

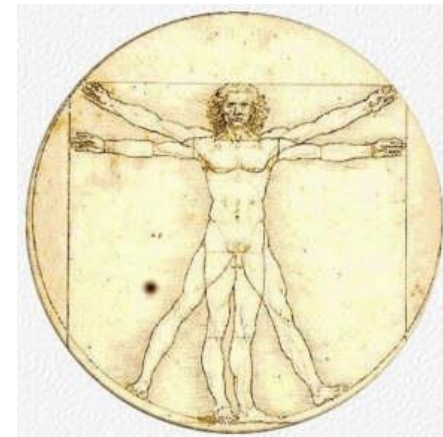
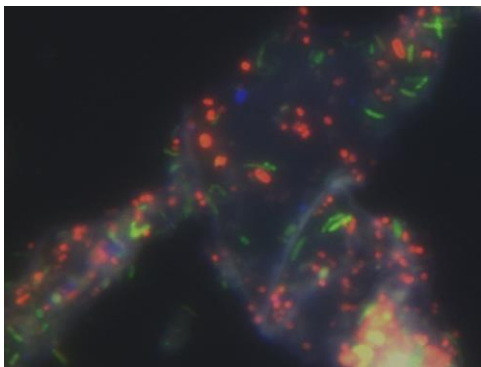


Diet, intestinal microbial communities and host health

Alan Walker

Rowett Institute of Nutrition and Health,
University of Aberdeen

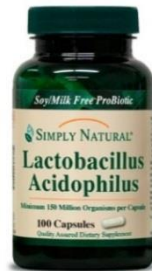
8/9/15



The human intestinal microbiota

- Human large intestine hosts an enormous number of microbes (“microbiota”)
 - 100,000,000,000,000 (10^{14}) bacterial cells
 - Greater than the number of human cells

- Thousands of different species colonise

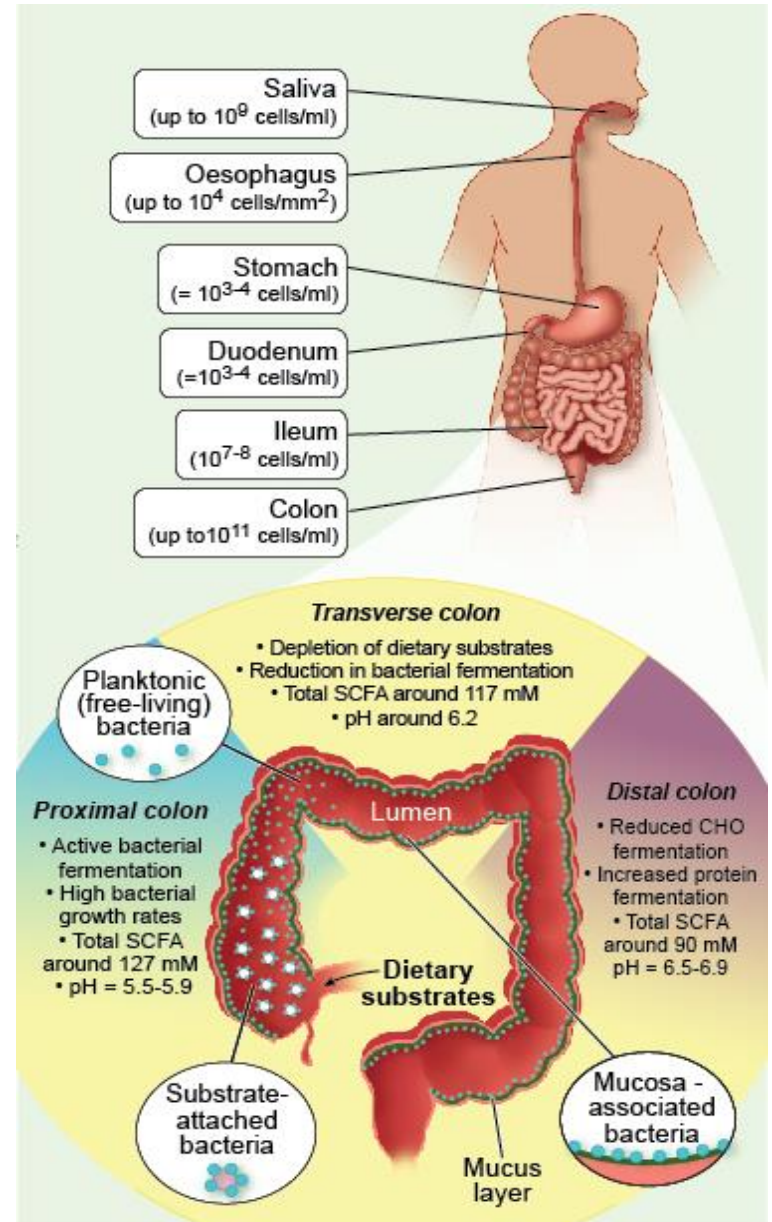


- Most are strict anaerobes
- Each host have a unique and largely stable microbiota

- The cumulative “microbiome” of these cells contains **400x** more unique genes than the human genome
 - est. 8 million vs ~20-25,000

- Plays a number of key roles in maintaining host health

- Enhances resistance against infection
- Immune system development/maintenance
- Beneficial compound production
- Breakdown dietary fibre



Principal substrates available for utilisation by intestinal microbes

Of dietary & intestinal origin:

Resistant starch

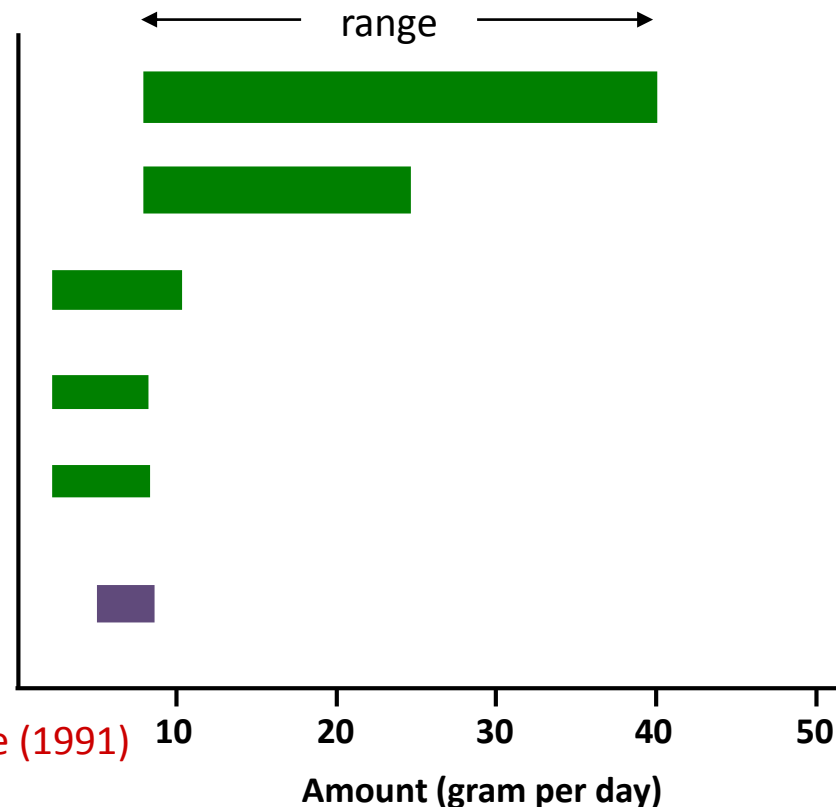
Non-starch polysaccharides

Unabsorbed sugars

Oligosaccharides

Dietary protein

Enzymes / secretions / mucus



Adapted from Cummings & Macfarlane (1991)

Digestibilities for plant cell wall polysaccharides – 7 subjects (Slavin *et al* J. Nut 1981)

Pure cellulose (Solka Flok)

minimal

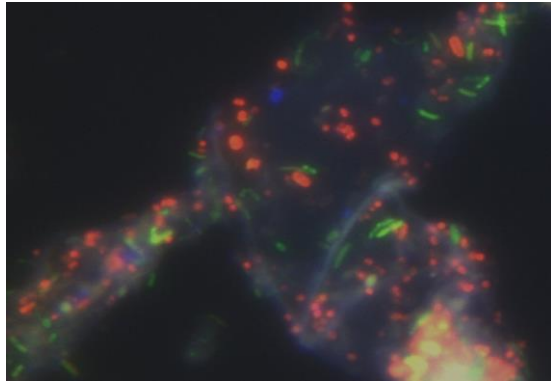
Cellulose (in normal diets)

69.7% (+/-10.7)

Hemicellulose

71.7% (+/- 5.4)

