Mass spectrometric characterisation of the circulating peptidome following oral glucose ingestion in control and gastrectomised patients

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Rationale: Meal ingestion triggers secretion of a variety of gut and endocrine peptides important in diabetes research which are routinely measured by immunoassays. However, similarities between some peptides (glucagon, oxyntomodulin and glicentin) can cause specificity issues with immunoassays. We used a liquid chromatography/tandem mass spectrometry (LC/MS/MS) methodology to unambiguously monitor multiple gut peptides in human plasma.

Methods: A simple acetonitrile-based protein precipitation step, followed by evaporation and solid-phase extraction, removed high-abundance proteins from samples prior to nano-LC/MS/MS analysis on an Orbitrap Q-Exactive Plus mass spectrometer using a data-dependent methodology. Database searching using PEAKS identified multiple gut-derived peptides, including peptides in the mid-pg/mL range. The relative levels of these and previously characterised peptides were assessed in plasma samples from gastrectomised and control subjects during an oral glucose tolerance test.

Results: Analysis of plasma extracts revealed significantly elevated levels of a number of peptides following glucose ingestion in subjects who had undergone gastrectomy compared with controls. These included GLP-1(7–36), GLP-1(9–36), glicentin, oxyntomodulin, GIP(1–42), GIP(3–42), PYY(1–36), PYY(3–36), neuropeptide Y, and C-peptide. Motilin levels decreased following glucose ingestion. Results showed good correlation with immunoassay-derived concentrations of some peptides in the same samples. The gastrectomy group also had higher, but non-glucose-dependent, circulating levels of peptides from PIGR and DMBT1.

Conclusions: Overall, the approach showed that a fast, generic and reproducible LC/MS/MS methodology requiring only a small volume of plasma was capable of the multiplexed detection of a variety of diabetes-related peptides.
1 | INTRODUCTION

The gut and pancreas produce a variety of peptides involved in the coordination of intestinal functions, nutrient assimilation, glucose homeostasis and appetite.\(^2\) Concentrations of peptides in the plasma are altered by fasting and feeding, and are routinely measured for diagnostic and research purposes using immunoassays employing high affinity antibodies. As the gut secretes more than 20 peptides,\(^2\) research into intestinal physiology is currently hindered by the costs of measuring multiple peptides in parallel and the availability of validated assays. Analysis of individual peptides, such as glucagon-like peptide-1 (GLP-1) and Peptide YY (PYY), has revealed that they play substantial roles in the gut-brain and gut-pancreatic axes, and supported the development of GLP-1-based therapies for the treatment of type 2 diabetes and obesity. There is great interest in developing new peptide-based therapies for metabolic and intestinal diseases, but gaining a deeper understanding of the physiology of peptide secretion in patients is a critical step in any such drug discovery pathway.

In view of the success of surgical bariatric procedures for the treatment of obesity and type 2 diabetes, there is great interest in understanding the underlying physiological mechanisms. One of the commonest and most effective bariatric procedures is Roux-en-Y gastric bypass (RYGB) surgery, which promotes weight loss (thus increasing insulin sensitivity) and enhances insulin secretion, resulting in rapid resolution of type 2 diabetes with at least partial remission in ~60% of RYGB-patients 1 year post-surgery.\(^3,4\) The mechanisms underlying these physiological changes are not fully resolved, but a considerable body of evidence points to important roles for peptides such as GLP-I and PYY,\(^5\) which exhibit profound post-prandial elevations after bariatric surgery. Post-surgical changes in other peptides have been less studied, with some reports of raised and others of unaltered post-prandial glucose-dependent insulinotropic polypeptide (GIP) excursions and more sporadic reports on the importance of other peptides which are elevated post-surgically such as neurotensin (Nts) for surgery outcomes.\(^6,7\)

The potential for liquid chromatography/mass spectrometry (LC/MS)-based methods to quantify peptides has been demonstrated previously, for example for proglucagon-derived peptides either following immuno-affinity based enrichment\(^8\) or after depletion of abundant plasma proteins through solvent precipitation followed by solid-phase extraction (SPE).\(^9\) Whilst these approaches have demonstrated good sensitivity and good correlation with existing immunoassays, they used targeted approaches with triple quadrupole based detection systems, requiring prior knowledge of the analyte under investigation. Alternatively, the plasma peptidome has been investigated after enzymatic protein digestion in an untargeted fashion, but the results are at least in part dominated by products from abundant plasma proteins, only partially resolved by specific pre-depletion,\(^10\) and interpretation might be complicated, when different peptides can be generated from the same prohormone as is the case for proglucagon-derived peptides. In our view a better approach for analysing peptides by mass spectrometry in an untargeted fashion is to avoid enzymatic digestion.\(^11\) We previously reported such an approach for plasma\(^12\) from patients with endocrine tumours and for sorted cells\(^13\) and tissue extracts from human brain\(^14\) and intestines.\(^15\)

