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<http://link.springer.com/article/10.1007/s10620-013-2844-1>

Please cite this article as: Le Leu, R.K., Young, G.P., Hu, Y., Winter, J. and Conlon, M., 2013. Dietary red meat aggravates dextran sulfate sodium-induced colitis in mice whereas resistant starch attenuates inflammation. *Digestive Diseases and Sciences*, 58(12), 3475-3482.

DOI 10.1007/s10620-013-2844-1

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2 Dietary Red Meat Aggravates Dextran Sulfate Sodium-Induced 3 Colitis in Mice Whereas Resistant Starch Attenuates 4 Inflammation

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7 Received: 6 March 2013 / Accepted: 9 August 2013
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9 Abstract

10 *Background* Although a genetic component has been
11 identified as a risk factor for developing inflammatory
12 bowel disease, there is evidence that dietary factors also
13 play a role in the development of this disease.

14 *Aims* The aim of this study was to determine the effects
15 of feeding a red meat diet with and without resistant starch
16 (RS) to mice with dextran sulfate sodium (DSS)-induced
17 colitis.

18 *Methods* Colonic experimental colitis was induced in
19 Balb/c mice using DSS. The severity of colitis was eval-
20 uated based on a disease activity index (based on body-
21 weight loss, stool consistency, rectal bleeding, and overall
22 condition of the animal) and a histological score. Estima-
23 tions were made of numbers of a range of different bacteria
24 in the treatment pools of caecal digesta using quantitative
25 real-time PCR.

26 *Results* Consumption of a diet high in red meat increased
27 DSS-induced colitis as evidenced by higher disease activity

and histopathological scores. Addition of RS to the red 28
meat diet exerted a beneficial effect in acute DSS-induced 29
colitis. Subjective analysis of numbers of a range of bac- 30
terial targets suggest changes in the gut microbiota abun- 31
dance were induced by red meat and RS treatments and 32
these changes could contribute to the reported outcomes. 33

Conclusions A dietary intake of red meat aggravates 34
DSS-induced colitis whereas co-consumption of resistant 35
starch reduces the severity of colitis. 36

Keywords Inflammation · Resistant starch · Red 38
meat · Gut microbiota · Dextran sulfate sodium 39

Abbreviations 40

DSS	Dextran sulfate sodium	41
RS	Resistant starch	42
RM	Red meat	43
IBD	Inflammatory bowel disease	44
UC	Ulcerative colitis	45
CRC	Colorectal cancer	46
SCFA	Short chain fatty acids	47
AIN	American Institute of Nutrition	48
Hi-maize	High amylose maize starch	49
DAI	Disease activity index	50
SRB	Sulfate-reducing bacteria	51
aps	Adenosine-5-phosphosulfate reductase gene	52

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Introduction 55

Inflammatory bowel diseases (IBD), including Crohn's dis- 56
ease and ulcerative colitis (UC), result from complex inter- 57
actions between environmental and genetic factors [1]. 58

59 Patients experience chronic relapsing symptoms that include
60 abdominal pain, diarrhoea, rectal bleeding and anaemia
61 resulting from intestinal inflammation, oedema and ulcera-
62 tion [2]. Although a genetic component has been identified as
63 a risk factor for developing IBD [3], there is evidence that
64 dietary factors may play a role in the development of IBD [4].
65 The incidence of IBD is high in western countries and is on
66 the increase in low-incidence areas such as southern Europe
67 and Asia, as well as developing countries that are now
68 adopting a westernised diet [5] [6].

69 A typical western diet is rich in red and processed meat
70 and poor in fruits and vegetables. Red meat has been
71 identified by the World Cancer Research Fund as a con-
72 vincing cause of colorectal cancer (CRC) [7] patients with
73 IBD also have a greater risk of developing CRC [8, 9]. In
74 contrast, a high intake of dietary fibre, fruit, or vegetables
75 may be protective against the development of IBD [10] and
76 also CRC [7, 11]. Short-chain fatty acids (SCFAs) are
77 products that are derived from fermentation of unabsorbed
78 dietary fibre and starch in the colon. The SCFA “butyrate”
79 is important for colonic integrity as it is the principal
80 energy source for the colonic epithelium, inhibits growth of
81 cancer cells in vitro and forces a more normal differenti-
82 ated phenotype [12, 13]. A deficiency of SCFAs in the
83 intestinal lumen is often related with epithelium atrophy
84 and inflammation. In UC, an overall impaired butyrate
85 metabolism has been reported in several studies [14]. In a
86 rodent model of dextran sulfate sodium (DSS)-induced
87 colitis, oral administration of sodium butyrate has been
88 shown to improve mucosal lesions and attenuate the
89 inflammatory profile of the intestinal mucosa and local
90 lymph nodes [15]. Also, Morita et al. [16] reported a pro-
91 tective effect of resistant starch (RS) in the form of high-
92 amylose cornstarch on trinitrobenzene sulfonic acid
93 (TNBS)-induced colitis in rats where enhancement of
94 mucosal protection was exerted possibly due to large bowel
95 SCFA production.

