lanes of 20% polyacrylamide gels (Novex, Invitrogen, Carlsbad, CA) submerged in trisborate running buffer (0.5× TBE; 44.5 mM, 1 mM EDTA, pH 8.0). The loaded gels were electrophoresed at 500 V for 12 minutes and then imaged at excitation and emission wavelengths of 302 nm and 500–580 nm, respectively (BioDoc-It M-26 transilluminator, UVP, Upland, CA). Gels were scanned (Storm 840 Workstation; Molecular Dynamics, Sunnyvale, CA) and calibrated with intensities by known concentrations (National Institutes of Health [NIH] Image J 1.440) to determine light absorption.

**Insulin receptor labeling**

Freshly isolated PBMC cells from a healthy volunteer were incubated with plasma from control fasting, control, pre-T2DM, and T2DM participants collected at baseline and at different time points after the meal or with spiked proteases (trypsin, elastase, and MMP-2). A PBMC suspension (50 μL) and plasma (150 μL) were incubated for 1 hour at 37°C. The cells were spread as a blood smear, fixed (10% formalin, neutral buffer), and labeled with a primary antibody against the extracellular domain of the insulin receptor (R-alpha-710 rabbit polyclonal antibody, Santa Cruz Biotech) followed by the biotin/avidin and Vector TMB peroxidase enzyme substrate. The cell images were collected using a bright-field microscope (40× and 80× objective) and digitally analyzed (NIH Image J 1.440) to determine light absorption as a measure of surface density for the extracellular domain of the insulin receptor.

**Glucose, inflammatory markers, and soluble adhesion molecules**

Glucose was determined using a standard glucose analyzer by the UCSD Medical Center Clinical Chemistry Laboratory. Circulating levels of C-reactive protein (CRP), serum amyloid A (SAA), soluble intercellular cell adhesion molecule-1 (sICAM-1), and soluble vascular cell adhesion molecule-1 (sVCAM-1) were determined by commercial enzyme-linked immunosorbent assay (ELISA) (MSD, Rockville, MD). Intra- and inter-assay coefficients were less than 7%.

**Statistical analyses**

Measurements are presented as mean ± standard error (SEM). Potential group differences were examined by analysis of variance (ANOVA) and, in response to the meal, repeated-measures ANOVA. Post hoc paired t-tests were used where significant group by time interactions were observed. Statistical significance was set at p ≤ 0.05. Correlations were examined using Pearson coefficients.

**Results**

**Study participants**

The 30 participants in the study included T2DM (n = 10); pre-T2DM (n = 10); controls (n = 7); and controls who fasted during the experiment (fasting controls, n = 3) (Table 2). Weight was significantly higher in T2DM when compared to controls (Table 2, p < 0.05) and to fasting controls (Table 2, p < 0.001). Pre-T2DM weight was significantly higher than fasting controls (Table 2, p < 0.05). Waist circumference and body mass index (BMI) were significantly higher in T2DM and pre-T2DM when compared to fasting controls (Table 2, p < 0.05), but not compared to control participants. By definition, fasting glucose levels were significantly higher in T2DM than in all other participants, and in pre-T2DM as compared to healthy controls (Table 2, p < 0.001). Systolic blood pressure (SBP) was significantly higher in T2DM compared to controls (Table 2, p < 0.05) and fasting controls (Table 2, p < 0.001).

**Baseline circulatory protease activity**

We observed higher baseline MMP-2/-9 and elastase activities in T2DM and in pre-T2DM as compared to controls (Figure 1A–B, p < 0.05) and fasting controls (Figure 1A–B, p < 0.001). Baseline trypsin activity was not statistically significant among the groups (Figure 1C).

**Postprandial increases in circulatory protease activity**

In control participants, MMP-2/-9, elastase, and trypsin increased significantly 15 minutes after the meal (Figure 2A–C, p < 0.05) and returned back to premeal values within a period of approximately 30 to 60 minutes post meal. Fasting controls showed no significant change in any protease activity.
Figure 1. Baseline protease activity. Mean baseline activity for (A) MMP-2/-9, (B) elastase, and (C) trypsin (*p < 0.05, **p < 0.001 versus T2DM and ##p < 0.001 versus pre-T2DM). Calibration curves in 1 x PBS spiked with different concentrations of (D) MMP-2/MMP-9, (E) elastase, and (F) trypsin (Cf = control fasting; p-T2DM = pre-T2DM).