In this study, we compared changes in the plasma peptidome during an oral glucose tolerance test (OGTT) in subjects after gastrectomy surgery (a procedure resulting in an anatomy very similar to RYGB) and control subjects, using an untargeted LC/MS/MS approach.

2 | METHODS AND MATERIALS

2.1 | Patients and plasma samples

Experiments were performed on plasma samples from a published study, which have previously been analysed by immunoassay for a range of gut and pancreatic peptides.\(^9\) The study was approved by the National Health Service Research Ethics Committee and conducted in accordance with the ethical standards of the Helsinki Declaration of 1975. In brief, following an overnight fast, all participants drank 50 g of glucose in 200 mL water within a 5-min period. Blood samples were collected into EDTA tubes (without any added protease inhibitors) immediately prior to glucose ingestion (time 0), and at 15, 30, 45, 60, 90, 120, 150, and 180 min post-ingestion. Samples were immediately placed on ice and centrifuged for 10 min at 3500 g at 4°C. Plasma aliquots (400 μL) were snap frozen on dry ice and stored at -80°C within 30 min of phlebotomy. Samples from one gastrectomy and one control subject were selected for the pilot study across all timepoints. Samples from 6 gastrectomy and 6 control subjects were selected for the main study analysis at 3 timepoints (0, 30 and 90 min).

2.2 | Chemicals

Acetonitrile (ACN), methanol, acetic acid and formic acid (FA) were purchased from Fisher Scientific (Pittsburgh, PA, USA). Dithiothreitol (DTT), iodoacetamide and bovine insulin were purchased from Sigma Aldrich (St Louis, MO, USA).

2.3 | Extraction of plasma samples

Plasma samples were thawed and extracted on ice to reduce peptidase-based degradation. Plasma (50 μL) was aliquoted in duplicate into a 2-mL 96-well plate and 300 μL of either 80% ACN in water or 80% ACN in water with 0.1% FA, both fortified with bovine insulin at 1 ng/mL, were added to each replicate to precipitate high molecular weight proteins; the addition of bovine insulin was only introduced during the main study and omitted in the pilot study. The samples were spun at 3900 g and the supernatants from each timepoint were combined and transferred to a Lo-bind Eppendorf plate and evaporated under oxygen-free nitrogen (OFN) at 40°C. The dried extracts were reconstituted into 200 μL of 0.1% FA and
vortexed before transferring into an Oasis HLB PRIME microelution 96-well plate (Waters, Milford, MA, USA) and washed with 200 \( \mu \)L of 0.1% FA and 200 \( \mu \)L of 5% methanol in 1% acetic acid in water (v/v/v). Peptides were eluted with 2 \( \times \) 30 \( \mu \)L aliquots of 60% methanol in water with 10% acetic acid (v/v/v) into a Lo-bind Eppendorf plate. The eluants were dried under OFN and reconstituted with 150 \( \mu \)L of 0.1% FA, of which 40 \( \mu \)L were injected onto the nano-LC/MS system. During the pilot study an additional reduction alkylation was performed after the SPE, which was, however, not found to be necessary for sample analysis and reliable detection of insulin. In brief in the pilot study dried SPE eluates were dissolved into 75 \( \mu \)L of 50mM ammonium bicarbonate with 10mM DTT and reduced at 60°C for 1 h. Peptides were alkylated by the addition of 15 \( \mu \)L of 100 mM iodoacetamide in 50 mM ammonium bicarbonate in the dark for 30 min. Then 20 \( \mu \)L of 1% FA was added and 40 \( \mu \)L of sample injected onto the nano-LC/MS system.