Fibre utilisation by gut microbes



complex polysaccharides

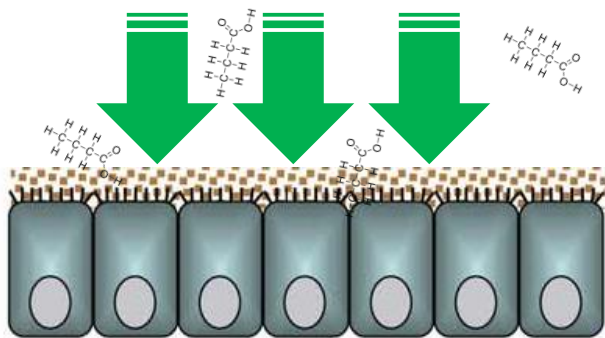
↓ Polysaccharide
degraders

oligo-, mono-saccharides

saccharolytic bacteria

↓ Anaerobic
fermentation

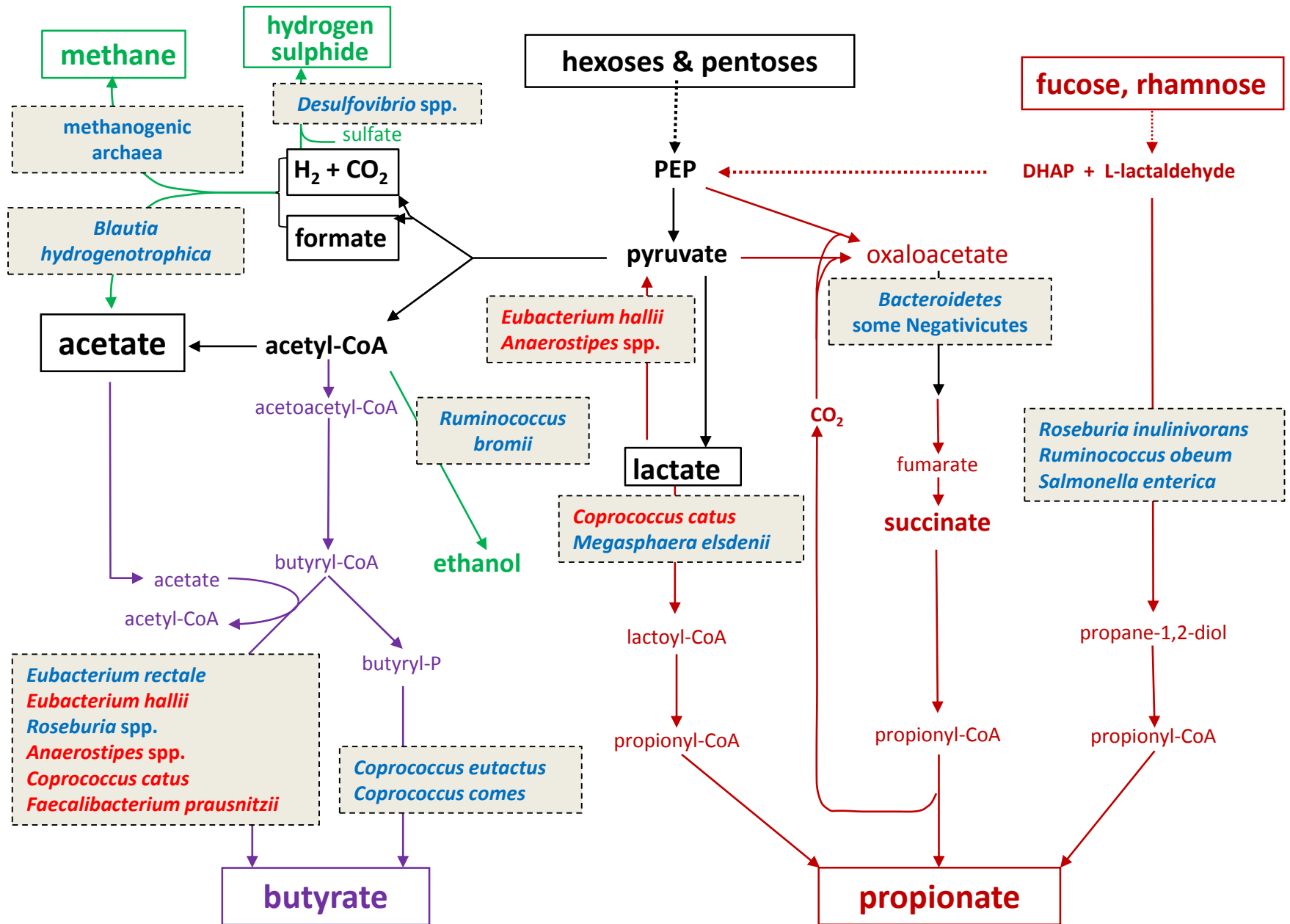
Short chain fatty acids



- Metabolise dietary components that escape digestion by human enzymes
 - Endows host with degradative capabilities they have not needed to evolve themselves
- Vitamin production
 - K, riboflavin (B₂), biotin (B₇), folic acid (B₉), cobalamin (B₁₂)
- Release of phytochemicals
 - Phenolic compounds etc
- Primary end products are short chain fatty acids
 - Acetate (C₂), propionate (C₃) and butyrate (C₄)
- SCFAs are symbiotic compounds
 - Gut epithelial cells grow on products of bacterial metabolism
 - Derive up to 70% of energy needs from bacterially-produced **butyrate**
 - Increases energy yield from diet (5 to 10% of caloric intake per day)

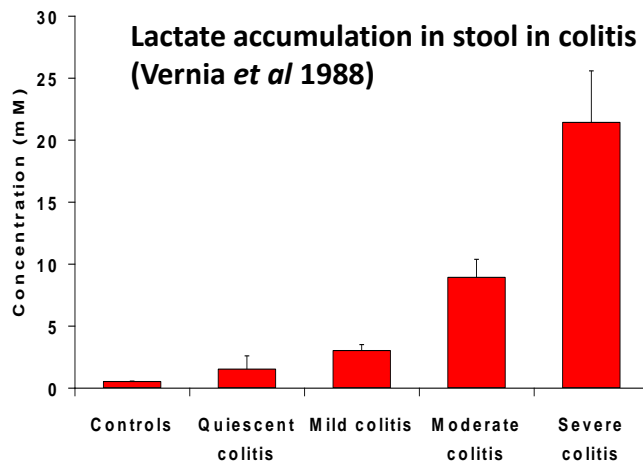
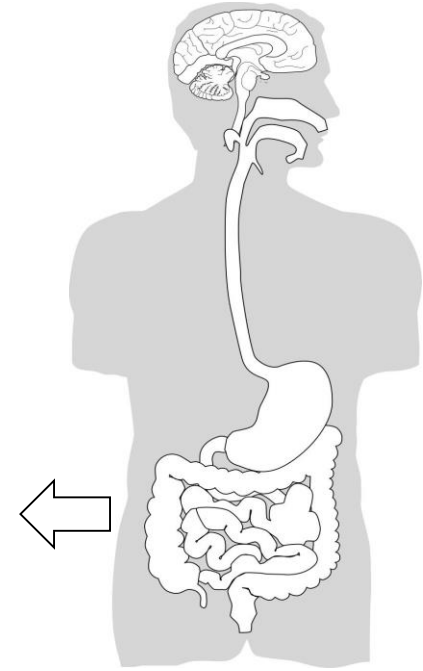


Major fermentation pathways



Impact of gut bacterial short chain fatty acids on the host

- Inhibition of histone deacetylase (*butyrate, propionate*)
- Altered mucosal gene expression, cell differentiation
- Protection against colorectal cancer, colitis (*butyrate*)
- Energy source for the colonic epithelium (*butyrate*)
- Anti-inflammatory effects (including stimulation of Tregs)
- Suppression of colitogenic pathogens (*acetate*)
- Stimulation of host receptors (FFAR2, FFAR3, GPR109)
- Influence on gut hormones (e.g. GLP-1, PYY) and satiety
- Influences upon gut transit, gut barrier function
- Peripheral energy supply, lipogenesis (*acetate*)
- Promote intestinal gluconeogenesis (*butyrate, propionate*)



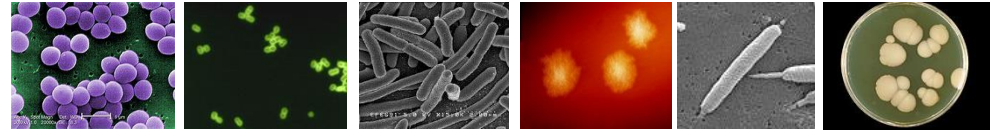
Lactate accumulation shown to be due mainly to reduced lactate utilization by other bacteria at pH 5.2 (¹³C lactate)

Belenguer, A. *et al* (2007) *A.E.M.* **73**, 6526-6533.



Host-associated microbes in disease

- Many diseases are caused by microbes that normally live asymptotically on the host

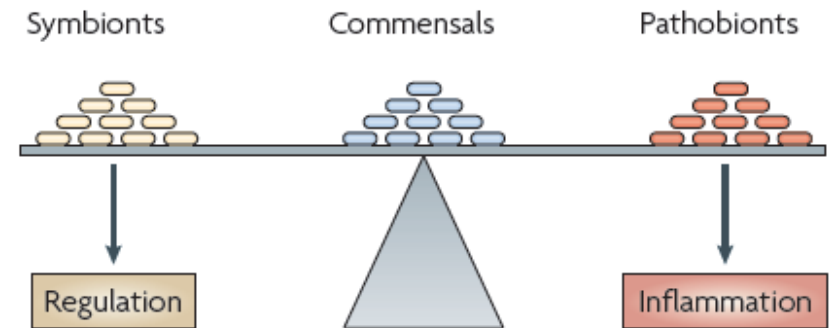


- e.g. *Staphylococcus aureus* (MRSA), Strep throat, gingivitis, acne, meningitis, pneumonia, *C. difficile* diarrhoea, thrush, UTIs, gastric cancer (*Helicobacter pylori*).

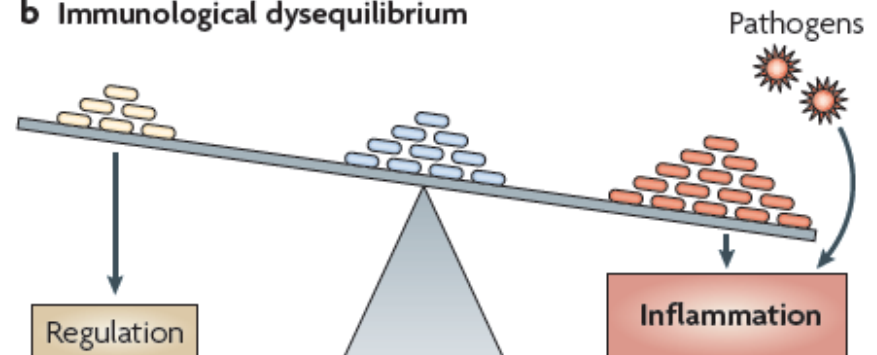
- A general imbalance (“dysbiosis”) in microbiota composition has been implicated in many disorders

- e.g. Inflammatory bowel diseases, bowel cancer, irritable bowel syndrome, diabetes, liver disease, allergies, atherosclerosis

a Immunological equilibrium



b Immunological dysequilibrium

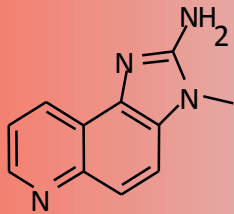


Impact of microbially derived metabolites on the host

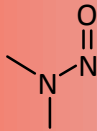


Damaging

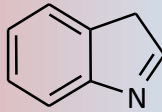
Heterocyclic Amines



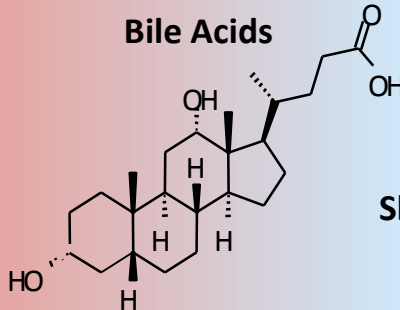
N-Nitrosamines



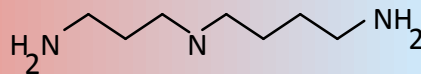
Indoles



Bile Acids



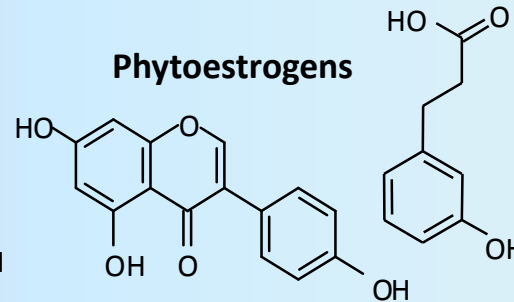
Polyamines



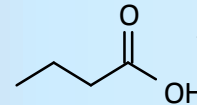
Protective

Anti-Inflammatory Molecules

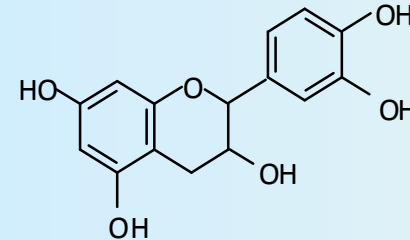
Phytoestrogens



Short Chain Fatty Acids



Anti-oxidant Molecules

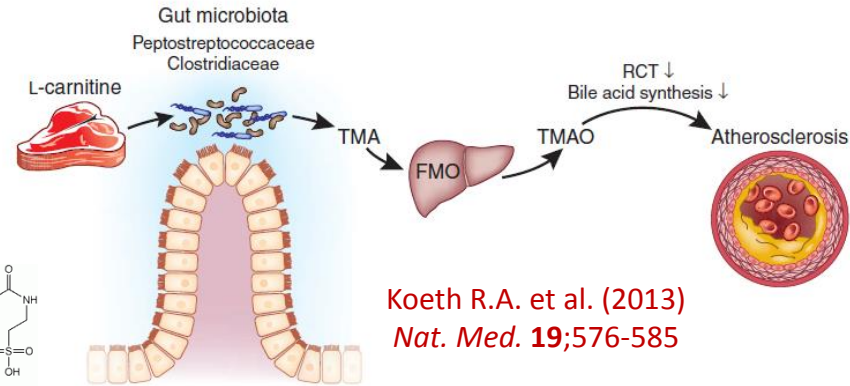


The "Western" diet, microbiota and host health



High-protein, reduced-carbohydrate weight-loss diets promote metabolite profiles likely to be detrimental to colonic health¹⁻⁴

