Diets high in resistant starch increase plasma levels of trimethylamine-N-oxide, a gut microbiome metabolite associated with CVD risk

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Abstract
Production of trimethylamine-N-oxide (TMAO), a biomarker of CVD risk, is dependent on intestinal microbiota, but little is known of dietary conditions promoting changes in gut microbial communities. Resistant starches (RS) alter the human microbiota. We sought to determine whether diets varying in RS and carbohydrate (CHO) content affect plasma TMAO levels. We also assessed postprandial glucose and insulin responses and plasma lipid changes to diets high and low in RS. In a cross-over trial, fifty-two men and women consumed a 2-week baseline diet (41 percentage of energy (%E) CHO, 40% fat, 19% protein), followed by 2-week high- and low-RS diets separated by 2-week washouts. RS diets were assigned at random within the context of higher (51–53%E) v. lower CHO (39–40%E) intake. Measurements were obtained in the fasting state and, for glucose and insulin, during a meal test matching the composition of the assigned diet. With lower CHO intake, plasma TMAO, carnitine, betaine and γ-butyrobetaine concentrations were higher after the high-v. low-RS diet (P < 0.01 each). These metabolites were not differentially affected by high v. low RS when CHO intake was high. Although the high-RS diet reduced postprandial insulin and glucose responses when CHO intake was low (P < 0.01 each), RS did not affect fasting lipids, lipoproteins, glucose or insulin irrespective of dietary CHO content. In conclusion, a lower-CHO diet high in RS was associated with higher plasma TMAO levels. These findings, together with the absence of change in fasting lipids, suggest that short-term high-RS diets do not improve markers of cardiometabolic health.

Key words: Trimethylamine-N-oxide: Resistant starch: Carbohydrate: Lipids: Insulin: Glucose: CVD

There is growing awareness that gut microbiotas have a substantial influence on human health and disease. Both animal and human studies have shown that gut microbial metabolism of dietary trimethylamines produces trimethylamine-N-oxide (TMAO)1–3, a metabolite associated with risk of CVD, independent of traditional CVD risk factors1,2,4. Studies from this group have also established that elevated plasma levels of carnitine, choline and betaine are associated with CVD risk because of their role in formation of TMAO1,2,5). More recently, another precursor of TMAO, γ-butyrobetaine, was shown to be associated with the development of atherosclerosis in a susceptible mouse model5). Together, these studies have fuelled interest in the potential for dietary modification to alter TMAO production6–8). Given the obligatory role of gut microbes in the conversion of trimethylamine-containing nutrients to TMAO1,2), it is of interest to determine whether dietary components associated with changes in gut microbial communities affect plasma concentrations of TMAO.

Dietary starches differ in their rates of digestion and absorption. Compared with most starches, resistant starches (RS) undergo limited digestion by α-amylases in the small intestine, but may be converted by amyloytic bacterial species in the colon to a range of metabolites including SCFA9). Differing forms of RS have been shown to rapidly alter the

Abbreviations: HOMA-IR, homoeostatic model assessment of insulin resistance; RS, resistant starches; TMAO, trimethylamine-N-oxide.

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composition of the human gut microbiota\(^{(10–12)}\). In view of this, and because production of TMAO is dependent on gut microbes\(^{(13)}\), we undertook a study to determine whether diets that differed in RS content affected plasma concentrations of TMAO, and to test whether any such effect was modified by total dietary CHO. In addition, we sought to confirm the attenuation in postprandial glucose and insulin responses by high RS intake\(^{(14–18)}\), and to examine changes in plasma lipids and lipoproteins whose associations with RS intake are less well established\(^{(15,16)}\).