### 2.4 | Nano-LC/MS/MS analysis

Peptide extracts were analysed using an Ultimate 3000 nano-LC system coupled to a Q Exactive Plus Orbitrap mass spectrometer (both from Thermo Fisher Scientific, San Jose, CA, USA). Extracts were loaded onto a 0.3 \( \times \) 5 mm peptide trap column (Thermo Fisher Scientific) at a flow rate of 30 \( \mu \)L/min and washed for 15 min before switching in line with a 0.075 \( \times \) 250 mm nano Easy column (Thermo Fisher Scientific) with a flow rate of 300 nL/min. The nano and trap column temperatures were both set at 45°C. The mobile phases were A: 0.1% FA in water (v/v) and B: 0.1% FA (v/v) in 80:20 ACN/water. Initial conditions were 2.5% B and held for 15 min. A ramp to 50% B was performed over 90 min, and the column was then washed with 90% B for 20 min before returning to the starting conditions for a further 20 min, totalling an entire run time of 130 min. Positive nano electrospray ionisation (ESI) analysis was performed using a spray voltage of 1.8 kV; the tune settings for the mass spectrometer used an S-lens setting of 70 V to target peptides of higher m/z values. A full-scan range of m/z 400–1600 was performed at a resolution of 75,000 before the top 10 ions of each spectrum were selected for MS/MS analysis. Existing ions selected for fragmentation were added to an exclusion list for 30 s.

### 2.5 | Database searching

The LC/MS data were searched using the PEAKS 8.5 software (BSI, Waterloo, Canada) against the human Uniprot database (downloaded 27-10-2017) using a non-specific digest setting. When extracts had been reduced and alkylated, a fixed carboxamidomethylation modification was applied to cysteine residues. Variable modifications included N-terminal acetylation, N-terminal pyroglutamate, C-terminal amidation and methionine oxidation. A false discovery rate (FDR) setting of 1% was used against a decoy database, and precursor and product ion tolerances were set as 10 ppm and 0.05 m/z units, respectively. The main study cohort data were put through the PEAKS software extension to identify potential biomarker peptides in the dataset, manually adding peak areas of bovine insulin as a normalising factor.

### 2.6 | Manual LC/MS data searching and peptide quantitation

The LC/MS/MS- and data-dependent acquisition (DDA)-based analyses combined with database searching failed to identify some of the expected gut peptides in all samples. However, in order to obtain a database match, peptides must both be selected for MS/MS fragmentation, and generate a suitably high-quality product ion spectrum for the PEAKS software to match against the database. Some gut peptides are present at concentrations in the low-pg/mL range; therefore, in the presence of other higher concentration plasma peptides, may not be selected for fragmentation. Furthermore, if they were selected for fragmentation, their product ion spectra might not contain sufficient data for a strong match. Therefore, in order to identify the presence of some of the peptides and to quantify other identified peptides, the theoretical m/z values for all peptides were used to interrogate the raw data using the Quan Browser software program (Thermo Fisher Scientific) (Table 1). The peak for each peptide was integrated at the expected retention time (RT), with a minimum signal-to-noise ratio of 3 required, default 9 smoothing added and using the genesis integration algorithm (example integration shown in Figure S1, supporting information). The data from specific peptides in the large cohort were normalised by expressing their peak areas as a ratio of the internal standard bovine insulin.

### 2.7 | Immunoassays

Immunoassays on these samples have been described previously.\(^9\) In brief, total GLP-1, total GIP and total PYY were measured using Meso Scale Discovery (Meso Scale Diagnostics, Rockville, MD, USA) assays according to the manufacturer’s instructions. Insulin concentrations were measured using the Liaison XL insulin system (DiaSorin, Milan, Italy). A total plasma volume of 500 \( \mu \)L was required to generate data for PYY, GIP, GLP-I and insulin.

### 3 | RESULTS

#### 3.1 | Full OGTT sample comparison in two subjects

A pilot study was performed to examine the plasma peptidome at multiple timepoints following a 50 g OGTT in one gastrectomy subject and one healthy control subject, generating data about which peptides were detectable, which appeared different following gastrectomy, and the best timepoints for further testing in a main
TABLE 1 List of peptides selected for manual data searching for quantitation in OGTT samples, along with the m/z values associated with the monoisotopic and multiple 13C isotope peaks