Wendy R Russell, Silvia W Gratz, Sylvia H Duncan, Grietje Holtrop, Jennifer Ince, Lorraine Scobbie, Garry Duncan, Alexandra M Johnstone, Gerald E Lobley, R John Wallace, Garry G Duthie, and Harry J Flint

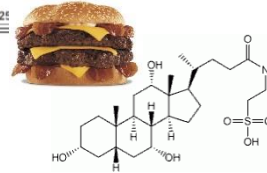


LETTER

doi:10.1038/nature11225

Dietary-fat-induced taurocholic acid promotes pathobiont expansion and colitis in *Il10*^{-/-} mice

Suzanne Devkota¹, Yunwei Wang¹, Mark W. Musch¹, Vanessa Leone¹, Hannah Fehlner-Peach¹, Anuradha Nadimpalli¹, Dionysios A. Antonopoulos², Bana Jabri¹ & Eugene B. Chang¹



nature COMMUNICATIONS

ARTICLE

Received 23 Jun 2014 | Accepted 14 Nov 2014 | Published 23 Dec 2014

DOI: 10.1038/ncomms6864 OPEN

Dietary cholesterol directly induces acute inflammasome-dependent intestinal inflammation

Fränze Progatzy¹, Navjyot J. Sangha¹, Nagisa Yoshida¹, Marie McBrien¹, Jackie Cheung¹, Alice Shia^{1,2}, James Scott², Julian R. Marchesi^{3,4,5,6}, Jonathan R. Lamb¹, Laurence Bugeon^{1*} & Margaret J. Dallman^{1*}

doi:10.1038/nature13793

ARTICLE

Artificial sweeteners induce glucose intolerance by altering the gut microbiota

Jotham Suez¹, Tal Korem^{2*}, David Zeevi^{2*}, Gili Zilberman-Schapira^{1*}, Christoph A. Thaiss¹, Ori Maza¹, David Israeli³, Niv Zmora^{4,5,6}, Shlomit Gilad¹, Adina Weinberger¹, Yael Kuperman¹, Alon Harmelin¹, Ilana Kolodkin-Gal¹, Hagit Shapiro¹, Zamir Halperin^{1,6}, Eran Segal¹ & Eran Elinav¹

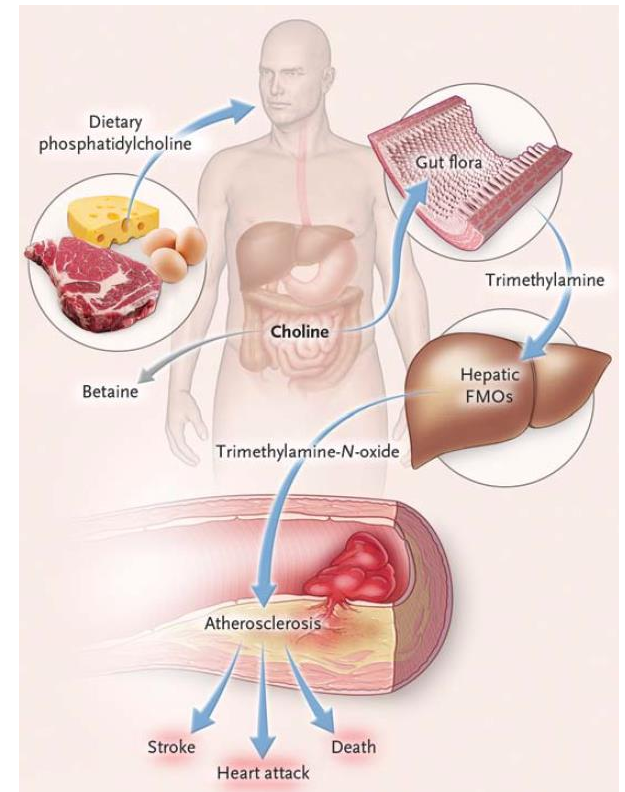


LETTER

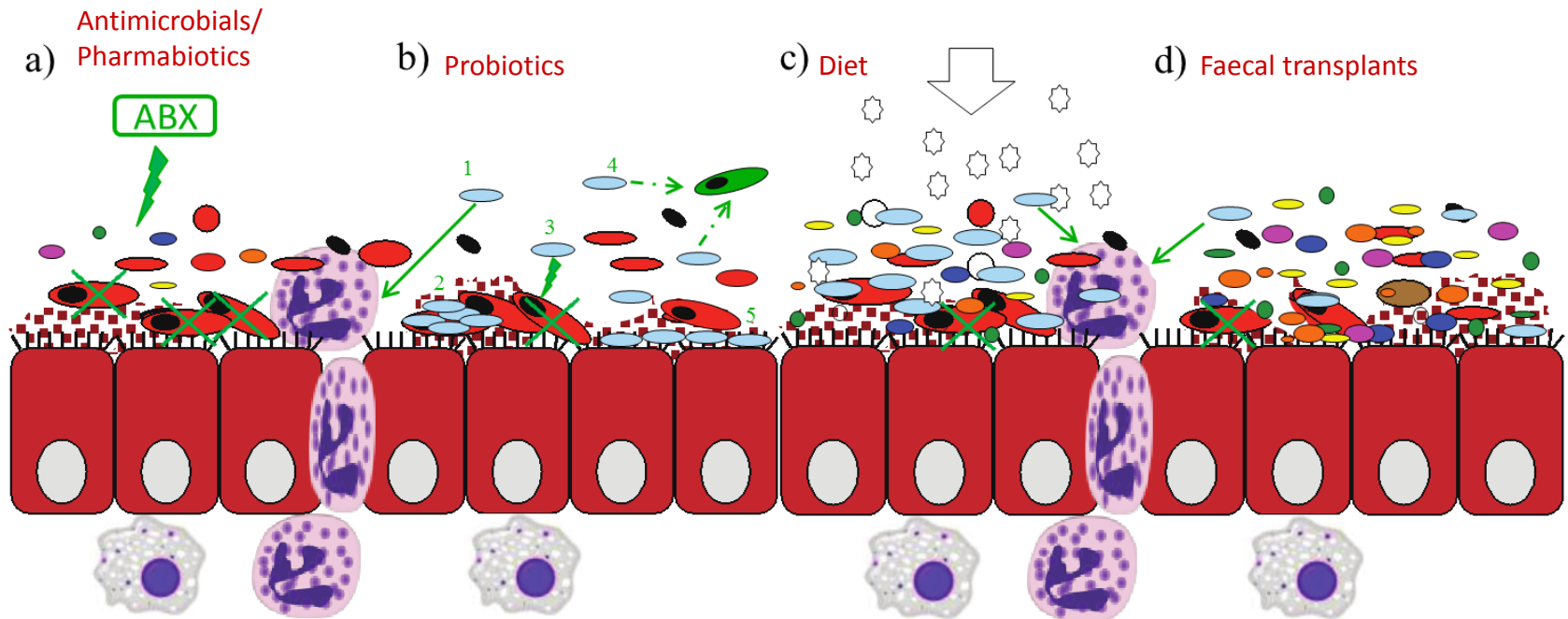
doi:10.1038/nature14232

Dietary emulsifiers impact the mouse gut microbiota promoting colitis and metabolic syndrome





Benoit Chassaing¹, Omry Koren², Julia K. Goodrich³, Angela C. Poole³, Shanthi Srinivasan⁴, Ruth E. Ley³ & Andrew T. Gewirtz¹



Altering the intestinal microbiota



Key:-

 Pathogen (e.g. *C. difficile*)  *Enterobacteriaceae*  Probiotic / beneficial microbe  Microbiota

- The aim of all of these approaches is to shift the composition of the microbiota to a more beneficial state
 - Is targeted manipulation possible via alterations in host diet?



Short- v long-term impacts of diet on the intestinal microbiota

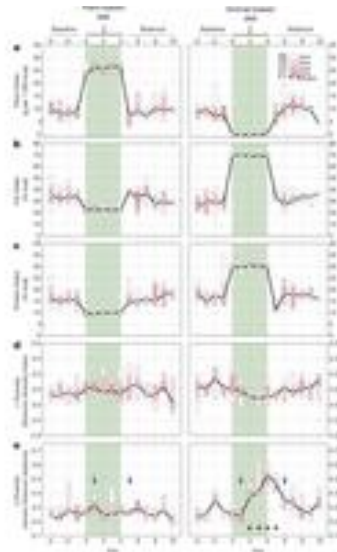
LETTER

doi:10.1038/nature12820

Diet rapidly and reproducibly alters the human gut microbiome

Lawrence A. David^{1,2†}, Corinne F. Maurice¹, Rachel N. Carmody¹, David B. Gootenberg¹, Julie E. Button¹, Benjamin E. Wolfe¹, Alisha V. Ling³, A. Sloan Devlin⁴, Yug Varma⁴, Michael A. Fischbach⁴, Sudha B. Biddinger³, Rachel J. Dutton¹ & Peter J. Turnbaugh¹

Figure 1: Short-term diet alters the gut microbiota.