**Methods**

**Study participants**

In all, fifty-two individuals (thirty-two women, twenty men) were recruited from participants of our previous dietary intervention studies and respondents to advertisements on the Internet. The sample included men (≥20 years) and post-menopausal women (defined as ≥43 years of age and amenorrhoea for ≥3 years or amenorrhoea for ≥1 but <3 years and plasma follicle-stimulating hormone concentrations elevated to the postmenopausal range) with BMI ≥20 and ≤35 kg/m\(^2\). All of them were non-smokers, had no history of CVD or other chronic diseases, and were not taking lipid- or glucose-lowering medications, blood thinning agents or hormones. Moreover, to permit testing of the insulin-lowering effects of RS, we also excluded individuals with relatively high insulin sensitivity as assessed by the homeostatic model assessment of insulin resistance (HOMA-IR) <50th percentile\(^{(19)}\) (based on HOMA-IR distributions of a comparable group of men and women screened for a previous study\(^{(20)}\); median: 2.1). Additional selection criteria included fasting glucose <7 mmol/l, total and LDL-cholesterol ≤90th percentile for age and sex, fasting TAG <5-65 mmol/l, blood pressure (BP) <150/90 mmHg, stable weight (<3% change) for at least 3 months before study onset and willingness to refrain from alcohol and dietary supplements during the study period.

The study protocol was approved by the Institutional Review Board of Children’s Hospital and Research Center of Oakland. All participants gave their written informed consent to take part in the study. Participants were provided with a list of clinical staff to contact should they need to discuss study procedures or report adverse events. This trial was registered at clinicaltrials.gov as NCT01027325.

**Study design and diets**

The present study was a controlled, randomised, cross-over dietary intervention conducted in an outpatient setting with weekly visits to our clinic located in Berkeley, CA. The logistical constraints of creating twenty-five different diets (five experimental diets, at five energy levels) required that the first twenty-six subjects enrolled into the study be assigned to the higher-CHO study arm and the second twenty-six to the lower-CHO study arm. Within each diet, a uniform random number generator was used to determine block sizes (two, four, six or eight subjects) and the sequence of the high- v. low-RS diets within each block, which were supplied to the project coordinator in sealed, numbered envelopes. The project statistician was the only person aware of the treatment assignment before subject enrolment.

The study design consisted of two arms: higher and lower total CHO intake with comparison of high RS v. low RS intake in random order in each arm (Fig. 1). All study participants (n=52) first consumed the lower-CHO baseline diet for 2 weeks, after which they followed the higher-CHO diet (the first twenty-six subjects recruited) or the lower-CHO diet (the second twenty-six subjects recruited). The high- and low-RS diets were each consumed for 2 weeks, separated by a 2-week washout, during which they were instructed to consume their habitual diet for 7 d, followed by repeating the baseline diet for an additional 7 d (Fig. 1). Clinic staff met with participants weekly to review and reinforce dietary patterns and ensure that body weight remained within ±3% of initial weight. Investigators, laboratory staff and study participants were blinded to the dietary assignment, whereas staff responsible for provision of food and monitoring of dietary compliance (nutritionist, study coordinator and nurse) was not.

The lower-CHO baseline diet was designed to match the macronutrient distribution of the lower-CHO study arm, but to be low in foods containing naturally occurring RS in order to facilitate limitation of RS intake. High- and low-RS contents of the diets (Table 1) were achieved by incorporating, respectively, a high-amylose maize starch (41·5 g RS/100 g starch, Hi-Maize 260; Ingredion Inc.) or a conventional, high-amylopectin maize starch (2·3 g RS/100 g starch, Melojel; Ingredion Inc.) into recipes. The resulting high-RS diets provided 19 g RS/4184 kJ (1000 kcal) for the lower-CHO study arm and 26 g RS/4184 kJ (1000 kcal) for the higher-CHO study arm, for an average daily intake of 48–66 g RS. These amounts are within ranges previously shown to affect human faecal microbiota composition\(^{(10–12)}\) as well as glycaemic control\(^{(22)}\).

Although rapidly digested maize starch was consumed mostly cooked, in baked goods and entrees, approximately 50% of the high-RS maize starch was consumed raw, mixed into beverages, fruit purees and soups (online Supplementary Table S1). Hi-Maize 260 maize starch was chosen on the basis of its high RS content and because such starches resist losing their granular structure under the range of processing conditions typically
Estimated values, based on published carnitine content of commonly consumed food products. Values shown are for 10 460 kJ (2500 kcal) menus.

Melojel maize starch was chosen on the basis of cooking make high-amylose starch resistant to enzymatic degradation. Melojel maize starch was chosen on the basis of cooking make high-amylose starch resistant to enzymatic degradation. Maintenance of the daily allotted energy and starch (e.g. 16 and 22 g of RS/meal for the high-RS diet for a subject consuming 10 460 kJ/d (2500 kcal/d); and 0-8 and 1-1 g RS/meal for the low-RS diet for a subject consuming 10 460 kJ/d (2500 kcal/d)).

