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 meal 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 starch (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
composition of the human gut microbiota\textsuperscript{(10–12)}. In view of this, and because production of TMAO is dependent on gut microbes\textsuperscript{(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\textsuperscript{(14–18)}, and to examine changes in plasma lipids and lipoproteins whose associations with RS intake are less well established\textsuperscript{(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\textsuperscript{(19)} (based on HOMA-IR distributions of a comparable group of men and women screened for a previous study\textsuperscript{(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 ≤1.65 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- vs. 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 vs. 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-amylopectin 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, Melojoy; 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\textsuperscript{(10–12)} as well as glycaemic control\textsuperscript{(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
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>
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<tbody>
<tr>
<td></td>
<td>High RS</td>
<td>Low RS</td>
<td>High RS</td>
</tr>
<tr>
<td><strong>CHO (%E)</strong></td>
<td>41</td>
<td>51</td>
<td>53</td>
</tr>
<tr>
<td><strong>RS (%E)</strong></td>
<td>10</td>
<td>0.6</td>
<td>8</td>
</tr>
<tr>
<td><strong>RS (g)</strong></td>
<td>66</td>
<td>4</td>
<td>48</td>
</tr>
<tr>
<td><strong>Protein (%E)</strong></td>
<td>19</td>
<td>22</td>
<td>22</td>
</tr>
<tr>
<td><strong>Fat (%E)</strong></td>
<td>40</td>
<td>27</td>
<td>26</td>
</tr>
<tr>
<td><strong>SFA</strong></td>
<td>9</td>
<td>6</td>
<td>7</td>
</tr>
<tr>
<td><strong>MUFA</strong></td>
<td>20</td>
<td>12</td>
<td>12</td>
</tr>
<tr>
<td><strong>PUFA</strong></td>
<td>9</td>
<td>7</td>
<td>6</td>
</tr>
<tr>
<td><strong>Choline (mg)</strong></td>
<td>118</td>
<td>97</td>
<td>99</td>
</tr>
<tr>
<td><strong>Choline (mg)§</strong></td>
<td>440</td>
<td>439</td>
<td>427</td>
</tr>
<tr>
<td><strong>Choline + carnitine (mg)</strong></td>
<td>558</td>
<td>536</td>
<td>526</td>
</tr>
<tr>
<td><strong>Glycaemic load</strong></td>
<td>40</td>
<td>39</td>
<td>39</td>
</tr>
<tr>
<td><strong>Cholesterol (mg)§</strong></td>
<td>302</td>
<td>321</td>
<td>321</td>
</tr>
<tr>
<td><strong>Food fibre (g)§</strong></td>
<td>28</td>
<td>24</td>
<td>27</td>
</tr>
</tbody>
</table>

CHO, carbohydrate; RS, resistant starch; %E, percentage of energy.
† Values shown are for 10-46 kJ (2500 kcal) menus.
‡ Calculated values, based on published carnitine content of commonly consumed foods(21).
§ Calculated values, Nutrition Data System for Research (University of Minnesota).
§§ Estimated values, based on published carnitine content of commonly consumed foods(21).

Plasma measurements. Plasma was prepared from blood samples obtained by venepuncture after an overnight fast, and collected in tubes containing Na2EDTA (1 g/l) and a preservative cocktail containing sodium azide, chloramphenicol succinate, gentamicin sulphate, PPACK dihydrochloride and aprotonin. 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)1,2,3. In brief, four volumes of methanol containing 10 µg MTAO-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 in tubes containing Na2EDTA (1 g/l) and subjected to microvial derivatisation with a product cocktail containing sodium azide, chloramphenicol succinate, gentamicin sulphate, PPACK dihydrochloride and aprotonin. Blood and plasma samples were maintained at 4°C until further processing.
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 (mmol/l)/22.5)\(^{(19)}\).

Total plasma cholesterol, TAG, HDL-cholesterol and glucose concentrations were measured enzymatically on a Liaysys 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 immuno-turbidimetric 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 D\(_2\)O to remove albumin. The IM instrument uses an electrospay 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/l). 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 × 16 = 32 faecal samples) and from twenty-three participants assigned to the lower-CHO study arm (2 × 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- v. 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- v. low-RS diets.