- Short term dietary regimes can result in reproducible *but limited* microbiota response

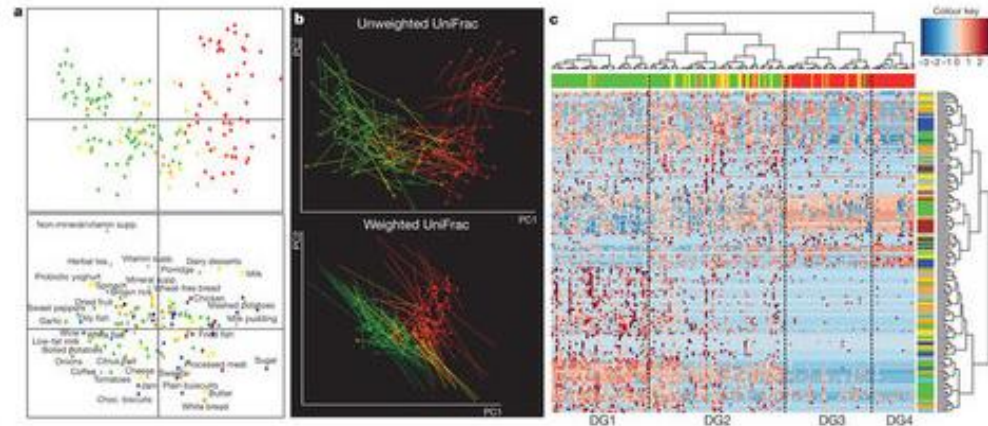
ARTICLE

doi:10.1038/nature11319

Gut microbiota composition correlates with diet and health in the elderly

Marcus J. Claesson^{1,2*}, Ian B. Jeffery^{1,2*}, Susana Conde³, Susan E. Power¹, Eibhlís M. O'Connor^{1,2}, Stobhán Cusack¹, Hugh M. B. Harris⁴, Mairead Coakley⁴, Bhuvanewari Lakshminarayanan⁴, Orla O'Sullivan⁴, Gerald F. Fitzgerald^{1,2}, Jennifer Deane⁵, Michael O'Connor^{5,6}, Norma Harnedy^{5,6}, Kieran O'Connor^{6,7,8}, Denis O'Mahony^{5,6,8}, Douwe van Sinderen^{1,2}, Martina Wallace¹, Lorraine Brennan⁹, Catherine Stanton^{2,4}, Julian R. Marchesi¹⁰, Anthony P. Fitzgerald^{3,11}, Fergus Shanahan^{2,12}, Colin Hill^{1,7}, R. Paul Ross^{2,4} & Paul W. O'Toole^{1,2}

Figure 2: Dietary patterns in community location correlate with separations based on microbiota composition.



- Changes in long-term dietary patterns illicit extensive changes in microbiota composition



Disappearing human microbiota?

- Have host behavioural changes in the urbanisation era introduced changes in microbiota composition?

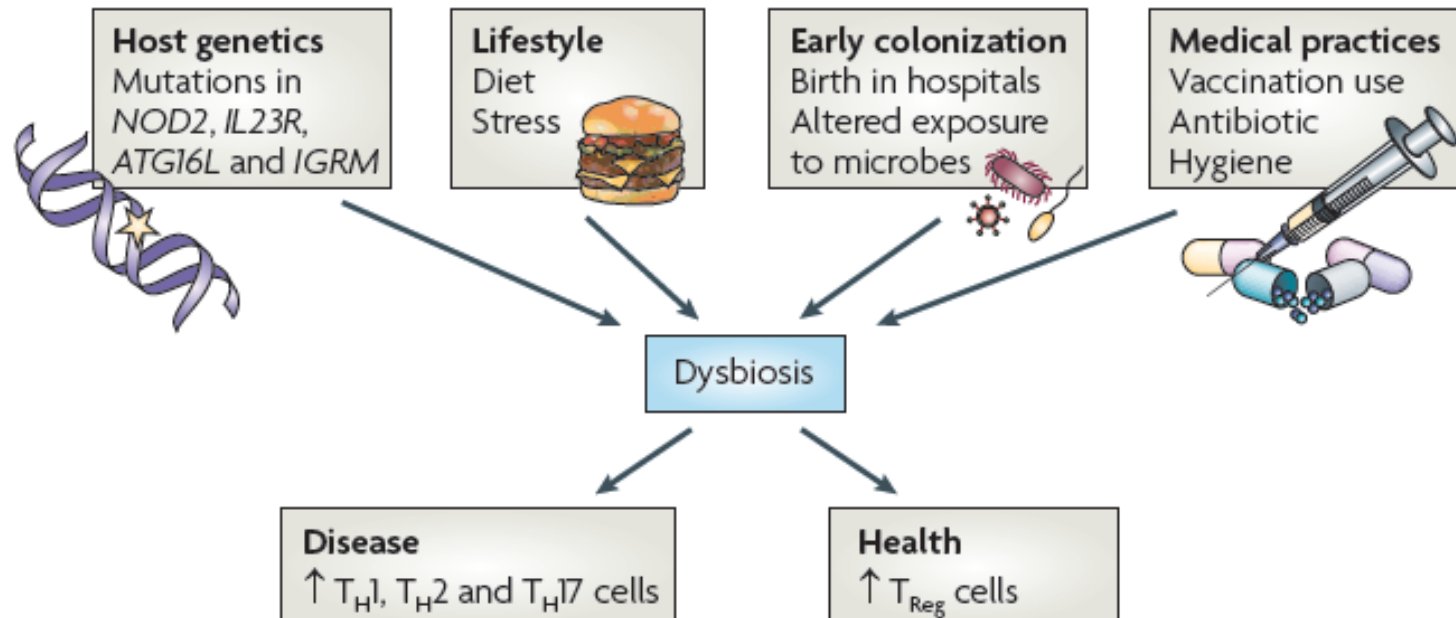
ESSAY

What are the consequences of the disappearing human microbiota?

Martin J. Blaser and Stanley Falkow

The 'disappearing microbiota' hypothesis [...] suggests [...] developments over the past century [...] contributed to a shift in the [...] species and types of microorganism in the gut

Hunter (2012) EMBO reports.13, 498–500

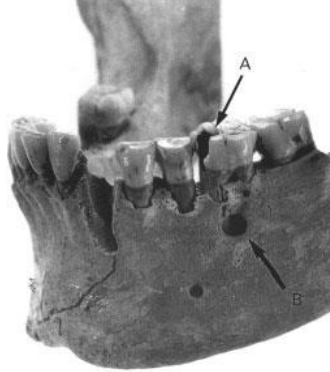


Link between diet, oral microbiota and health

Hunter-gatherer



Neolithic agriculturist



Medieval agriculturist

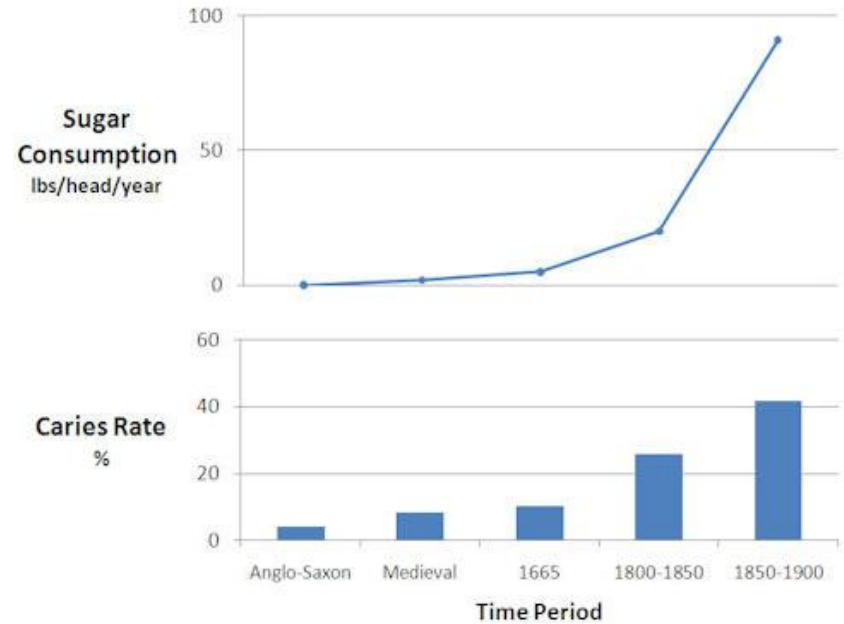
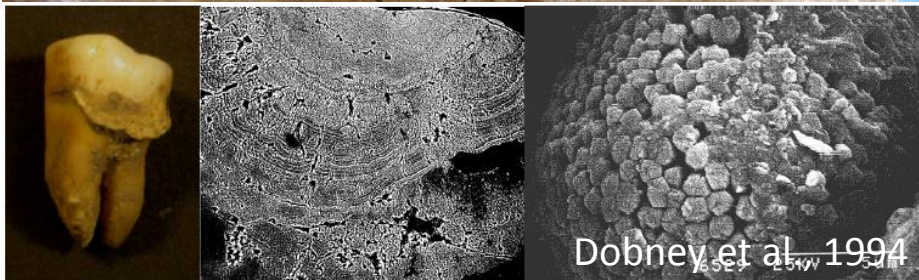
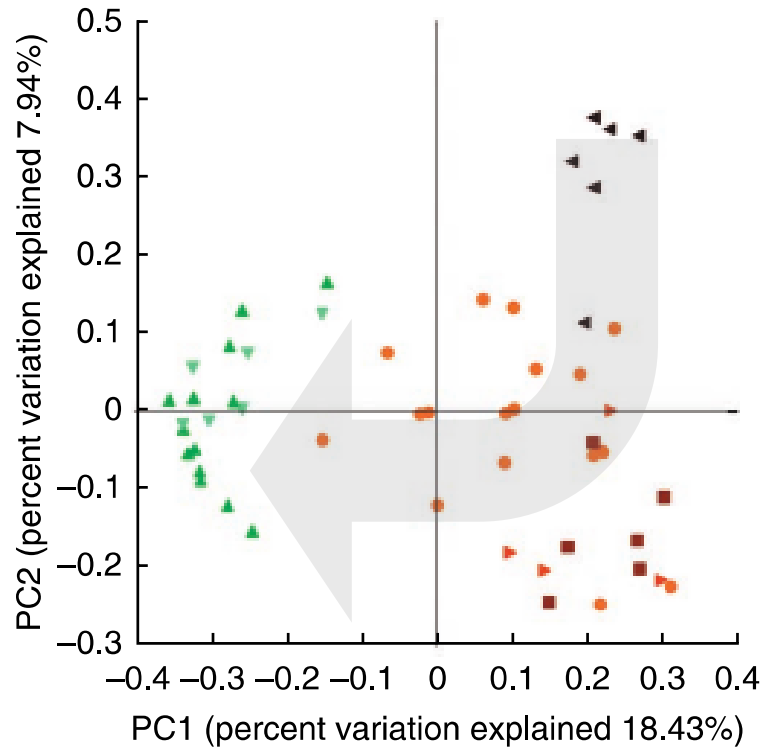


Image: Dr Jo Buckburry (re-plotted from Moore and Corbett 1978)
<http://www.leeds.ac.uk/yawya/bioarchaeology/Dental%20disease.html>