Table 1. Composition of baseline and experimental diets†

<table>
<thead>
<tr>
<th></th>
<th>Baseline/ washout diet</th>
<th>Higher-CHO arm</th>
<th>Lower-CHO arm</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>High RS</td>
<td>Low RS</td>
<td>High RS</td>
</tr>
<tr>
<td>CHO (%E)</td>
<td>41</td>
<td>51</td>
<td>53</td>
</tr>
<tr>
<td>RS (%E)</td>
<td>10</td>
<td>0-6</td>
<td>8</td>
</tr>
<tr>
<td>RS (g)</td>
<td>66</td>
<td>4</td>
<td>48</td>
</tr>
<tr>
<td>Protein (%E)</td>
<td>19</td>
<td>22</td>
<td>22</td>
</tr>
<tr>
<td>Fat (%E)</td>
<td>40</td>
<td>27</td>
<td>26</td>
</tr>
<tr>
<td>SFA</td>
<td>9</td>
<td>6</td>
<td>7</td>
</tr>
<tr>
<td>MUFAs</td>
<td>20</td>
<td>12</td>
<td>12</td>
</tr>
<tr>
<td>PUFA</td>
<td>9</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>Carnitine (mg)‡</td>
<td>118</td>
<td>97</td>
<td>99</td>
</tr>
<tr>
<td>Choline (mg)§</td>
<td>440</td>
<td>439</td>
<td>427</td>
</tr>
<tr>
<td>Choline + carnitine (mg)§</td>
<td>558</td>
<td>536</td>
<td>526</td>
</tr>
<tr>
<td>Glycaemic load§</td>
<td>302</td>
<td>321</td>
<td>321</td>
</tr>
<tr>
<td>Cholesterol (mg)§</td>
<td>146</td>
<td>118</td>
<td>97</td>
</tr>
<tr>
<td>Food fibre (g)§</td>
<td>28</td>
<td>24</td>
<td>27</td>
</tr>
</tbody>
</table>

CHO, carbohydrate; RS, resistant starch; %E, percentage of energy.

* P < 0-05 compared with all other diets.
† Values shown are for 10-460 kJ (2500 kcal) menus.
‡ Estimated values, based on published carnitine content of commonly consumed foods.
§ Calculated values, Nutrition Data System for Research (University of Minnesota).
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Laboratory measures

Quantification of resistant starch. The RS content of the test starchy foods was analysed by a modified AOAC method 2009.01, using a Megazyme K-INTDF assay kit (Megazyme International Ireland Ltd).

Plasma measurements. Plasma was prepared from blood samples obtained by venepuncture after an overnight fast, and collected in tubes containing Na2EDTA (1-4 g/l) and a preservative cocktail containing sodium azide, chloramphenicol succinate, gentamicin sulphate, PPACK dihydrochloride and aprotinin. Blood and plasma samples were maintained at 4°C until further processing.

Trimethylamine-N-oxide, choline, betaine, γ-butyrobetaine and carnitine. Analyses were performed in plasma samples stored at 80°C using a stable-isotope dilution HPLC with online electrospray ionisation tandem MS (LC/ESI/MS/MS)†. In brief, four volumes of methanol containing 10 μM TMAO–trimethyl-d9 (d9-TMAO), betaine–trimethyl-d9 (d9-betaine), choline–trimethyl-d9 (d9-choline), γ-butyrobetaine–trimethyl-d9 (d9-γ-butyrobetaine) and carnitine–trimethyl-d9 (d9-carnitine) were added to plasma as internal standard to precipitate protein. Following centrifugation, the supernatant was collected for LC/MS/MS assay. Supernatants (10 μl) were analysed by injection into a silica column (4-6×250 mm, 5 μm Luna silica; cat. no. 00G-4274-E0; Phenomenex) at a flow rate of 0-8 ml/min interfaced with an API 5000 MS (AB SCIEX). Precursor–product ion transitions at m/z 76 → 58, m/z 104 → 60, m/z 118 → 59, m/z 140 → 60, m/z 162 → 60, m/z 85 → 66, m/z 113 → 69, m/z 127 → 68, m/z 155 → 69 and m/z 171 → 69 were used for TMAO, choline, betaine, γ-butyrobetaine, carnitine, d9-TMAO, d9-betaine, d9-carnitine, d9-γ-butyrobetaine and d9-carnitine, respectively. Increasing concentrations of TMAO, choline, betaine, γ-butyrobetaine and carnitine standards were spiked to control plasma to abstain from alcohol and dietary supplements during the study. The staff nutritionist used menu checklists, grocery receipts and information gathered from weekly interactions to assign a compliance score (1-5-point scale, where 5 is indicative of high compliance) for each study participant.