96 The DSS-induced colitis mouse model provides an
97 experimental model that displays many symptoms similar
98 to those seen in human UC, such as diarrhoea, bloody
99 faeces, body weight loss, mucosal ulceration, and short-
100 ening of the colorectum [17]. In the present study, we
101 determined the effects of feeding a diet high in red meat
102 with and without RS on DSS-induced colitis in Balb/c
103 mice.

104 Methods

105 Animals and Diets

106 Thirty-two male Balb/c mice were obtained from the
107 Animal Resource Centre, Perth, Western Australia, and

108 housed in controlled conditions of 22 ± 2 °C (SD),
109 80 ± 10 % humidity, and 12-h light/dark cycle. Mice were
110 acclimatized for a minimum of 1 week before com-
111 mencement of the trial. Mice were then divided into four
112 groups ($n = 8$) and fed one of four experimental diets
113 (Table 1) for a period of 12 days. The experimental diets
114 were modified forms of the AIN-76a standard for purified
115 diets for rats and mice. The first group “Control” con-
116 sumed the modified AIN-76a diet. The second group “RS”
117 consumed high amylose maize starch (Hi-maize[®] 260;
118 National Starch and Food innovation, Bridgewater, NJ,
119 USA) at a level of 10/100 g diet. The third group “RM”
120 consumed cooked red meat at a level of 30/100 g diet. The
121 fourth group “RM + RS” consumed cooked red meat at a
122 level of 30/100 g diet and high amylose maize starch at a
123 level of 10/100 g diet.

124 High amylose maize starch (Hi-maize 260), was used as
125 the source of resistant starch and was supplied by the
126 National Starch and Chemical Company. Hi-maize 260 has
127 been shown to contain approximately 50 % resistant starch
128 [18] and was added at a level of 10/100 g diet; therefore, a
129 total of 5 % resistant starch was added to the diet. This
130 proportion of starch consumed as RS in this RS-containing
131 diet is feasible in the context of the human diet and is not
132 likely to create any serious problem of side effects such as
133 flatulence and bloating [19]. Lean, minced rump steak was
134 purchased, cooked at medium temperature on a gas hot-
135 plate with continuous mixing to prevent the meat from
136 burning, and oven-dried overnight before grinding to
137 powder. Total nitrogen level of the cooked/dried red meat

Table 1 Composition of experimental diets

Ingredient	Control	RS	RM	RM + RS
Casein	20	20	0	0
Red meat	0	0	30	30
Corn starch	15	5	15	5
Sucrose	37.93	37.93	31.13	31.13
High amylose maize starch ^a	0	10	0	10
Sunflower seed oil	16.8	16.8	16.8	16.8
Lard ^b	3.2	3.2	0	0
α -cellulose	2	2	2	2
L-cysteine	0.3	0.3	0.3	0.3
Choline	0.12	0.12	0.12	0.12
Mineral mix ^c	3.5	3.5	3.5	3.5
Vitamin mix ^c	1	1	1	1
Methionine	0.15	0.15	0.15	0.15

^a High amylose maize starch (Hi-maize 260TM) used as the source of resistant starch

^b AIN-76 vitamin and mineral mixtures

^c Lard was added to the Control and RS diets to balance each diet for saturated fat and to give a total fat content of 20 %