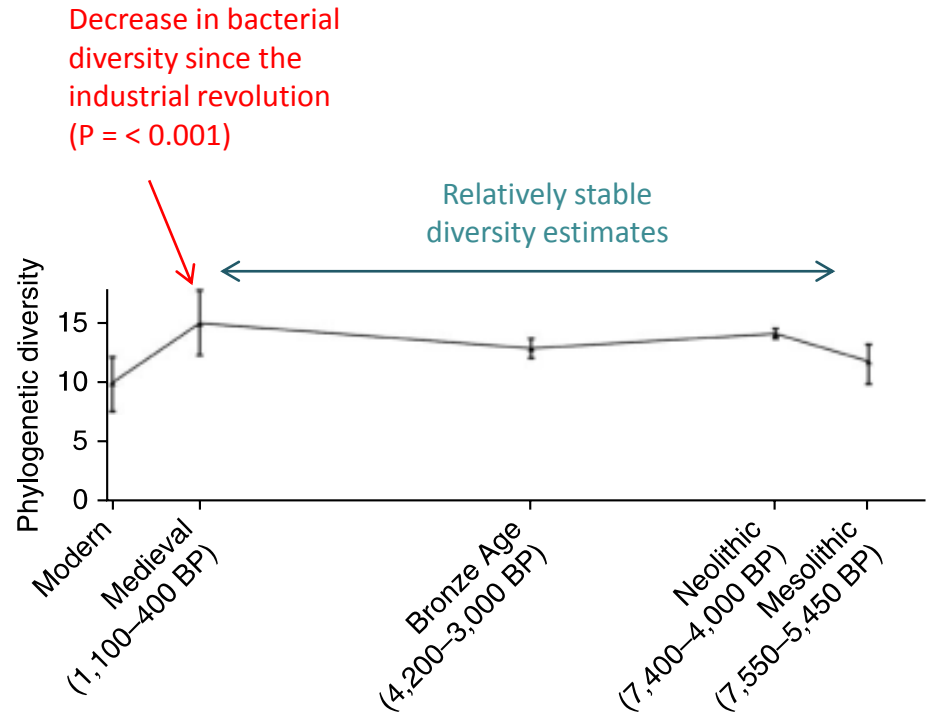
- Calcified plaque – one of the only preserved records of bacteria
- Densely colonised by oral microbiota

- Increased caries rate in skeletal records is linked to increased consumption of carbohydrates
- Unknown whether or not these changes were accompanied by shifts in microbiota composition

Oral microbiota changes through history

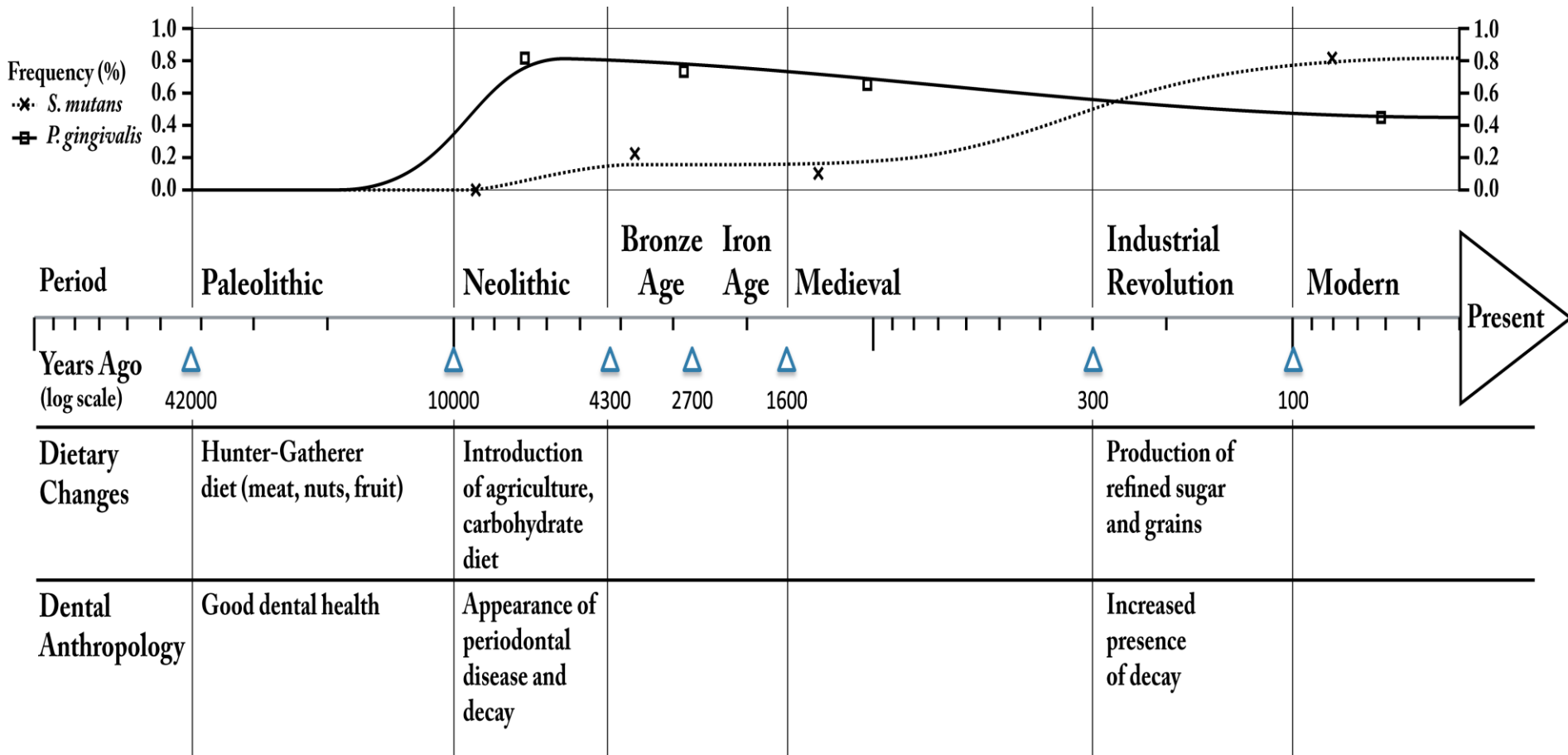


- ▲ Mesolithic ($n = 6$)
- ▶ Bronze Age ($n = 4$)
- Neolithic ($n = 6$)
- Medieval ($n = 18$)
- ▼ Modern calculus ($n = 6$)
- ▲ Modern plaque ($n = 13$)



- Non-pathogenic *Ruminococcaceae* associated with hunter-gatherers
- Decay-associated *Veillonellaceae* increase post-farming

Changes in predominant oral pathogens as a result of diet and culture

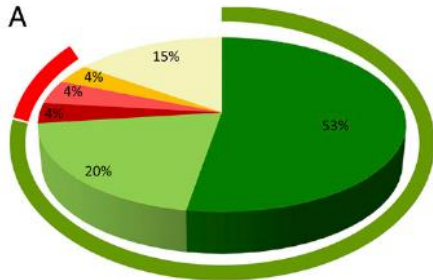


- These pathogens do not appear to be prominent in hunter-gatherers
- *Streptococcus mutans* became dominant relatively recently
- Shifts correlate with human behavioural changes (e.g. diet)

Regional variations in gut microbiota composition

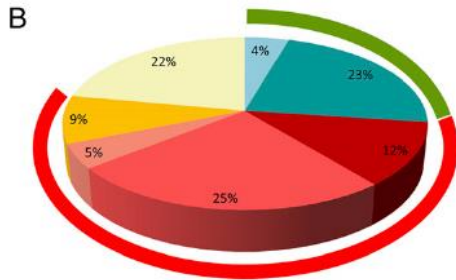
- We may need to reconsider what we think of as a normal “healthy” intestinal microbiota

De Filippo et al. PNAS (2010)



BF

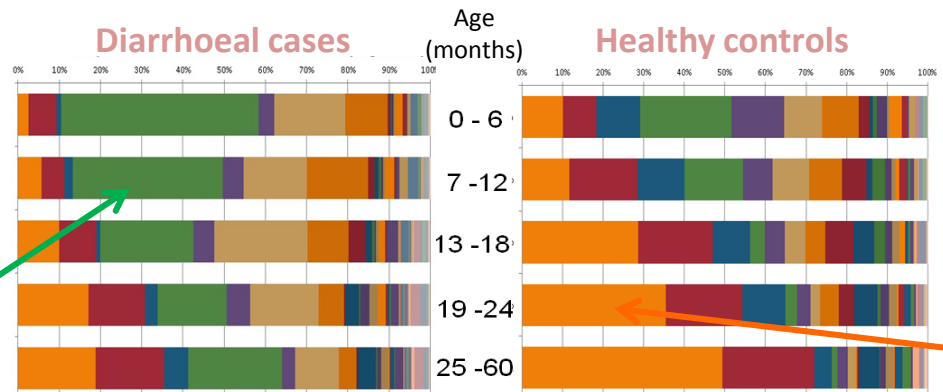
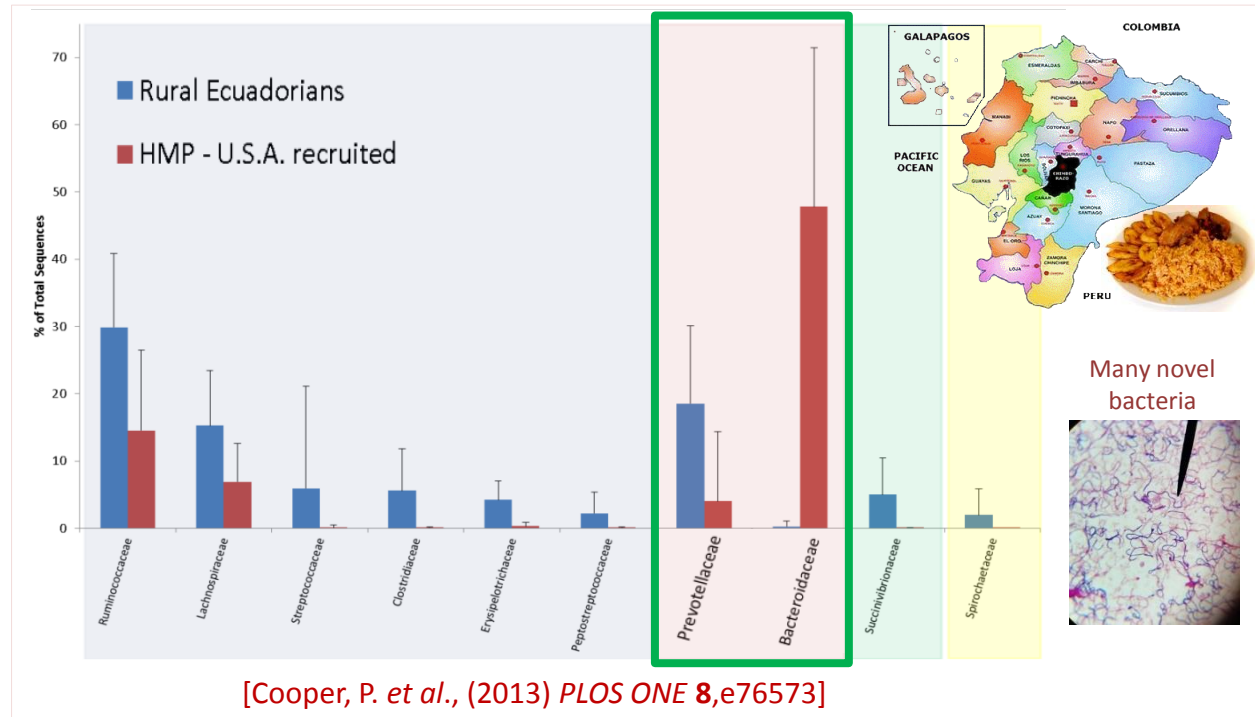
- Preotella } Bacteroidetes
- Xylanibacter } Bacteroidetes
- Acetomaculum } Firmicutes
- Faecalibacterium } Firmicutes
- Subdoligranulum } Firmicutes
- Others } Firmicutes