Figure 2. Postprandial protease activity and glucose levels. MMP-2/-9 activity, elastase, trypsin, and glucose in control, and control fasting (A–D) and in pre-T2DM and T2DM participants (E–H) (*p < 0.05 versus time 0 within group, and *p < 0.05 control versus T2DM). Linear correlations of blood glucose levels and (I) MMP-2/-9 activity (p < 0.001), (J) elastase activity (p < 0.001), and (K) trypsin activity (p < 0.001) (p-T2DM = pre-T2DM).
The T2DM group showed an initial 15-minute postmeal increase in elastase activity, which continued to remain elevated to the 60-minute time point (Figure 2F, \( p < 0.01 \)).

Among all study participants, we observed a positive correlation between blood glucose during the meal and MMP-2/-9 activity (Figure 2I, \( p < 0.001 \)), elastase activity (Figure 2J, \( p < 0.001 \)), and trypsin activity (Figure 2K, \( p < 0.001 \)).

**Insulin receptor density reduction in PBMC after incubation with plasma**

PBMCs incubated for 1 hour with baseline plasma from T2DM and pre-T2DM had significantly lower levels of insulin receptor density compared to those incubated with plasma from control participants (Figure 3A, \( p < 0.001 \)). PBMCs incubated with T2DM plasma also showed significantly lower levels of insulin receptor density when compared to cells incubated with pre-T2DM plasma (Figure 3A, \( p < 0.05 \)).

Insulin receptor density on PBMCs incubated with plasma collected at different time points from fasting control participants remained the same throughout the 5-hour observation period (Figure 3B). In nonfasting controls, PBMC insulin receptor density decreased significantly when incubated with plasma collected 45 minutes after the meal (Figure 3C, \( p < 0.01 \)). Insulin receptor density decreased significantly when incubated with pre-T2DM plasma collected at 30 and 60 minutes after the meal (Figure 3D, \( p < 0.01 \)). For T2DM, the insulin receptor density in the PBMCs showed no statistically significant changes before and after the meal (Figure 3E).

There was a significant decrease in insulin receptor density in cells incubated with plasma from all groups compared to cells incubated with \( 1 \times \) PBS (Figure 3A, \( p < 0.001 \)). Incubation of PBMCs with 5 nM of purified trypsin, elastase, and MMP-2 spiked into \( 1 \times \) PBS produced a significant decrease in insulin receptor density on the cell membrane (\( p < 0.05 \)).

**Glucose, Inflammatory markers, and soluble adhesion molecules**

Postprandial glucose levels increased significantly in all participants, except fasting controls (\( p < 0.001 \)) (Figures 2 and 4).

Levels of inflammatory markers and soluble adhesion molecules rose in the circulation of control participants after the meal: CRP values increased significantly at 45 and 60 minutes (Figure 4A, \( p < 0.05 \)) while the SAA values rose significantly at 45, 60, and 120 minutes after the meal (Figure 4B, \( p < 0.05 \)). The sICAM-1 values increased significantly at 45 and 120 minutes (Figure 4C, \( p < 0.05 \)), while the sVCAM-1 values rose at 45, 60, and 120 minutes after the meal (Figure 4, \( p < 0.05 \)). No such changes were observed for T2DM or pre-T2DM participants (Figure 4 F–J).

Among all participants, at baseline we observed negative correlations between blood glucose and plasma CRP levels (Figure 4K, \( p < 0.001 \)), SAA (Figure 4L, \( p < 0.001 \)), sICAM-1 (Figure 4M, \( p < 0.001 \)), and sVCAM-1 (Figure 4N, \( p < 0.001 \)).