- 138 was determined by the Dumas method [20], and the total
139 protein content was calculated to be 73 %. Saturated fat
140 content of the red meat was 6 % when analysed by a
141 standard fat extraction method [21]. Moisture content of
142 the meat was found to be 10 % by weighing known
143 amounts of meat product and drying overnight to calculate
144 moisture lost from the sample. Final diet preparations were
145 placed into air-sealed containers and stored at 4 °C, with
146 fresh food in the mouse cage bowls replaced daily.
- 147 The Flinders University of South Australia Animals
148 Welfare Committee approved all experimental procedures.
- 149 Induction of Colitis
- 150 Experimental colitis was induced by adding DSS (molec-
151 ular weight 36-50 kDa; MP Biomedicals) to the drinking
152 water at a level of 3 % for the first 5 days of the study. All
153 mice received standard tap water from day 6 to day 12 of
154 the study.
- 155 Tissue Collection
- 156 Mice were anaesthetised with a 10 % ketamine and 10 %
157 metotomidine solution at 75 mg/kg and decapitated 7 days
158 after DSS treatment. After dissection, the colon was
159 removed and placed into a 10 % buffered formalin solution
160 containing 3.6 % formaldehyde for 24 h and transferred to
161 70 % ethanol for histologic processing. Tissue was rehy-
162 drated through gradient alcohols and embedded in paraffin
163 wax for histological assessment.
- 164 Histopathological Analysis
- 165 Colon sections (5 µm) were stained with haematoxylin and
166 eosin and were independently and randomly coded so that
167 dietary groups were not known to the pathologist. Eight
168 randomly selected fields (magnified ×100) were viewed
169 under a light microscope, and each section was graded and
170 averaged according to the method described by Cooper
171 et al. [22]. The severity of mucosal injury was graded as
172 follows: grade 0, normal—intact colonic crypt; grade 1,
173 slight—cystic dilatation of crypts; grade 2, mild—loss of
174 basal 1/3 of crypts; grade 3, moderate—loss of basal 2/3 of
175 crypts; grade 4, severe—loss of entire crypt with surface
176 epithelium remaining intact.
- 177 Disease Activity Index Assessment
- 178 Mice were scored daily using a Disease Activity Index
179 (DAI) based on weight loss, stool consistency, rectal
180 bleeding, and overall condition of the animal [23].
181 Each of these elements was scored on a 0–3 scale, with 0
182 representing no disease symptom and 3 representing severe
disease symptom. Weight loss was scored as 0 representing
no weight loss compared to the original weight, 1 repre-
senting a weight loss of less than 5 %, two representing a
weight loss of between 5 and 10 %, and three representing
a weight loss of more than 10 % of the original weight. The
grading of each variable was scored from 0 to 3. Data are
the sum of scores for four independent variables.
- Bacterial Quantification
- Caecal digesta collected from each mouse was combined
into treatment group pools (insufficient material was
available for individual analysis). DNA was extracted
from 0.25 g of each pool using the repeated bead beating
plus column method of Yu and Morrison [24] and then
used for estimation of numbers of target bacteria using
quantitative real-time PCR (qRT-PCR). Each pool was
analysed in quadruplicate. PCR reactions were carried out
on a CFX Connect 96 real-time PCR detection system
(Bio-Rad, Hercules, CA, USA) in a volume of 10 µl.
Each reaction contained 1 µl DNA template, 5 µl SsoFast
EvaGreen Supermix, 0.2 µl bovine serum albumin (0.5 µl
DMSO used for SRB_aps reaction), primers (according
to references below) and PCR-grade water. Bacterial
assays were performed according to previous publications:
Akkermansia muciniphila, *Bifidobacterium* spp. (84 °C
step before fluorescence acquisition performed in this
study), *Clostridium coccooides* group, *Clostridium leptum*
group, *Escherichia coli* and *Faecalibacterium prausni*
[25]; SRB_aps and total bacteria [26]; *Enterococcus* spp.
and *Parabacteroides distasonis* [27]; *Ruminococcus bro-*
mii (conditions like *F. prausnitzii* except 30 s annealing)
primers used were he-10F and he-10R from [28]; *Rumi-*
nococcus gnavus (conditions like *F. prausnitzii* except
58 °C annealing) [29]; *Bacteroides–Prevotella* (conditions
like *R. gnavus* except 45 s annealing and 700 nM primer)
[30]. A series of eight tenfold dilutions of a sample-
derived standard for each amplicon were analysed with
samples to estimate bacterial abundance and PCR effi-
ciency. It was not possible to examine differences
between groups using statistical tests due to the lack of
sample replication (due to the requirement for sample
pooling).
- Statistical Analysis
- Qualitative DAI and semi quantitative histological severity
scores were analysed using the non-parametric Kruskal–
Wallis test with pairwise comparisons. For all analyses,
 $P < 0.05$ was considered significant. All data are expressed
as the geometric mean ± standard error of the mean
(SEM). Statistical comparisons were made using IBM
SPSS for Windows software package V20.0 (Chicago, IL).