EU

- Alistipes } Bacteroidetes
- Bacteroides } Bacteroidetes
- Acetomaculum } Firmicutes
- Faecalibacterium } Firmicutes
- Roseburia } Firmicutes
- Subdoligranulum } Firmicutes
- Others } Firmicutes

Escherichia/Shigella

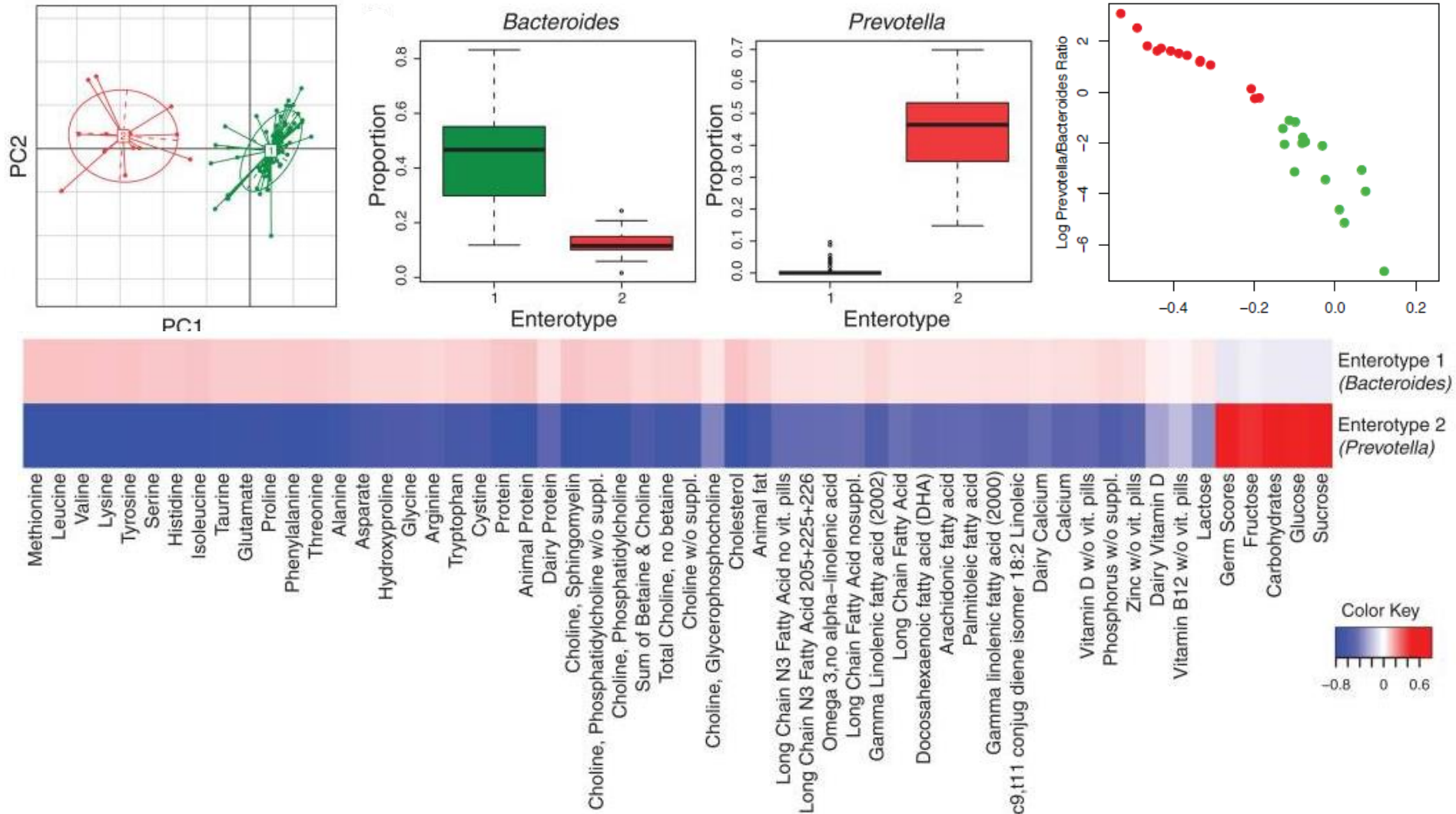


Children in :
 Kenya
 Mali
 The Gambia
 Bangladesh

Prevotella

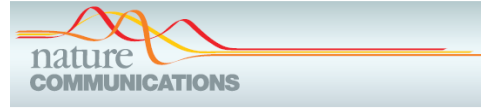
Links between host diet and microbiota structure

- Microbiota structures are associated with long term dietary consumption patterns



Links between host diet and microbiota activity

- O'Keefe *et al* performed 2-week food exchanges
- African Americans were fed a high-fibre, low-fat African-style diet and rural Africans a high-fat, low-fibre western-style diet
- Resulted in measurable changes in health biomarkers
 - ↑ butyrogenesis, ↓ secondary bile acid synthesis in the African Americans



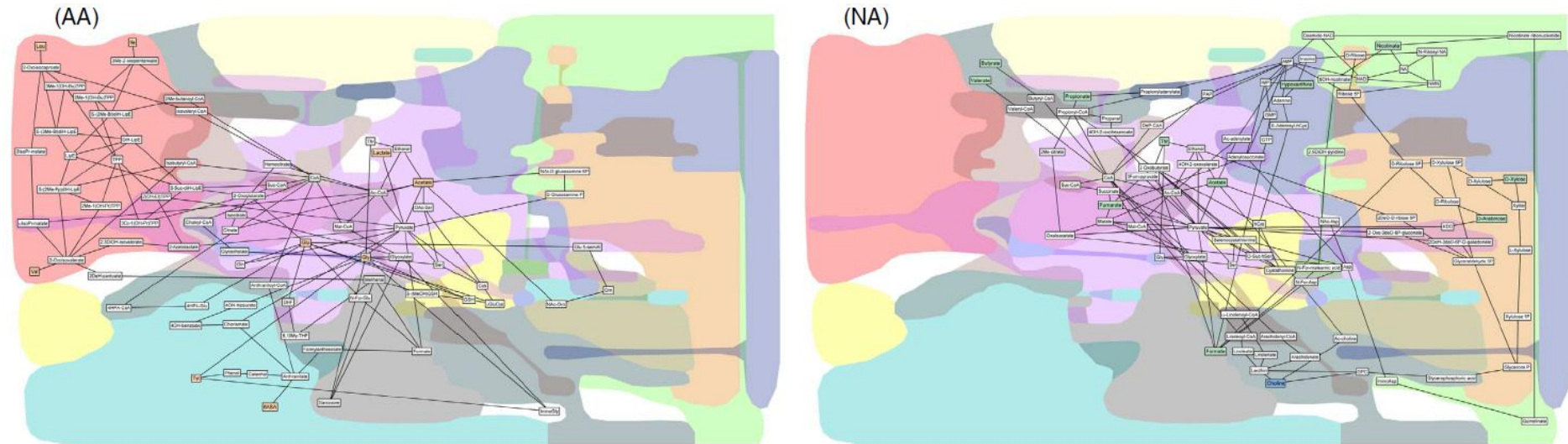
ARTICLE

Received 23 May 2014 | Accepted 20 Jan 2015 | Published 28 Apr 2015

DOI: 10.1038/ncomms7342

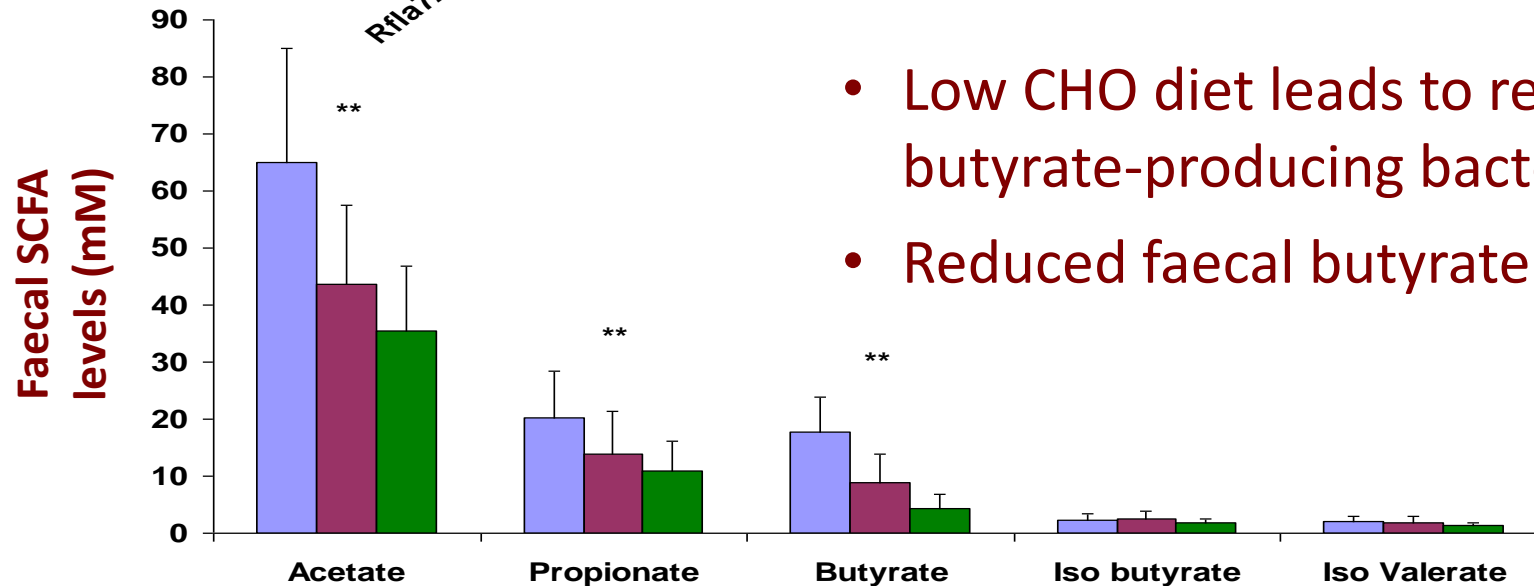
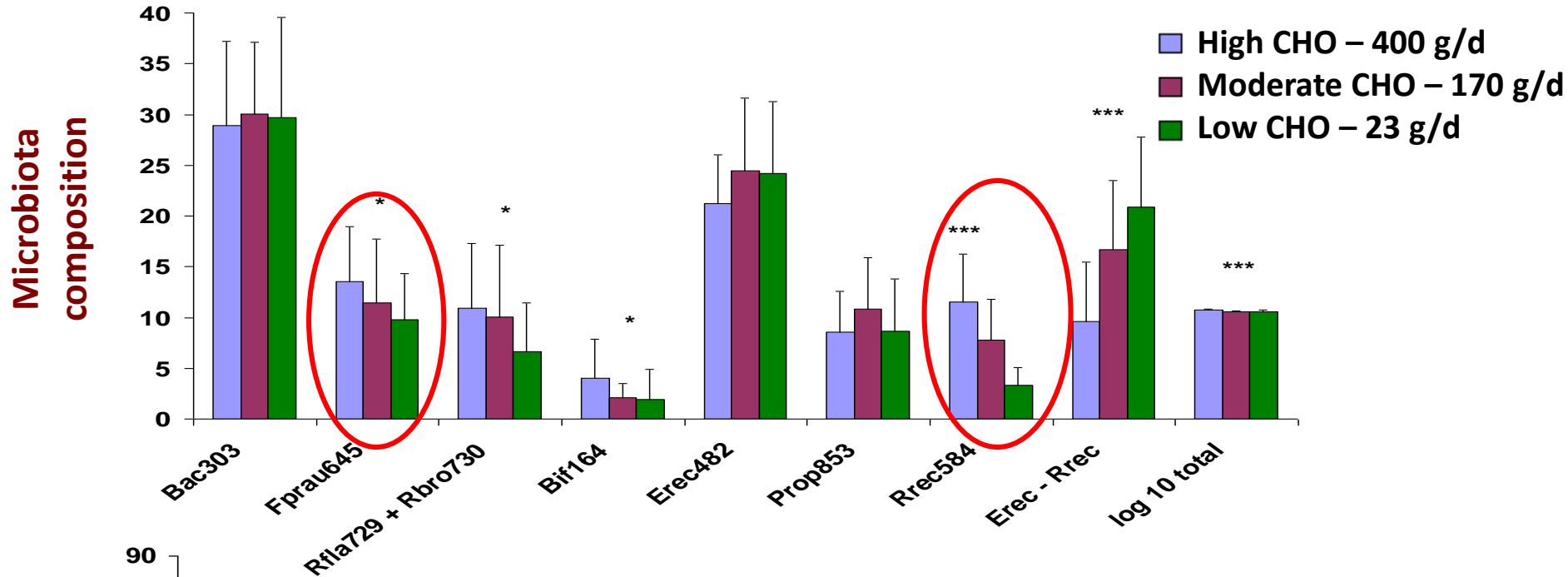
Fat, fibre and cancer risk in African Americans and rural Africans