| Peptide name | Charge (z) | m/z values | RT (min) |
|--------------|------------|------------|---------|
| GRPP         | 4          | 846.63, 846.88, 847.13, 847.38 | 43      |
| OXN          | 7          | 636.46, 636.60, 636.75, 636.89 | 58      |
| Glicentin    | 7          | 1157.84, 1157.98, 1158.13, 1158.27, 1158.41, 1158.56 | 56      |
| GLP-I 7–36 amide | 4 | 824.91, 825.18, 825.43 | 72      |
| GLP-I 9–36 amide | 4 | 772.90, 773.15, 773.40, 773.65, 773.90 | 77      |
| PYY 1–36 amide | 7 | 616.60, 616.75, 616.89, 617.04 | 60      |
| PYY 3–36 amide | 7 | 579.30, 579.45, 579.59 | 58      |
| Insulin (intact) | 5 | 1162.14, 1162.34, 1162.54, 1162.74, 1162.94 | 66      |
| Insulin A-chain | 2 | 1306.05, 1306.55, 1307.05, 1307.55 | 66      |
| Insulin B-chain | 5 | 709.35, 709.55, 709.75, 709.95, 710.15 | 60      |
| C-peptide    | 3          | 1007.17, 1007.51, 1007.84, 1008.18 | 75      |
| Bovine insulin (intact) | 5 | 1147.13, 1147.33, 1147.53, 1147.73, 1147.93, 1148.13 | 65      |
| GIP propeptide | 7 | 455.24, 455.39, 455.53, 455.67 | 31      |
| GIP 1–42     | 6          | 831.25, 831.41, 831.58, 831.75, 831.91 | 62      |
| GIP 3–42     | 7          | 792.23, 792.40, 792.56, 792.73, 792.90 | 60      |
| Neurotensin  | 3          | 558.31, 558.64, 558.98 | 43      |
| Motilin      | 5          | 540.48, 540.68, 540.88, 541.08 | 48      |
| Adrenomedullin (45–92) | 8 | 640.08, 640.20, 640.45, 640.58 | 48      |
| Augurin (42–68) | 6 | 498.11, 498.28, 498.45, 498.61 | 42      |

Note. Extracted ions had a tolerance of ±0.01 m/z units. Peptide m/z values were taken either from the PEAKS results or from a previous peptidomics study. See supporting information for extracted ion chromatograms, experimentally acquired m/z values and theoretical m/z values for chosen charge states.

A number of circulating peptides were detected, including gut and pancreatic peptides, fibrinogen fragments, hepcidin, thymosin, bradykinin and angiotensin (Tables S1 and S2, supporting information). A number of these peptides are known to be “sticky” peptides – in particular insulin and GLP-I; however, the high amount of peptides that is retained by the relatively crude extraction, and the use of Lo-bind consumables, minimises the loss of these peptides to non-specific binding to consumables. Many of the identified gut-derived peptides afterwards showed clear time-dependent changes on OGTT, as shown in Figure 1. Previously published enzyme-linked immunosorbent assay (ELISA) results from these two subjects are shown in Figure S2 (supporting information).

Extracts from the gastrectomy subject returned more gut peptide identifications than the control subject, in particular peptides from the proglucagon gene, which included OXN, active GLP-1 7–36 amide and GLP-1 9–36 amide, the inactive cleavage product of dipeptidyl peptidase-4 (DPP4) digestion: their levels over the OGTT can be seen in Figure 1A–C. Another intestinally proglucagon-derived peptide, glicentin, comprising the N-terminal part of proglucagon, including both the GRPP and the oxyntomodulin sequence, which has 68 amino acids – too large to be identified by PEAKS, which has a cut-off of 65 amino acids. Manual examination of the raw data for the expected m/z value of its [M+7H]+ charge state showed that glicentin was present in the gastrectomy subject, but not the control subject (Figure 1D). The only other proglucagon-derived peptide that we were able to detect was GRPP, which was detectable in both the post-gastrectomy subject and the control subject, although at lower levels in the latter (Figure 1E).

The analysis also identified peptides from GIP and motilin, a peptide involved in gut motility, both of which are expressed at highest levels in the proximal small intestine (duodenum/jejunum). Motilin was readily detectable in both subjects and levels dropped after glucose ingestion in both cases (Figure 1F). With the exception of active GIP 1–42 (Figure 1G), which we could not detect in the control subject, GIP-derived peptides (GIP-prepeptide, representing the first cleaved peptide, N-terminal to the active hormone and GIP 3–42, an inactive product of GIP 1–42 digestion by DPP4) (Figure 1H,I) were readily detectable in both subjects, and they rose after the OGTT, reaching higher levels in the gastrectomy samples. Neurotensin, a peptide thought to arise mostly from the distal small intestine, rose after the OGTT, as shown in Figure 1J. Previously published immunoassay-derived insulin concentrations in the same samples published previously were corroborated in the standard Uniprot database, whereas the first eighteen N-terminal amino acids of PYY 3–36 amide and DPP4-cleaved PYY 3–36 amide (Figure 1K,L) were detected in the gastrectomy, but not the control subject.