Fasting blood samples were collected on two consecutive days following completion of the baseline diet (days 13, 14) and at the end of each diet period (days 27, 28 and days 55, 56). A 3-h meal tolerance test was administered on days 28 and 56 (the concluding day of each experimental diet) with blood samples collected in the fasting state and 0-5, 1, 2 and 3 h after consumption of a meal representative in macronutrient composition to the assigned experimental diet. The different high- and low-RS meals were designed to correspond to the CHO content of the lower- or higher-CHO study arms (40% v. 52 percentage of energy (%E) as CHO), and to provide one-third of the daily allotted energy and starch (e.g. 16 and 22 g of RS/meal for the high-RS diet for a subject consuming 10 460 kJ/d (2500 kcal/d); and 0-8 and 1-1 g RS/meal for the low-RS diet for a subject consuming 10 460 kJ/d (2500 kcal/d)).
generate calibration curves with the y-axis as the peak area ratio to their respective internal standards for determining plasma concentrations of TMAO, betaine, choline, γ-butyrobetaine and carnitine, respectively.

**Glucose, insulin and lipids.** Plasma insulin concentrations were measured by an ELISA (EZHI-14K Human Insulin ELISA kit; Millipore). HOMA-IR was calculated from plasma insulin and glucose concentrations (insulin (mU/l) x glucose (nmol/l)/22.5)\(^{19}\).

Total plasma cholesterol, TAG, HDL-cholesterol and glucose concentrations were measured enzymatically on a Liasys 330 Clinical Chemistry System (AMS Diagnostics), and LDL-cholesterol was calculated using the Friedewald formula\(^{25}\).

Quality control of lipid measurements was maintained through the standardisation programme of the Centers for Disease Control-National Heart, Lung and Blood Institute. Plasma apo B and apo AI were analysed on the same machine by immunoturbidimetric assays using the ITA reagent kit (Bacton Assay Systems)\(^{26,27}\).

Particle concentrations of VLDL, intermediate-density lipoprotein and LDL subfractions in plasma were determined by ion mobility (IM) as described previously\(^{28}\). This method uniquely allows for direct particle quantification following brief ultracentrifugation in D2O to remove albumin. The IM instrument uses an electrospary to create an aerosol of particles that pass through a dynamic mobility analyzer coupled to a particle counter. Particle numbers are measured in pre-specified particle diameter intervals and converted to plasma particle concentrations (nmol). LDL diameter is also measured at the peak of LDL particle distribution\(^{28}\).

**Faecal DNA extraction and sequencing.** Faecal samples were collected at the end of each dietary intervention (high RS and low RS) from sixteen participants assigned to the higher-CHO study arm (2 x 16 = 32 faecal samples) and from twenty-three participants assigned to the lower-CHO study arm (2 x 23 = 46 faecal samples). From these samples, total genomic DNA was extracted in duplicate using the MoBio PowerSoil DNA extraction kit with additional heat lysis for 5 min at 60°C (MoBio Laboratories). PCR were used to amplify DNA, using the F515/R806 primer to target the V3/V4 region of the 16S rRNA gene, and the reverse primer construct also contained a twelve-base error-correcting Golay code\(^{29}\). 16S rRNA was sequenced as described in the online Supplementary Methods. Sequence data were analysed using the Quantitative Insights into Microbial Ecology pipeline version 1.7\(^{30}\), as described in the online Supplementary Material.