**Discussion**

In the animal literature, unchecked proteolytic activity has been shown to cleave the extracellular domain of the insulin receptor, leading to deficient insulin binding and signaling (3, 4). While there have been limited human data examining this issue, elevated levels of “soluble” insulin receptor fragments have been observed in the plasma of T2DM patients (5). The findings from this study support the hypothesis that a potential mechanism leading to insulin resistance and
T2DM may be the presence of digestive proteases from the lumen of the intestine in the peripheral circulation, due to an elevated mucosal permeability in the small intestine. We observed an elevation in elastase and MMP-2/-9 activity in the circulation of pre-T2DM and T2DM as compared to controls. In addition, and consistent with the animal literature (3–5), PBMCs incubated with plasma exhibiting this proteolytic activity showed a decrease in the density of the insulin receptor ectodomain. These findings serve to document that proteases cleave artificial substrates for enzyme activity detection when added to them, and that proteases present in plasma can cause a significant decrease in the membrane density of the insulin receptor ectodomain.

Extracellular cleavage of the insulin receptor was not limited to individuals with overt signs of T2DM. Even in non-symptomatic control participants, we detected a postprandial transient elevation of protease activity in the circulation, which was associated with a reduced insulin receptor density on cells incubated with their plasma collected in a postprandial period. Overall, the evidence links an elevation in plasma protease activity, membrane depletion of insulin receptor, and an increase in blood glucose levels and inflammatory markers in response to consumption of a high-calorie/high-carbohydrate meal. While few studies have directly examined carbohydrate load on proteases, a study of lean non-T2DM men found that, as compared to a high-fat meal, an isoenergetic low-fat (higher carbohydrate) meal led to higher MMP-2 and MMP-9 levels, which were associated with higher glucose levels (13). The authors speculated that hyperglycemia may induce MMP-2 and MMP-9 expression from key cellular sources of MMPs, namely, endothelial cells and macrophages. The study did not assess elastase or trypsin.

Previous efforts to study proteases in T2DM have yielded conflicting results and have focused mainly on plasma MMP-2 and MMP-9 levels. Some reports indicate no correlation between plasma levels of MMP-2 and -9 and T2DM (14), while others show elevated levels of MMP-2 and -9 in T2DM (15–17), or lower levels of MMP-2 and -9 after an oral glucose tolerance test for T2DM (18). These discrepancies may be due to the limitations in previous assay techniques. For example, immunoassays, such as ELISAs, use antibodies that do not distinguish between the active and inactive forms of proteases; moreover, they require ample preprocessing of the samples. The novel electrophoretic assay used in this report bypasses these limitations by (1) measuring protease activity in whole blood and not just in plasma or serum, (2) detecting protease activity derived from nanomolar (as compared to micromolar) levels of proteases, (3) determining only the activity of proteases (and

![Figure 4](image-url). Postprandial levels of CRP, SAA, sICAM-1, and sVCAM-1 in control and control fasting (A–D) and in pre-T2DM and T2DM (F–J) for 5 hours (*p < 0.05 when compared to time 0 for control participants). Linear correlations of blood glucose levels and (k) CRP (p < 0.001), (l) SAA (p < 0.001), (m) sICAM-1 (p < 0.001), and (n) sVCAM-1 (p < 0.001).

Figure 4. Postprandial levels of CRP, SAA, sICAM-1, and sVCAM-1 in control and control fasting (A–D) and in pre-T2DM and T2DM (F–J) for 5 hours (*p < 0.05 when compared to time 0 for control participants). Linear correlations of blood glucose levels and (k) CRP (p < 0.001), (l) SAA (p < 0.001), (m) sICAM-1 (p < 0.001), and (n) sVCAM-1 (p < 0.001).
not only protein levels), and (4) working with a small blood sample volume (3.5 μL) (10–12).