The LC/MS analysis readily detected insulin A, B and C peptides (Figure 1M–O), the time-profiles of which mirrored the immunoassay-derived insulin concentrations in the same samples. The plasma concentrations of insulin and its C-peptide are about 2 orders of magnitude higher than those of proglucagon-derived peptides, and are well within the sensitivity of the LC/MS system, as we have previously demonstrated. A correlation of the insulin ELISA concentration against the B-chain peptide peak area across these two
participants gave an $R^2$ value of 0.9849, showing very comparable data between the two analytical approaches, despite the LC/MS data not being transformed or normalised in any way.

### 3.2 Peptidomics analysis of 6 gastrectomy and 6 control subjects

We next analysed plasma samples from 6 gastrectomy subjects and 6 control subjects taken at 0, 30 and 90 min after the 50 g OGTT, using the same analytical protocol but omitting the reduction/alkylation step (leaving insulin and other disulphide-bonded peptides intact). The total time taken to acquire the LC/MS/MS data was approximately 3.5 days of instrument time. The PEAKS output identified similar peptides to those found in the pilot study (Table S3, supporting information), including a number of distinct products from the PYY, proglucagon and GIP genes, together with motilin and C-peptide. Peak areas of all previously described peptides were subsequently generated by interrogation of the raw data using the Quan Browser software, along with peak areas of intact insulin and the internal standard bovine insulin. The addition of bovine insulin as an internal standard enabled normalisation of the peak area for each peptide to that of bovine insulin in the same sample, generating semi-quantitative peak area ratios for each analyte. The peak areas of the detected bovine insulin internal standard over the 36 nano-LC/MS analyses were consistent, with a coefficient of variance (CV) of 11.9%, indicating that the extraction process and LC/MS analysis were robust and reproducible.

The peak area ratios of the selected peptides at 0, 30 and 90 min after the OGTT are depicted in Figure 2. Confirming the pilot data and previously generated results from immunoassays,9 the plasma levels of insulin, PYY, proglucagon-derived peptides and neurotensin were elevated after the OGTT in gastrectomy subjects compared with control subjects, whereas GIP-derived peptides were largely similar between the groups. As we have previously analysed several gut hormones in these samples by immunoassays, using commercial kits against total GLP-1, total GIP, total PYY and insulin, we examined the performance of the LC/MS approach, by comparing the LC/MS results against the corresponding immunoassay values (Figure 3). Across the 12 subjects, there was excellent correlation between insulin levels measured with the two assay methods ($R^2 = 0.9837$). The total GLP-1 determined by Immunoassay correlated reasonably with the peak area ratio for GLP-1 9–36 amide (the major circulating form of GLP-1 detected by LC/MS; $R^2 = 0.73$), and slightly better for GRPP ($R^2 = 0.84$), which is co-released from intestinal L-cells but can also arise from glucagon-producing pancreatic alpha-cells. Individual

![Figure 1](image-url)  
Plasma peptide peak area time courses for one gastrectomy and one control participant in the pilot study. Peptide peak areas of selected peptides as measured by LC/MS/MS in two subjects over a 50 g OGTT.
GIP-derived peptide LC/MS data correlated well with the total GIP immunoassay results. GIP prepeptide, comprising the cleaved peptide cleaved from the prohormone on the N-terminal side of GIP, was more readily detectable by LC/MS than GIP 1–42 or 3–42 but its levels correlated less well with the immunoassay than GIP 3–42. The total PYY measured by immunoassay correlated well with peak area ratios for PYY 3–36 amide ($R^2 = 0.93$), whereas the correlation against PYY 1–36 amide alone was weaker, at $R^2 = 0.78$.