232 **Results**233 **Clinical Symptoms and DAI**

234 No mortality was observed in the control treatment,
 235 whereas 1 mouse died from each of the RS and
 236 RS + RM groups and 3 mice died from the red meat
 237 group. The DAI score was monitored daily over the
 238 12 days (5 days DSS treatment followed by 7 days tap
 239 water). DAI scores are shown in Fig. 1 and statistical
 240 outcomes in Table 2. Significant differences in DAI
 241 scores were evident as early as day 2 with the RM
 242 treatment group having significantly higher scores than
 243 all other treatment groups; this pattern was maintained to
 244 day 5. There were no differences seen on days 6
 245 between the different groups. On day 7, the RM group
 246 was significantly higher than the RS group. On day 8,
 247 the RM group was significantly higher than the Control
 248 and RS groups. On days 9 and 10, the RM group dis-
 249 played higher DAI compared to the RS group. No dif-
 250 ferences were observed on days 11 and 12.

251 **Histopathology Analysis**

252 Histologically, the DSS model of colitis is characterized by
 253 a disruption in crypt architecture, reduced crypt area and
 254 increased inflammatory infiltrate. Figure 2 shows a repre-
 255 sentative samples from each dietary group. Mice consum-
 256 ing the red meat diet (RM) had significantly higher
 257 histological severity scores than the Control group and the
 258 RS group (Fig. 3).

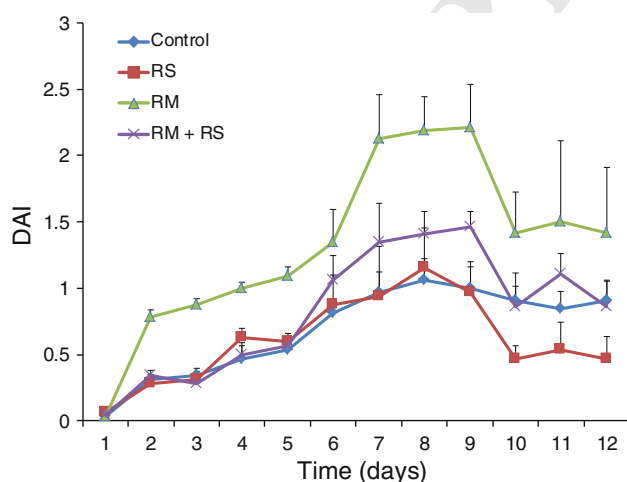


Fig. 1 Disease activity index (DAI) scores in mice monitored daily over the 12 days (5 days DSS treatment followed by 7 days tap water)

Table 2 Disease activity index (DAI) scores during the 12 days mice were fed the different diets

	Control	RS	RM	RM + RS
D1	0.03 ± 0.03	0.06 ± 0.04	0.03 ± 0.03	0.03 ± 0.03
D2	0.31 ± 0.04 a	0.28 ± 0.03 a	0.78 ± 0.06 b	0.34 ± 0.05 a
D3	0.34 ± 0.04 a	0.31 ± 0.06 a	0.87 ± 0.04 b	0.28 ± 0.03 a
D4	0.47 ± 0.10 a	0.62 ± 0.07 a	1.00 ± 0.05 b	0.50 ± 0.10 a
D5	0.53 ± 0.10 a	0.59 ± 0.07 a	1.10 ± 0.07 b	0.56 ± 0.08 a
D6	0.81 ± 0.11	0.88 ± 0.22	1.34 ± 0.25	1.06 ± 0.18
D7	0.97 ± 0.16 ab	0.94 ± 0.38 a	2.13 ± 0.33 b	1.34 ± 0.30 ab
D8	1.06 ± 0.17 a	1.15 ± 0.30 a	2.19 ± 0.25 b	1.40 ± 0.18 ab
D9	1.00 ± 0.21 ab	0.97 ± 0.23 a	2.21 ± 0.32 b	1.46 ± 0.11 ab
D10	0.90 ± 0.13 ab	0.68 ± 0.10 a	1.35 ± 0.31 b	1.10 ± 0.16 ab
D11	0.84 ± 0.16	0.54 ± 0.20	1.50 ± 0.61	1.10 ± 0.15
D12	0.90 ± 0.19	0.46 ± 0.18	1.42 ± 0.49	0.86 ± 0.20