**Statistical analysis**

On the basis of published data comparing high- vs. low-RS diets\(^ {15,16}\), a sample size of fifty-two participants was estimated to provide 80% power (5% significance) to detect a significant metabolic effect of RS, as manifest by 15 and 50% changes in postprandial insulin and glucose responses (AUC), respectively, a 19% change in plasma TAG, and a 13% change in small dense LDL between the high- vs. low-RS diets.

Statistical analyses were performed using ANOVA and crossover experiments procedure of Stata 11.1 (StataCorp LP). The effects of high vs. low RS were estimated by ANOVA for a crossover design that involved the random assignment of subjects to high and low RS, and included effects due to RS, CHO and their interaction. These analyses also tested effects of dietary sequence (i.e. high- following low-RS diets vs. low- following high-RS diets), and no significant diet order effects were observed for any of the measures of response (data not shown). The analyses were repeated within each CHO condition for a simple cross-over design that included only RS effects. Transformation of data that were not normally distributed (carnitine, choline, insulin, HOMA-IR, TAG and HDL-cholesterol) did not affect the results.

**Results**

**Participant retention and baseline characteristics**

A total of fifty-two participants (twenty men and thirty-two women) completed the study. The flow diagram of participant recruitment and withdrawal is illustrated in Fig. 2. On average, these individuals were middle aged (mean 44 (SD 14) years), normotensive (systolic BP: 119 (sd 14) mmHg, diastolic BP: 70 (sd 8) mmHg), and overweight or obese as characterised by their BMI (51 (sd 2) kg/m²), body fat (38 (sd 7) %) and/or waist circumference (107 (sd 8) cm, men; 101 (sd 7) cm, women). HOMA-IR ranged from 2.1 to 20.4 at screening (mean 3.87 (sd 2.90); median: 3.0).

With the exception of baseline plasma carnitine levels, which were lower in those randomised to the lower-carbohydrate diet, baseline characteristics of participants did not differ significantly between those in the lower- and higher-CHO study arms (Table 2). Adjustment for differences in baseline plasma carnitine levels between high- and low-CHO groups did not affect microbiome metabolite responses to diets high vs. low in RS.

**Compliance with dietary protocol**

Participants were highly compliant with the dietary protocol, with nutritionist-reported mean compliance scores of 4.7 (sd 0.7) (on a scale of 1–5). Self-reported gastrointestinal symptoms and perceived satiety during high and low RS intake were consistent with high dietary adherence, with significantly increased frequency of flatulence, fullness, loss of appetite and burping and significantly increased intensity of abdominal cramps, flatulence and fullness after the high-RS diets (online Supplementary Fig. S1). High RS intake also increased the reported number of weekly bowel movements in participants assigned to the higher-CHO diets (12 (sd 7) bowel movements/week with high RS and 9 (sd 5) bowel movements/week with low RS, P = 0.005).

**Documentation of adverse events**

No serious adverse events were reported (online Supplementary Table S2).
Gut microbiome derived metabolites

Fasting plasma carnitine, betaine, \( \gamma \)-butyrobetaine and TMAO concentrations were significantly higher after the high-\( \nu \) low-RS diet in the lower-CHO treatment arm (Table 3), but not the higher-CHO treatment arm (\( P > 0.38 \) for all metabolites), resulting in a significant CHO by RS interaction for these metabolites. Plasma choline concentration was not significantly affected by starch digestibility. Additional analyses showed that plasma TMAO levels were not correlated with the sum of plasma choline and carnitine, both dietary precursors of TMAO (\( P = 0.53 \)).

Gut microbial taxa associated with plasma trimethylamine-N-oxide concentrations

Faecal samples were collected in a subgroup of thirty-nine participants for microbial community analysis. Consistent with findings in the group as a whole (\( n = 52 \)), plasma TMAO concentrations were significantly higher after the high-\( \nu \) low-RS diets (\( +35 (sd = 2.35) \) and \( +3.14 (sd = 1.74) \) for all taxa, respectively; \( P = 0.0008 \)) in these thirty-nine participants. Microbial community analysis of these samples identified significant positive and negative correlations between multiple taxa and plasma TMAO levels (Fig. 3, \( P < 0.05 \) for all taxa).