### 3.3 PEAKSQ analysis from 6 gastrectomy and 6 control subjects

Analysis using the PEAKSQ module, manually adding the bovine insulin peak area as a normalising factor, enabled interrogation of the entire dataset for plasma peptidomic differences between control and gastrectomy subjects. Across all timepoints, a number of likely false positives were detected, including peptides from fibrinogen and globins, and closer interrogation of the data revealed that the PEAKSQ software was selecting up to three peptides for quantitation out of the many identified from the same parent protein, whereas other peptides from the same parent exhibited either no differences or changes in the opposite direction. In the dataset collected 30 min after glucose ingestion, PEAKSQ correctly identified that insulin, GIP and proglucagon products were higher in gastrectomy than control participants, supporting the data presented in Figures 1 and 2, but did not identify differences in any other known and identified bioactive peptides. Across all samples, PEAKSQ identified raised levels of peptide fragments from two larger proteins, PIGR (polymeric immunoglobulin receptor) and DMBT1 (Deleted in malignant brain...
tumours 1) (Figure 4), which are both known to be enriched in the gastrointestinal tract. PIGR has a large extracellular domain involved in binding IgA and IgM for translocation across epithelia, a single transmembrane domain and a short intracellular C-terminus. Peptides identified from PIGR included the sequences 598–639, 598–648, 604–639, 605–648, 607–648, 607–648, 610–648 and 604–648, which mainly comprise the C-terminus of the extracellular domain (19–638) and part of the transmembrane domain (639–661). Across all time points, all peptides derived from PIGR had higher peak areas in gastrectomy than control subjects (e.g. $p = 0.009$ for fragment 598–648 by two-way analysis of variance (ANOVA)). One peptide fragment from DMBT1 (amino acids 2385–2413 from the C-terminus) was higher in plasma from gastrectomy patients than controls ($p = 0.017$ by two-way ANOVA). Figure 4 also shows the peak areas of two unrelated peptides that were detected in the plasma for comparison. For these two peptides, augurin 42–68 (a C-terminal fragment of a propeptide containing residues 32–68) and adrenomedullin 45–92, which is an intact propeptide sequence, no significant differences between the control and gastrectomised subjects were observed.

4 | DISCUSSION

We have demonstrated that a simple, high-throughput and inexpensive plasma peptide extraction methodology can be combined with nano-LC/MS/MS analysis to study gross changes in the plasma peptidome following gastrectomy surgery. Insulin and C-peptide were readily detectable by LC/MS/MS in all participants and correlated well with immunoassay-derived concentrations across the full range of the fasting and stimulated levels found in the subjects tested. Gut peptides circulate at lower concentrations than insulin, and were more difficult to detect by LC/MS/MS, although in the gastrectomy
samples we readily identified a number of gut hormones believed to contribute to metabolic improvements after bariatric surgery (GLP-1, OXN, GIP, PYY and neurotensin). We previously reported substantially elevated plasma levels during an OGTT in this group for GLP-1 and PYY measured by immunoassays and the multiplex LC/MS/MS results reported here correlate relatively well with the historical data. Post-gastrectomy anatomy is strikingly similar to post-RYGB anatomy (with the additional total removal of the stomach remnant in the former), but in the predominantly lean post-gastrectomy cohort the excessive insulin secretion often results in post-prandial hypoglycaemia, which can be alleviated by GLP1R-blockage, with similar observations having been reported in RYGB-patients after weight loss.

Most gut peptides, however, were below the detection limit in control subjects, and only identifiable in a few control subject samples after interrogation of the raw data. For example, the active form of GLP-1 (GLP-1 7–36 amide) was not detected in plasma from the control subject as normal concentrations are less than 10 pmol/L, below the detection limit of our generic nano-LC/MS approach. However, where immunoassay data were available, the LC/MS peak area ratios for post-OGTT gut hormone levels in the gastrectomy group correlated well with immunoassay-derived concentrations. This indicates that the developed method is inherently quantitative, and is therefore applicable for the further development of fully quantitative studies using peptide standards and stable isotope labelled internal standards. Arguably, our results suggest that nano-LC/MS approaches are well suited for monitoring multiple peptides in parallel in small plasma samples. The sensitivity achieved was in the low tens of picograms per millilitre of plasma, which could potentially be improved upon by using more targeted selected reaction monitoring (SRM)-based analysis rather than the full-scan function used in the data-dependent acquisition technique on the Orbitrap. Indeed, we have reported post-OGTT glucagon excursions quantified by LC/MS/MS in these patients and the controls using a targeted approach. However, in its current guise, the approach could be used for monitoring gut peptide release in post-gastric bypass patients. Other groups have studied the plasma peptidome of patients post-RYGB by LC/MS and detected raised oxyntomodulin (OXN) levels, but their approach involved substantial sample work-up including enzymatic digestion of target peptides which complicates interpretation of the source of the resulting peptides as OXN also contains sequences present in both glucagon and glicentin (two other peptides produced from the proglucagon gene, which are easily distinguished by our method). In this context, although the presence of raised plasma glucagon after gastric bypass has been reported, our analysis did not identify glucagon in the plasma despite elevated glicentin and OXN (Figure 1) and we previously have shown similar relatively small glucagon-excursions in the control and post-gastrectomy patients.