Rows with different letters are significantly different at $P < 0.05$

259 **Caecal Bacterial Analysis**

260 Estimations were made of numbers of a range of different
 261 bacteria in caecal digesta were quantified using qRT-PCR
 262 and are shown in Table 3. The caecal digesta from mice in
 263 each treatment group was pooled to provide sufficient
 264 material for DNA extraction and analysis. Although sta-
 265 tistical analyses were not possible due to a lack of sample
 266 replication, a subjective comparison of means suggests a
 267 combination of red meat and RS treatment resulted in
 268 reduced numbers of *C. coccooides*, *Enterococcus* spp. and
 269 *E. coli* relative to other groups, and effects of red meat
 270 treatment on *F. prausnitzii*, *P. distasonis*, *A. muciniphila*,
 271 *Bifidobacteria* and the *C. leptum* group.

272 **Discussion**

273 The findings of the current investigation demonstrate that a
 274 diet high in red meat can increase the severity of DSS-
 275 induced colitis in mice whereas co-consumption of RS
 276 appears to reduce the severity of red meat-induced effects.
 277 Mice consuming the red meat diet alone demonstrated
 278 increased morbidity and mortality, heightened histological
 279 damage in the colon and enhanced DAI scores (from day 2
 280 to day 5). Addition of resistant starch appeared to protect
 281 against DSS-induced colitis, as it was observed that mice
 282 fed RS together with red meat had fewer mortalities, the
 283 enhancement of DAI by red meat through day 2 to day 5
 284 was ameliorated and the histopathology score was not
 285 significantly different from controls.

286 Epidemiological evidence suggests that diet plays a role
 287 in IBD [6]. Incidence rates of IBD have increased over the
 288 years in populations adopting a westernised diet [5, 6].

Fig. 2 Histological analysis of DSS treated mice. **a** Colon section from control fed mouse showing normal architecture (HE, $\times 100$); **b** colon section from RS fed mouse showing normal architecture (HE, $\times 100$); **c** colon section from red meat (RM) fed mouse showing crypt inflammation and moderate damage (HE, $\times 100$); **d** colon section from RM + RS fed mouse showing inflammation and minor damage (HE, $\times 100$), the tissue damage was less severe than in C damage (HE, $\times 100$)