Fasting and postprandial insulin and glucose

Although high- and low-RS diets did not affect fasting concentrations of insulin and glucose (Table 4), the high-RS test

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Table 2. Baseline characteristics

<table>
<thead>
<tr>
<th></th>
<th>Higher-CHO study arm</th>
<th>Lower-CHO study arm</th>
<th>( P ) (high v. low CHO)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>Mean ( \pm ) sd</td>
<td>Mean ( \pm ) sd</td>
<td></td>
</tr>
<tr>
<td>BMI (kg/m(^2))</td>
<td>24.7 ( \pm ) 14.1</td>
<td>24.3 ( \pm ) 13.0</td>
<td>0.39</td>
</tr>
<tr>
<td>Glucose (mmol/l)</td>
<td>5.52 ( \pm ) 0.48</td>
<td>5.54 ( \pm ) 0.43</td>
<td>0.84</td>
</tr>
<tr>
<td>Insulin (mU/l)</td>
<td>11.2 ( \pm ) 5.2</td>
<td>10.8 ( \pm ) 8.7</td>
<td>0.85</td>
</tr>
<tr>
<td>HOMA-IR</td>
<td>2.74 ( \pm ) 1.26</td>
<td>2.69 ( \pm ) 2.35</td>
<td>0.93</td>
</tr>
<tr>
<td>TMAO (( \mu )mol/l)</td>
<td>5.19 ( \pm ) 3.19</td>
<td>4.16 ( \pm ) 2.27</td>
<td>0.18</td>
</tr>
<tr>
<td>Carnitine (( \mu )mol/l)</td>
<td>33.7 ( \pm ) 6.1</td>
<td>30.2 ( \pm ) 5.2</td>
<td>0.03</td>
</tr>
<tr>
<td>Choline (( \mu )mol/l)</td>
<td>6.57 ( \pm ) 1.37</td>
<td>6.60 ( \pm ) 1.62</td>
<td>0.93</td>
</tr>
<tr>
<td>Betaine (( \mu )mol/l)</td>
<td>36.1 ( \pm ) 8.1</td>
<td>32.9 ( \pm ) 7.7</td>
<td>0.16</td>
</tr>
<tr>
<td>( \gamma )-Butyrobetaine (( \mu )mol/l)</td>
<td>0.91 ( \pm ) 0.26</td>
<td>0.90 ( \pm ) 0.21</td>
<td>0.77</td>
</tr>
<tr>
<td>Total cholesterol (mmol/l)</td>
<td>4.47 ( \pm ) 0.77</td>
<td>4.39 ( \pm ) 0.64</td>
<td>0.70</td>
</tr>
<tr>
<td>LDL-cholesterol (mmol/l)</td>
<td>2.83 ( \pm ) 0.77</td>
<td>2.75 ( \pm ) 0.53</td>
<td>0.59</td>
</tr>
<tr>
<td>TAG (( \mu )mol/l)</td>
<td>1.11 ( \pm ) 0.29</td>
<td>1.15 ( \pm ) 0.50</td>
<td>0.76</td>
</tr>
<tr>
<td>HDL-cholesterol (mmol/l)</td>
<td>1.13 ( \pm ) 0.20</td>
<td>1.12 ( \pm ) 0.23</td>
<td>0.87</td>
</tr>
<tr>
<td>Apo B (mg/l)</td>
<td>790 ( \pm ) 135</td>
<td>740 ( \pm ) 154</td>
<td>0.22</td>
</tr>
<tr>
<td>Apo A1 (mg/l)</td>
<td>1138 ( \pm ) 129</td>
<td>1115 ( \pm ) 114</td>
<td>0.51</td>
</tr>
</tbody>
</table>

CHO, carbohydrate; HOMA-IR, homoeostatic model assessment of insulin resistance (insulin (mU/l) × glucose (mmol/l)/22.5).