The peptidomics approach identified some non-glucose-dependent peptides that appeared to differentiate the gastrectomy from the control subjects. These peptides were derived from proteins that have been attributed to host responses to infection in the gut (PIGR and DMBT1) and were higher in concentration in the gastrectomy group.

FIGURE 4 Peak area ratios of plasma peptides that were glucose independent. Peak area ratios for the peptides indicated, measured by LC/MS/MS. Samples were taken at t = 0, 30 and 90 min following a 50 g OGTT in 6 healthy control and 6 gastrectomised individuals. PIGR 598–648 is illustrative of a range of PIGR peptides, and together with DMBT (2385–2413) was higher in gastrectomised than control individuals. Augurin (42–68) and ADM (45–92) are shown as examples of peptides that did not differ between groups.
PIGR binds polymeric immunoglobulins on the basolateral epithelial surface, transports them to the apical membrane in vesicular structures, and is then cleaved to release its immunoglobulin cargo into the gut lumen. Our detection of PIGR-derived peptides in the plasma probably reflects either cleavage occurring at the basolateral membrane, or reabsorption of cleaved PIGR peptides from the lumen. Our finding that several circulating PIGR-derived peptides contained part of the transmembrane domain suggests that cleavage may involve gamma-secretase. Release of the PIGR extracellular domain or PIGR-derived peptides into the circulation has not been described previously, and further studies will be required to determine whether PIGR-derived plasma peptides have biological activity. DMBT1 is a large secreted protein found in intestine and saliva and is also known as salivary agglutinin, surfactant pulmonary-associated D-binding protein, and hensin. DMBT1 is reported to play a role in intestinal microbial defence, and is upregulated in individuals with inflammatory bowel disease and other diseases of the intestinal tract. As both PIGR and DMBT1 have been implicated in host defence, we speculate that their detection at higher levels post-gastrectomy may reflect an increased load of intestinal microbiota, as gastrectomy patients frequently suffer from small intestinal bacterial overgrowth and PIGR expression is known to be activated by microbial products such as lipopolysaccharides (LPS).

5 CONCLUSIONS

The described peptidomics approach employs a generic protein precipitation approach (followed by SPE) for enriching for circulating peptides while removing high-abundance and high molecular weight proteins such as albumin and immunoglobulins. The approach requires only small volumes of plasma (100μL) and is a fast, generic, reproducible and inexpensive method for studying an under-researched area, the plasma peptidome. Whilst the method was used in a semi-quantitative fashion, it generated data that showed a good correlation with existing immunologically derived plasma peptide concentrations. The peptidomics analysis identified similar increases in known bioactive peptides after gastrectomy; however, the sensitivity of the approach was not sufficient to detect peptides circulating in the low-ng/mL concentrations in the control subjects. Whilst no new glucose-dependent peptide changes were detected, peptides from DMBT and PIGR appeared to be raised after gastrectomy, and further studies will be required to investigate whether they could be used as biomarkers for intestinal infection or inflammation. These data have shown that, with a single extraction, LC/MS-based peptidomics analyses can identify and monitor large numbers of circulating peptides with a wide variety of masses and chemical properties. We have shown good correlation against existing ELISA systems when the LC/MS/MS approach was able to detect selected peptides, suggesting that LC/MS can be seen at the very least as complementary to ELISAs. Whilst the LC/MS approach was not as sensitive as the ELISA it did use a fifth of the volume required in the four immunoassay approaches, with a comparable price per sample. Further quantitative applications of this approach would require a shift from an untargeted peptidomics system to targeted triple quadrupole analyses to unlock the full potential of LC/MS/MS for plasma peptide quantitation.

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD016690 and 10.6019/PXD016690.

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**SUPPORTING INFORMATION**

Additional supporting information may be found online in the Supporting Information section at the end of this article.

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