The baseline elevation of MMP-2/-9 and elastase activity in T2DM may be responsible for the reduction of insulin receptor density and their resulting poor blood glucose control. Proteases, such as elastase, MMP-2, and MMP-9, not only are capable of reshaping the extracellular matrix (19) and activating other proteases, but also are capable of cleaving extracellular receptors (20, 21). Here we present evidence that freshly isolated PBMCs incubated with plasma from T2DM or with purified proteases (MMP-2, elastase, and trypsin) exhibit significant depletion of their insulin receptor density. These results are consistent with the evidence for soluble insulin receptors in the circulation of T2DM patients and in vitro cleavage of the insulin receptor by a protease (5, 6). In addition to insulin receptor cleavage, receptor internalization may also occur under these circumstances. The finding that cells incubated with proteases spiked into 1 × PBS also showed depletion of the insulin receptor supports the hypothesis that cleavage of the insulin receptor is a significant process. The exact fate of receptors in these patient groups subject to ectodomain cleavage and the rate of reconstitution into the membrane from endoplasmic pools of newly synthesized receptors remain to be determined in the future.

A major source for the proteolytic activity in the circulation of T2DM may be the intestine, where proteases derived from the pancreas need to be active as a requirement for daily digestion. The evidence that a single high-calorie/high-carbohydrate meal produces an immediate rise in protease activity after the meal in control participants, whereas this did not change significantly in fasting controls, suggests that the increase of pancreatic proteases in the circulation may be linked to digestion. In control participants, the meal also caused an initial increase in soluble adhesion molecules and inflammatory markers and an initial decrease in the insulin receptor density in cells incubated with plasma collected 45 minutes after the meal. In contrast to control participants, T2DM had a significant initial increase after the meal in elastase activity only and no significant depletion in insulin receptor density. The elevation in elastase activity in T2DM could be caused not only by an increase in pancreatic elastase, which can be derived from the intestine and the pancreas itself, but also from neutrophil elastase, which can be derived from the intestine and the pancreas. The increase of pancreatic proteases in the circulation may be causal not only for the diversity of cell dysfunctions that accompany T2DM, but also for the development of insulin resistance. The concept that the digestive system, and in particular pancreatic proteases, may be associated with the development of insulin resistance and T2DM, offers a possible explanation for the hypothesis that the digestive system, and in particular pancreatic proteases, may be associated with the development of insulin resistance and T2DM. In response to a typical high-calorie/high-carbohydrate meal, pancreatic proteases that are normally compartmentalized inside the intestinal lumen may reach the circulation due to an increase in intestinal permeability. Once in the systemic circulation, these pancreatic proteases can degrade biomolecules. Proteases may be responsible for the reduction of the insulin receptor on cells and impairing glucose control. Many membrane receptors have extracellular domains that may be subject to cleavage by proteases, which could be the reason for the diversity of cell dysfunctions that accompany T2DM. Blockage of proteolytic activity in circulation may be a therapeutic target for T2DM, and a prior proof-of-principle of this concept, studies indicate that the broad metalloprotease inhibitor doxycycline improved the overall health of T2DM (7).

Conclusion

Despite the high prevalence of T2DM, the molecular mechanisms for the development of insulin resistance have not yet been fully elucidated. The results of this study provide evidence for the hypothesis that the digestive system, and in particular pancreatic proteases, may be associated with the development of insulin resistance and T2DM. In response to a typical high-calorie/high-carbohydrate meal, pancreatic proteases that are normally compartmentalized inside the intestinal lumen may reach the circulation due to an increase in intestinal permeability. Once in the systemic circulation, these pancreatic proteases can degrade biomolecules. Proteases may be responsible for the reduction of the insulin receptor on cells and impairing glucose control. Many membrane receptors have extracellular domains that may be subject to cleavage by proteases, which could be the reason for the diversity of cell dysfunctions that accompany T2DM. Blockage of proteolytic activity in circulation may be a therapeutic target for T2DM, and a prior proof-of-principle of this concept, studies indicate that the broad metalloprotease inhibitor doxycycline improved the overall health of T2DM (7).

Acknowledgments

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Conflicts of interest
P.R.T. has no disclosures related to this manuscript. She is a consultant for Sanofi/Regeneron,Novo-Nordisk,Boehringer-Ingelheim,Janssen,Pfizer and Amgen. She is a stock holder of Cardero Therapeutics. G.W.S.-S. owns shares in Leading Bioscience Inc., a company developing treatments for shock. P.J.M. has no disclosures related to this manuscript.

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References