* Data were analysed by ANOVA for a cross-over design.
Resistant starch and cardiometabolic risk

Table 3. Plasma concentrations of carnitine, choline, betaine, γ-butyrobetaine and trimethylamine-N-oxide (TMAO) after 2 weeks of diet with differing amounts of resistant starch (RS) and carbohydrate (CHO)* (Mean values and standard deviations)

<table>
<thead>
<tr>
<th></th>
<th>Higher-CHO study arm</th>
<th></th>
<th>Lower-CHO study arm</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>SD</td>
<td>Mean</td>
<td>SD</td>
</tr>
<tr>
<td>Carnitine (μmol/l)</td>
<td>32.9</td>
<td>7.2</td>
<td>32.3</td>
<td>4.9</td>
</tr>
<tr>
<td>Choline (μmol/l)</td>
<td>5.92</td>
<td>1.43</td>
<td>6.07</td>
<td>1.28</td>
</tr>
<tr>
<td>Betaine (μmol/l)</td>
<td>34.1</td>
<td>8.3</td>
<td>34.5</td>
<td>7.6</td>
</tr>
<tr>
<td>γ-Butyrobetaine (μmol/l)</td>
<td>0.92</td>
<td>0.25</td>
<td>0.91</td>
<td>0.23</td>
</tr>
<tr>
<td>TMAO (μmol/l)</td>
<td>4.04</td>
<td>1.90</td>
<td>3.66</td>
<td>1.58</td>
</tr>
</tbody>
</table>

* Data were analysed by ANOVA for a cross-over design.

Fig. 3. Pearson’s correlations between relative abundance of taxa and plasma trimethylamine-N-oxide (TMAO) concentrations. An OTU table was filtered at a minimum depth of 5000 sequences per sample, summarised at the genus level, and filtered to exclude genera less than 0.05% abundant. Relative abundances of taxa were correlated to TMAO values for each sample.

meals produced significantly lower postprandial insulin and glucose responses, expressed as incremental AUC (IAUC), compared with low-RS test meals (Table 4 and online Supplementary Fig. S2). These differences were largely due to the differential effect of RS on the 0-5-h postprandial glucose response (P=0.0001) and the 1-h postprandial insulin response (P=0.007).

Consuming higher-CHO compared with lower-CHO test meals acutely did not affect the IAUC for glucose, but resulted in significantly higher postprandial insulin responses at all time points after the meal (online Supplementary Fig. S2), expressed as IAUC (P=0.001, Table 4). There were no significant CHO by RS interactions for postprandial glucose or insulin responses (P=0.49 and P=0.66, respectively).

Fasting lipids and lipoproteins

With the exception of plasma TAG and large VLDL particles, which were increased by high- v. low-CHO diets (P=0.02 and P=0.002, respectively), fasting plasma lipids, lipoproteins and apoproteins were not affected by starch digestibility or the amount of CHO in the diet (Tables 4 and 5).

Body weight

Changes in body weight were minimal (Table 4), although a reduction with low v. high RS in the low-CHO arm (87.7 (sd 12.8) vs. 88.3 (sd 12.8) kg) was significant at P<0.05. Adjustment for change in body weight did not significantly affect the gut microbiome-derived metabolite or glycaemic and lipoprotein responses to the high- and low-RS diets (data not shown).

Discussion

We report that intake of dietary RS can modulate circulating levels of TMAO, a metabolite that is associated with increased future risk of major cardiovascular events(1,2,4). The production
of TMAO is dependent on gut microbes and arises from dietary precursors such as choline, carnitine, phosphatidylcholine and γ-butyrobetaine, which are first converted by colonic bacteria to trimethylamine. Trimethylamine is then absorbed and rapidly oxidised to TMAO by hepatic flavin monooxygenases.

The association of TMAO with CVD has been ascribed in part to inhibition of reverse cholesterol transport, changes in cholesterol and bile acid metabolism, and increased macrophage foam cell formation. In more recent studies, TMAO has also been linked to development of vulnerable plaque, both through activation of arterial endothelial cells, and through a direct effect on intracellular Ca signalling in platelets, promoting a prothrombotic phenotype. Notably, in a susceptible mouse model, inhibition of microbial trimethylamine production from choline was recently shown to reduce plasma levels of TMAO. Rather, our finding suggests that both higher CHO and carbohydrate (CHO) intake were significantly increased by high RS intake, although this effect was dependent on total dietary CHO. Specifically, the TMAO-raising effect of RS was observed with a CHO intake of 39–40% of energy, whereas with CHO intake >50% of energy levels of TMAO were yet higher and independent of RS content. This finding suggests that both higher CHO intake alone and high RS intake alone are sufficient to promote the production of trimethylamine by the colonic microbiota, and that both must be reduced in order to attenuate this process.