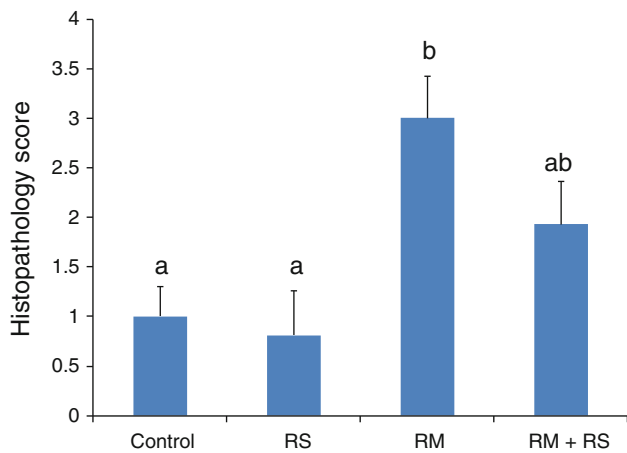
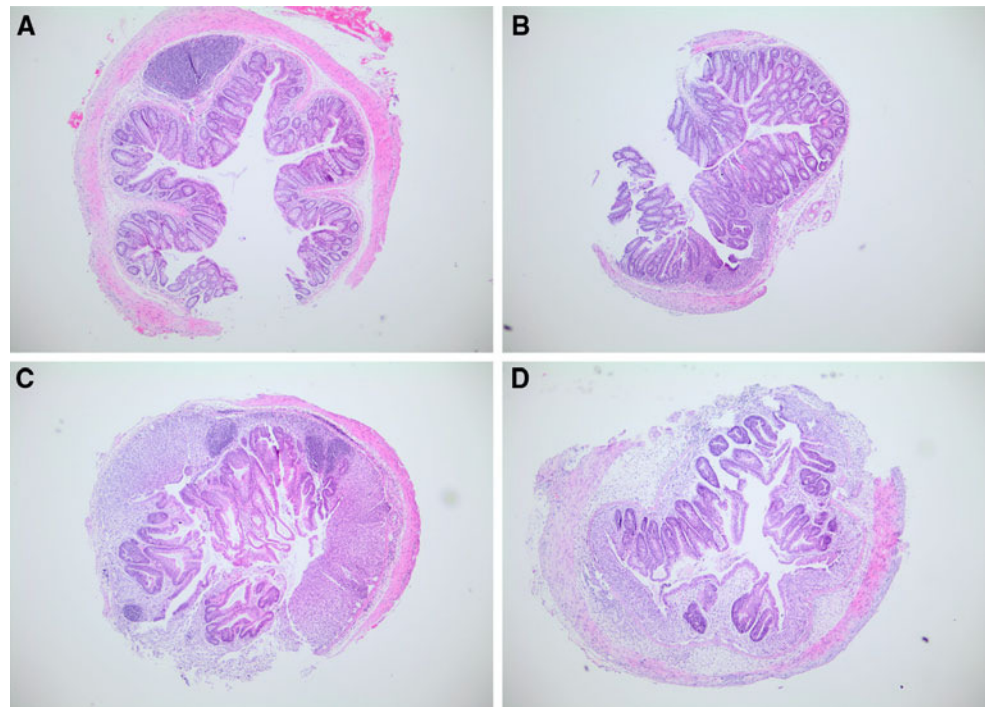


Fig. 3 Histopathology severity scores. Bars with different superscript letters are significantly different at $P < 0.05$

289 Animal protein, particularly red meat, [31–33], has been
 290 singled out as a possible risk factor as contributing to the
 291 development of IBD. Plausible explanations of why
 292 increased red meat intake may contribute to IBD may
 293 include increased delivery of amino acids and heme to the
 294 colon where they undergo fermentation and metabolism by
 295 the colonic microbiota [34], which results in the generation
 296 of potentially toxic substances such as ammonia, amines,
 297 N-nitroso compounds, phenols, cresols and hydrogen sul-
 298 fide [35, 36]. Increased dietary heme from haemoglobin in
 299 red meat can form reactive oxygen species, [37] Sesink
 300 et al. [38] showed that dietary heme increases luminal
 301 cytotoxicity which causes damage to the colonic

epithelium. Previous animal studies by us have also shown 302
 that red meat consumption results in a thinning of the 303
 colonic mucus layer and increases damage to the colono- 304
 cytes in the form of DNA strand breaks [39] or pro- 305
 mutagenic adducts [40]. 306

Mice consuming RS along with the red meat diet had 307
 reduced clinical signs of colitis when compared to mice fed 308
 only the red meat diet. Furthermore, the RM + RS mice 309
 did not differ from the control mice for either histopa- 310
 thological severity or daily DAI scores. There are a number 311
 of potential reasons why RS may improve or prevent 312
 colonic inflammation. RS is the portion of starch that 313
 resists digestion in the small intestine and enters the large 314
 bowel, and so contributes to total dietary fibre intake [41, 315
 42]. In the large bowel, RS is fermented by the microbiota, 316
 resulting in the production of butyrate which improves 317
 colonic physiology [42, 43] as well as providing a major 318
 source of energy for the growth of microorganisms [44]. 319
 Although SCFA levels were not measured in the current 320
 study, we have previously reported significant increases in 321
 total SCFA and butyrate in mice and rats consuming sim- 322
 ilar dietary RS levels to those used in the present study [40, 323
 45]. Additional studies have also shown that adding RS to a 324
 diet high in red meat profoundly alters protein and carbo- 325
 hydrate fermentation in a manner that can be interpreted as 326
 constituting a more favourable luminal environment [40, 327
 46–48]. 328

The gut bacterial population profiles of individuals with 329
 IBD are altered compared to healthy individuals, including 330
 a reduced overall diversity of microbes [28, 29, 49]. In this 331