Statistical analyses were performed using ANOVA and cross-over experiments procedure of Stata 11.1 (StataCorp LP). The effects of high v. low RS were estimated by ANOVA for a cross-over 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 v. 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. Log-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 (31 (SD 2) kg/m\(^2\)), body fat (38 (SD 7) %) and /or waist circumference (107 (SD 8) cm, men; 101 (SD 7) cm, women). HOMA-IR ranged from 2.46 to 4.6 (median: 3.10). 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 v. 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 flatus, 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).
Analysed concentrations were significantly higher after the high-Chol treatment arm (Table 3), but not the higher-Chol treatment arm ($P>0.38$ for all metabolites), resulting in a significant Cho by RS interaction for these metabolites. Plasma cho line 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-Cho, low-RS diets ($t=3.5$ (s.e. 2.35) and $t=3.1$ (s.e. 1.74), 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).

**Gut microbiome derived metabolites**

Fasting plasma carnitine, betaine, $\gamma$-butyrobetaine and TMAO concentrations were significantly higher after the high-Cho, low-RS diet in the lower-Chol treatment arm (Table 3), but not the higher-Chol 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 ($P=0.53$).

**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
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>
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</thead>
<tbody>
<tr>
<td></td>
<td>High RS</td>
<td>Low RS</td>
<td>P (high v. low RS)</td>
<td>High RS</td>
</tr>
<tr>
<td>Carnitine (μmol/l)</td>
<td>Mean</td>
<td>SD</td>
<td>Mean</td>
<td>SD</td>
</tr>
<tr>
<td>Choline (μmol/l)</td>
<td>32.9</td>
<td>7.2</td>
<td>32.3</td>
<td>4.9</td>
</tr>
<tr>
<td>Betaine (μmol/l)</td>
<td>9.2</td>
<td>34.1</td>
<td>8.3</td>
<td>34.5</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>6.0</td>
<td>0.44</td>
<td>6.6</td>
<td>0.58</td>
</tr>
</tbody>
</table>

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

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 \((P=0.001, \text{Table 4})\). There were no significant CHO by RS interactions for postprandial glucose or insulin responses \((P=0.049)\) 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 \((87.7 \text{ (SD 12.8) kg})\) 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\(^{(3,24)}\). 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 mono-oxygenases.

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 microbially trimethylamine production from choline was recently shown to reduce plasma levels of TMAO and to inhibit the development of atherosclerotic lesions. Moreover, in two different mouse models of atherosclerosis, anti-sense oligonucleotide targeting of hepatic flavin mono-oxygenase 3 has been shown to similarly inhibit TMAO formation and development of atherosclerosis.

Resident gut micro-organisms are rapidly modulated by variation in intake of starches, and these changes may vary in conjunction with differences in starch digestibility. It is known that starches that are relatively resistant to intestinal digestion are subject to fermentation by amylolytic bacterial digestion are subject to fermentation by amylolytic bacterial digestion. Notably, in a susceptible mouse model, inhibition of microbial trimethylamine production from choline 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 total dietary CHO. 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. 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

**Table 4. Body weight and plasma insulin, glucose and lipid concentrations after 2 weeks of diet with differing amounts of resistant starch (RS) and carbohydrate (CHO)**

<table>
<thead>
<tr>
<th></th>
<th>Higher-CHO study arm</th>
<th>Lower-CHO study arm</th>
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<tr>
<td></td>
<td>High RS</td>
<td>Low RS</td>
</tr>
<tr>
<td>Weight (kg)</td>
<td>Weight</td>
<td>Mean</td>
</tr>
<tr>
<td>Fasting insulin (mU/l)</td>
<td>8.6</td>
<td>4.5</td>
</tr>
<tr>
<td>Fasting glucose (mmol/l)</td>
<td>5.26</td>
<td>0.55</td>
</tr>
<tr>
<td>IAUC insulin (mU/l per h)</td>
<td>132.8</td>
<td>73.6</td>
</tr>
<tr>
<td>IAUC glucose (mmol/l per h)</td>
<td>1.85</td>
<td>1.62</td>
</tr>
<tr>
<td>Total cholesterol (mmol/l)</td>
<td>4.30</td>
<td>0.71</td>
</tr>
<tr>
<td>LDL-cholesterol (mmol/l)</td>
<td>2.66</td>
<td>0.48</td>
</tr>
<tr>
<td>TAG (mmol/l)</td>
<td>1.23</td>
<td>0.42</td>
</tr>
<tr>
<td>HDL-cholesterol (mmol/l)</td>
<td>1.08</td>
<td>0.17</td>
</tr>
<tr>
<td>Apo B (mg/l)</td>
<td>762</td>
<td>141</td>
</tr>
<tr>
<td>Apo A1 (mg/l)</td>
<td>1121</td>
<td>143</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
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<th>Higher-CHO study arm</th>
<th>Lower-CHO study arm</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>High RS</td>
<td>Low RS</td>
</tr>
</tbody>
</table>
| ILD, intermediate-density lipoprotein; LDL ppd, LDL peak particle diameter.