Stephen J.D. O'Keefe¹, Jia V. Li², Leo Lahti^{3,4}, Junhai Ou¹, Franck Carbonero^{5,†}, Khaled Mohammed¹, Joram M. Posma², James Kinross², Elaine Wahl¹, Elizabeth Ruder⁶, Kishore Vipperla¹, Vasudevan Naidoo⁷, Lungile Mtshali⁷, Sebastian Tims³, Philippe G.B. Puylaert³, James DeLany⁸, Alyssa Krasinskas⁹, Ann C. Benefiel⁵, Hatem O. Kaseb¹, Keith Newton⁷, Jeremy K. Nicholson², Willem M. de Vos^{3,4,10}, H. Rex Gaskins⁵ & Erwin G. Zoetendal³



Pathways	Tricarboxylic acid (TCA) cycle	TCA anaplerotic metabolism	Aromatic and indole compounds	Lipid and fatty acid related metabolism	Bile acid metabolism	Branch-chain amino acid metabolism	Nicotinamide metabolism
	Coenzyme A metabolism	Purine and pyrimidine metabolism	Glycolysis and amino sugar metabolism	1-carbon and related metabolism	Sulphur metabolism	Urea cycle and related metabolites	Lysine metabolism
Metabolites	Higher after African diet	Higher after African-American diet	Higher in African home environment	Higher in African-American home environment	Higher in urine after African-American diet, higher in faeces after African diet		

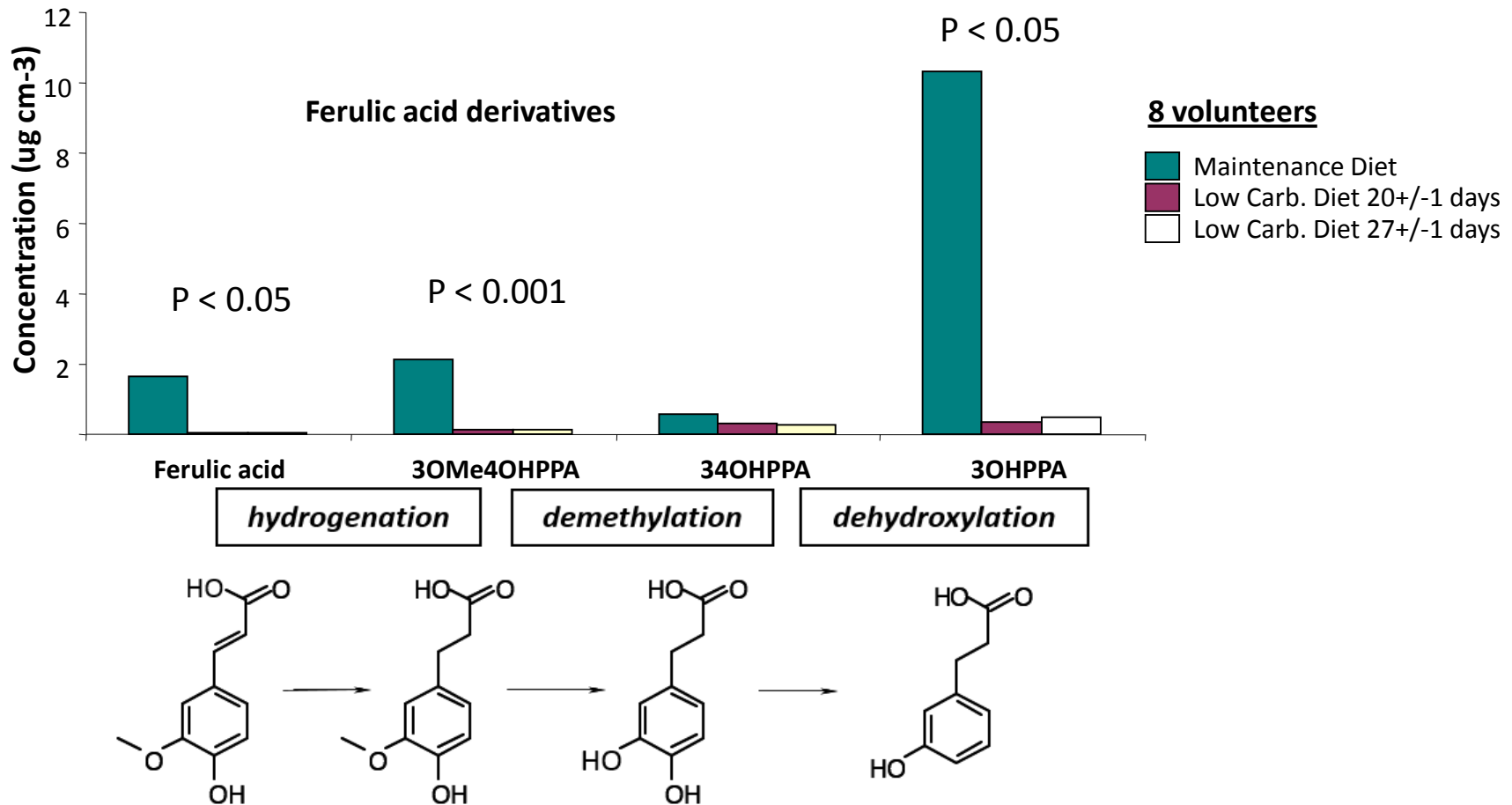
Impact of low carbohydrate weight loss diets



- Low CHO diet leads to reduction in butyrate-producing bacteria
- Reduced faecal butyrate levels

** P < 0.001

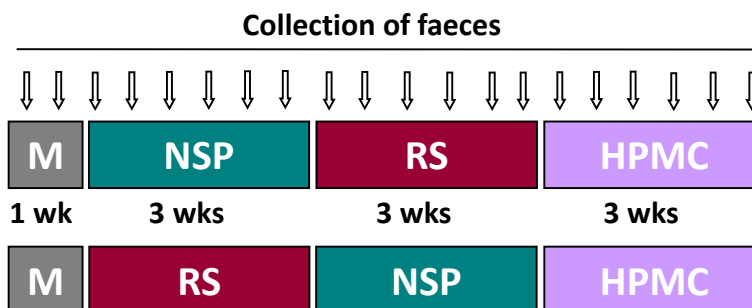
Major fibre derived phenolics in faecal samples



- Low carbohydrate, high protein intake resulted in reduced concentrations of potentially cancer-protective plant phenolic derivatives

Resistant starch vs non-starch polysaccharide diet

14 obese male volunteers with metabolic syndrome (mean age 54 years, mean BMI 39.4 kg/m²)



Mean dietary intake [g/d]:

Diet	CHO	Starch	RS	NSP	Protein	Fat
M	427	230	5	28	103	126
NSP	427	138	2	42	102	136
RS	434	275	26	13	109	127
HPMC	201	110	3	22	144	63

} Weight maintenance

} Weight loss

CHO: carbohydrate

M: Weight maintenance, mixed diet (55% energy from carbohydrates)