Author Proof

Table 3 Numbers of target bacteria in treatment pools of cecal digesta

Target	Numbers per g digesta (Mean)			
	Control	RS	RM	RM + RS
<i>Akkermansia muciniphila</i>	1.72×10^8	1.15×10^8	3.99×10^6	1.18×10^7
<i>Bacteroides-Prevotella</i> group	3.58×10^8	4.9×10^8	1.13×10^9	NA
<i>Bifidobacterium</i> spp.	1.99×10^8	2.47×10^8	3.63×10^5	8.92×10^5
<i>Clostridium coccoides</i> group	7.07×10^8	1.33×10^9	5.39×10^8	5.17×10^5
<i>Clostridium leptum</i> group	1.08×10^8	1.98×10^8	1.44×10^6	9.21×10^6
<i>Enterococcus</i> spp.	2.38×10^7	9.20×10^6	1.83×10^6	1.72×10^5
<i>Escherichia coli</i>	5.09×10^8	1.58×10^8	1.94×10^9	5.70×10^5
<i>Faecalibacterium prausnitzii</i>	1.35×10^7	2.14×10^7	3.30×10^5	2.31×10^6
<i>Parabacteroides distasonis</i>	3.90×10^7	3.81×10^7	6.05×10^6	1.59×10^5
<i>Ruminococcus bromii</i>	9.15×10^4	1.82×10^5	NA	3.91×10^4
<i>Ruminococcus gnavus</i>	6.73×10^6	1.06×10^7	1.02×10^5	2.98×10^5
SRB_aps	1.48×10^7	1.93×10^7	NA	NA

SRB Sulfate-reducing bacteria, aps adenosine-5-phosphosulfate reductase gene, NA not available

study, we have examined effects of treatment on gut populations of a range of bacteria that are implicated in IBD or bowel health broadly. Our targets included *F. prausnitzii*, *R. bromii*, *P. distasonis*, the *C. coccoides* group and the *C. leptum* group that are associated with fermentation of complex carbohydrates and production of SCFA, and generally thought to provide benefit. Numbers of the latter two groups are also low in IBD [49], and *F. prausnitzii* is of additional interest due to its anti-inflammatory effects and lower numbers in the gut of individuals with colitis [50, 51]. Populations of *A. muciniphila* and *R. gnavus*, which contribute to mucus turnover and are altered in IBD [29], were also examined. Other targets were accepted markers of bowel health (*Bifidobacterium* spp. and *Lactobacillus* spp.), bacteria often associated with poor health outcomes (*E. coli*, *Enterococcus* spp.), and some groups that may play a role in health (*Bacteroides-Prevotella*, sulfate-reducing bacteria). Although the contribution of bacteria to the increased colonic damage that can occur in response to diets high in red meat is poorly defined, it is likely that they have a role as many of the products that are produced in the gut following bacterial fermentation of proteins are toxic. Similarly, bacteria are implicated in the protection against dietary protein-induced increases in colonic DNA damage that occurs in response to consumption of RS, primarily because production of SCFA via bacterial action, especially of butyrate, correlates strongly with protection [52]. In our study, we were unable to carry out definitive analyses of the gut microbiota due to constraints related to the amount of digesta available. However, our subjective analysis of numbers of a range of bacterial targets suggests there were changes in the abundance of some bacteria in response to red meat and RS treatments, and these changes could contribute to the

reported outcomes. Some of the changes suggested by our limited microbial data, such as drops in numbers of *A. muciniphila* and bacteria belonging to the *C. coccoides* and *C. leptum* groups in response to the red meat diet in DSS-treated mice, are also observed in the large bowel mucosa of humans with Crohn's disease [29, 49], suggesting similar mechanisms may be at play in our DSS animal model of colitis.

In conclusion, dietary red meat worsens the histopathology, inflammatory indicators and clinical signs in DSS-induced colitis, whereas resistant starch added to a high red meat diet reduces the severity of colitis. Changes in the gut microbiota by consumption of red meat and resistant starch may play a role in the modulation of the severity of the DSS-induced colitis. Further studies are required to elucidate the mechanisms involved in the worsening of colitis by red meat and beneficial effects of resistant starch in a suitable model.

Acknowledgments This work was supported by the National Health and Medical Research Council (grant ID 535079) and CSIRO Preventative Health National Research Flagship.

Conflict of interest None.

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