* Data were analysed by ANOVA for a cross-over design.
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\(^{(3)}\), 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\(^{(38,39)}\), 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 1.9–2.6-fold higher than in earlier interventions\(^{(44–46)}\), but we found no effect of RS on fasting plasma lipids or lipoproteins. The short-term nature of the current intervention may also be a factor, but earlier studies showing reductions in cholesterol and TAG with high- \( v \) low-RS diets at 4 weeks, but not at 8 and 13 weeks\(^{(15,16)}\), suggest that the effects of RS on plasma lipids are transitory. Notably, we observed that, independent of starch digestibility, higher-CHO diets increased plasma TAG and large VLDL particle concentrations, and promoted a shift in LDL particle distribution towards more medium and small LDL (Supplementary Fig. S4), in keeping with the recognised effect of carbohydrates on features of atherogenic dyslipidaemia\(^{(47–51)}\), and in overall agreement with the recent OmniCarb study\(^{(52)}\), which found that plasma TAG were increased by higher CHO intake, but were not influenced by starch quality as assessed by the glycaemic index.

Strengths of our study include a design that, for the first time, allowed testing of high \( v \), low RS in the context of both higher- and lower-CHO diets, lack of confounding effects from other nutrients that were matched across diets, and strict dietary control achieved by the preparation and provision of most study foods. This differs from previous studies in which test starches were provided in the form of supplements that individuals consumed with their self-selected diet\(^{(15,46,53,54)}\), with only one intervention conducted in a controlled setting\(^{(16)}\).

A limitation of our study is that the protocol and randomisation scheme required that all foods be prepared in advance, flash-frozen and stored until consumed, typically within 1–2 months. Starch processing conditions have been shown to affect their functionality and susceptibility to enzymatic degradation. When heated in excess water, high-amylpectin starches become highly digestible as a result of gelatinisation, a process that results in disruption of starch crystalline structure and swelling of starch granules. Upon cooling and storage, gelatinised starch may undergo retrogradation during which amylose and, to a lesser extent, outer branches of amylopectin re-align into more ordered crystalline structures that are less susceptible to degradation by \( \alpha \)-amylases\(^{(55)}\). Therefore, we cannot rule out the possibility that in our study freezing and storage may have promoted retrogradation of gelatinised starch products in a manner that rendered them more resistant to digestion, thus attenuating differential metabolic effects of high- and low-RS diets. However, in an earlier study, storage time, freezing, thawing and re-heating did not affect the RS content of high- and low-amylase muffins\(^{(45,46)}\). Also of note, re-heating of starch-based foods may promote the re-dispersion of crystallised starch chains and restoration of starch digestibility\(^{(56,57)}\). In the present study, regular maize starch in the low-RS diet was incorporated mostly into entrees and baked goods, which, after freezing, were thawed and re-heated before consumption. The diets were otherwise consumed in a manner consistent with how individuals eat on a day-to-day basis. Under these conditions, and despite a 16-fold difference in the RS content of the high- and low-RS diets at time of preparation, we found no differences in their effects on fasting plasma glucose, insulin, lipids and lipoproteins.

Another limitation of our study is the short-term duration of the dietary intervention. As was also shown in an acute feeding study with egg yolk\(^{(53)}\), our findings demonstrate that changes in TMAO levels in response to dietary modification can occur rapidly. Our findings are also consistent with 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 soya\(^{(59)}\) or low glycaemic load carbohydrates\(^{(60)}\), typically deemed beneficial to cardiometabolic health. Hence, although there is strong evidence for the relation of TMAO to atherosclerotic 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

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