It is unlikely that the increase in plasma TMAO with the high-RS diet was due to higher dietary intake of carnitine and choline. In fact, the sum of dietary carnitine + choline, both dietary precursors of TMAO, was slightly lower for the high-RS diet v. low-RS diet in the lower-CHO study arm. Moreover, the sum of plasma choline + carnitine levels was not correlated with plasma TMAO levels. Rather, our findings suggest that differential
effects of high \( v \). Low RS on gut microbial composition led to increased TMAO concentrations with high RS intake.

In keeping with the obligatory role of gut microbiota in producing TMAO\(^{(13)}\), analysis of the microbial composition of faecal samples showed that the proportions of certain taxa were correlated with plasma TMAO levels. Although recent studies have delineated biochemical processes involved in the microbial conversion of choline and carnitine to TMAO\(^{(50–52)}\), little is known of the diversity of microbial taxa that can contribute to this process. One recent study examined seventy-nine human microbial isolates spanning several common phyla observed in the human gut and identified several human commensals with TMAO-producing activity\(^{(40)}\). Although it is not possible from the present results to determine the contribution of specific microbial communities to the diet-induced changes in TMAO levels observed here, it is intriguing that some that were inversely correlated with TMAO change – namely, Lachnospiraceae and Clostridiaceae (Fig. 3) – were also recently found to be associated with lower plasma TMAO levels in mice\(^{(35)}\).

Finally, the extent to which products of RS fermentation (e.g. SCFA) may have influenced the associations of these microbial communities with TMAO requires further study – for example, by examination of these associations in conjunction with measurements of faecal fatty acids and other metabolites at multiple time points after RS feeding.

In agreement with earlier observations\(^{(14–18,22)}\), we report significantly attenuated insulin and glucose responses to meals providing 16–22 g RS. A strength of our study is that this was observed in the context of physiological meals that were balanced and matched for fat, protein and food fibre, which can markedly affect the digestion and absorption of RS\(^{(41)}\). These results suggest a potential utility for RS in improving meal-to-meal regulation of blood glucose. SCFA, particularly acetate and propionate generated from colonic fermentation by resident bacteria, have also been implicated in the insulin sensitising effects of RS\(^{(42,43)}\).

Although earlier studies have suggested that the lipid-lowering effects of RS may be dependent upon high levels of intake\(^{(15,16)}\), this is not supported by our findings. In the present study, test starches were provided in amounts 1–2 g RS. A strength of our study is that this was achieved with both high- and low-RS diets at time of preparation, we found no effect of RS on fasting plasma lipids or lipoproteins.

Despite findings, earlier demonstrations of rapid alterations in microbial community structure with RS intake\(^{(10–12)}\), and suggest that such changes in gut microbiota promote generation of TMAO in a setting of lower carbohydrate, higher fat intake. However, it remains to be determined whether these effects are sustained with longer-term dietary interventions.

In light of the health benefits generally ascribed to RS, and of epidemiological evidence linking high fibre intake to reduced CVD risk\(^{(58)}\), the increase in TMAO with RS is contrary to what might be expected. Earlier dietary intervention studies have also shown increased abundance of TMAO after diets high in soy\(^{(59)}\) or low glycaemic load carbohydrates\(^{(60)}\), typically deemed beneficial to cardiometabolic health. Hence, although there is strong evidence for the relation of TMAO to athero-sclerotic CVD, we cannot conclude that the dietary effects on TMAO observed here would translate into changes in risk for
CVD. Furthermore, whether increases in TMAO are clinically relevant in the context of a concomitant improvement in glycaemic control, as is commonly observed with RS, remains to be established.

In conclusion, our study showed that, in the context of a lower-CHO diet, high RS intake resulted in significantly higher plasma concentrations of TMAO, a novel CVD risk biomarker. In keeping with earlier findings, RS blunted the postprandial glucose and insulin responses to meals consumed acutely, but average daily intake of 49–68 g RS did not affect fasting plasma lipids, lipoprotein particle concentrations, glucose or insulin. Together, these observations support the conclusion that at least in the short term high RS intake does not improve biomarkers of cardiometabolic health.

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Supplementary material
For supplementary material/s referred to in this article, please visit https://doi.org/10.1017/S0007114516004165

References