NSP : High non-starch polysaccharides (added bran), low RS

RS: High resistant starch (Type III), reduced NSP

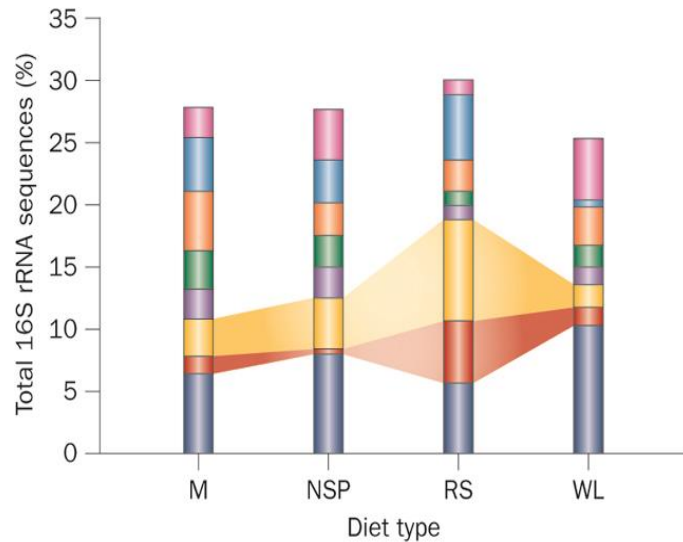
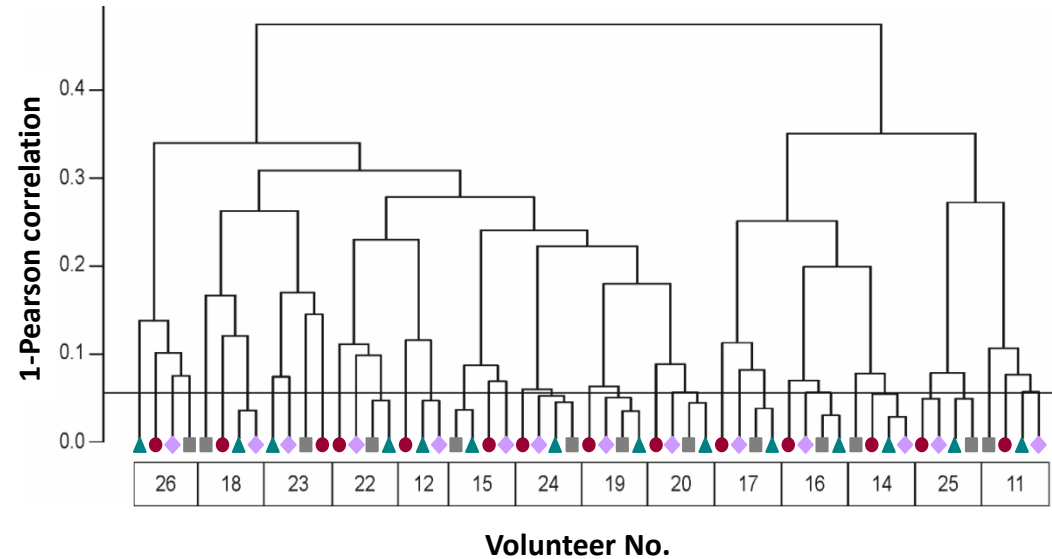
HPMC: Reduced calorie intake. Increased % protein, moderate carbohydrate



Resistant starch vs non-starch polysaccharide diet

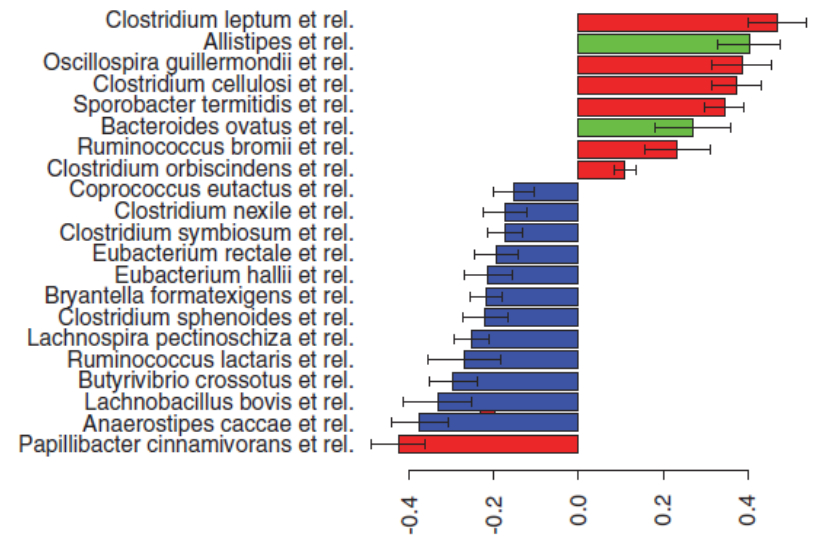
- Samples cluster by donor, not by diet
- Sub-group of bacteria are highly responsive to both the NSP and RS-enriched diets

- More *Ruminococcaceae* species increase with RS
- More *Lachnospiraceae* species increase with NSP

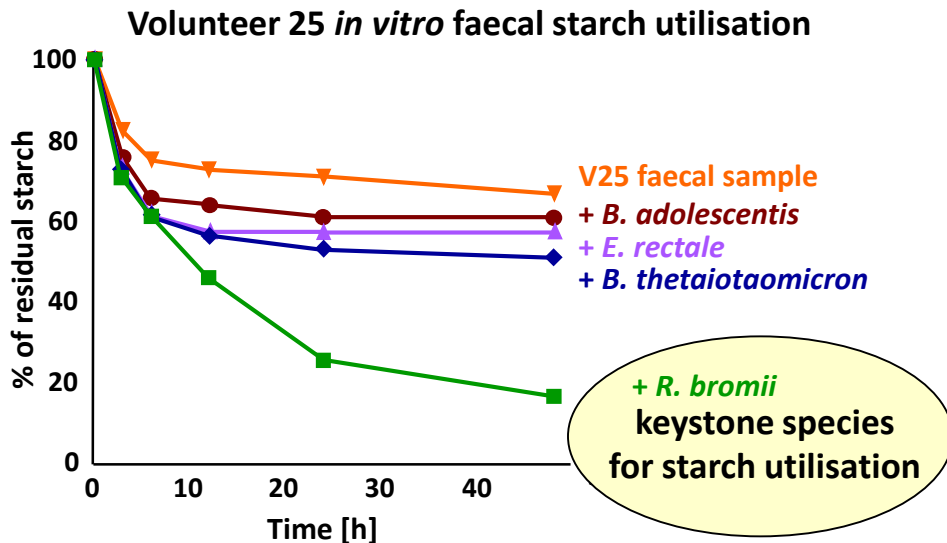
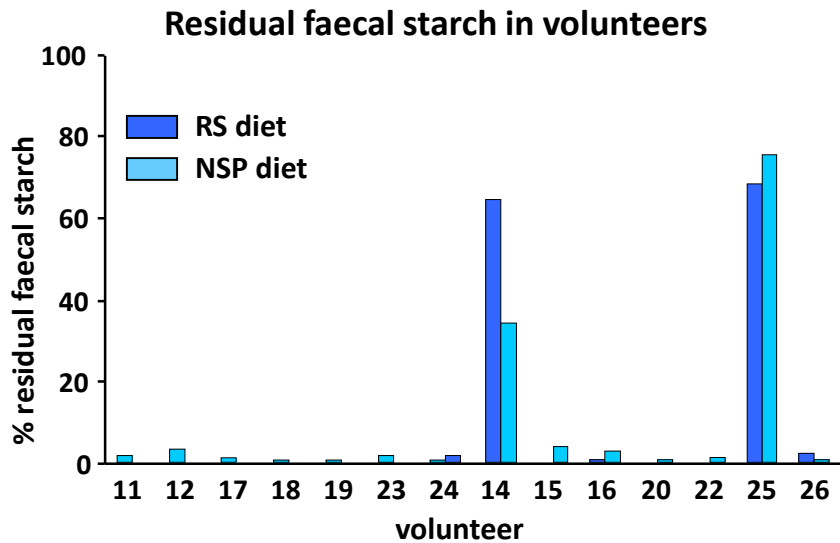
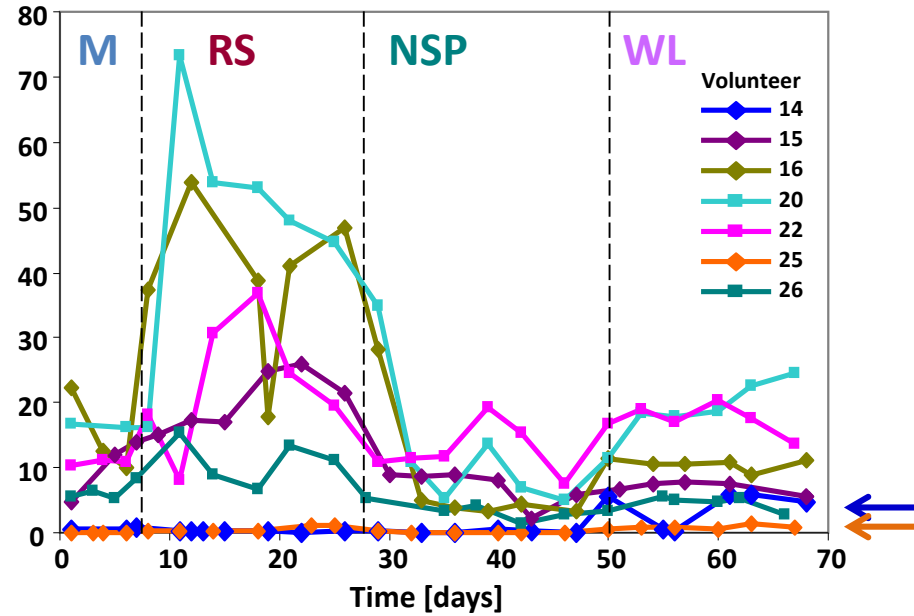
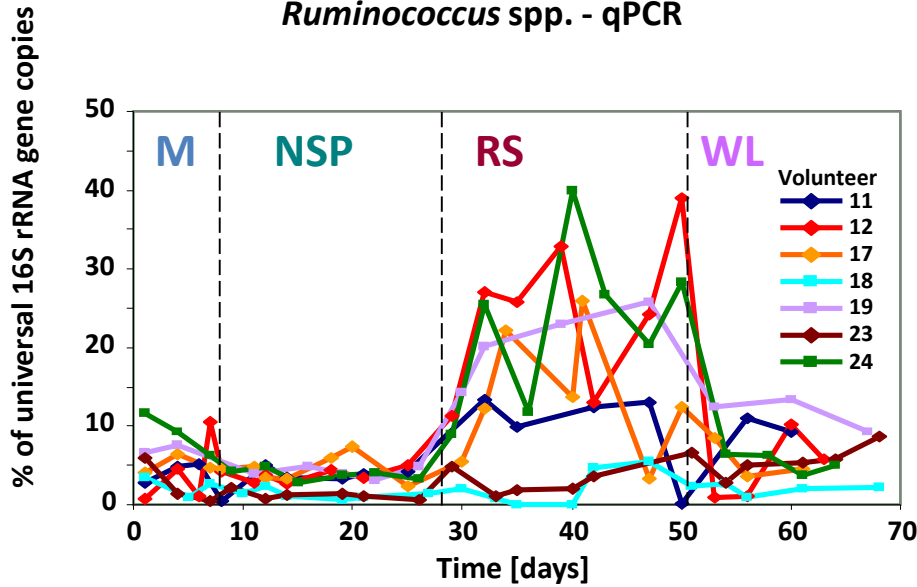


- *Bacteroides vulgatus*
- *Colinsella aerofaciens**
- *Clostridium clostridioforme*
- *Anaerostipes hadrus*
- *Eubacterium hallii*
- *Eubacterium rectale‡*
- *Ruminococcus bromii‡*
- *Faecalibacterium prausnit*

Stimulated by NSP Stimulated by RS



Keystone species within the microbiota



Links between diet, microbiota and health

Wheat, oats



Resistant starch



Pectin



Protein



NSP-degraders

Butyrivibrio fibrisolvens Bu
Bacteroides ovatus Pr Ac Su
Ruminococcus spp. Ac
Bacteroides xylanisolvens Pr Ac Su
Bacteroides cellulosilyticus Pr Ac Su

Starch degraders

Ruminococcus bromii Fo Ac Et
Eubacterium rectale Bu
Bifidobacterium adolescentis La Ac
Bacteroides thetaiotaomicron Pr Ac Su

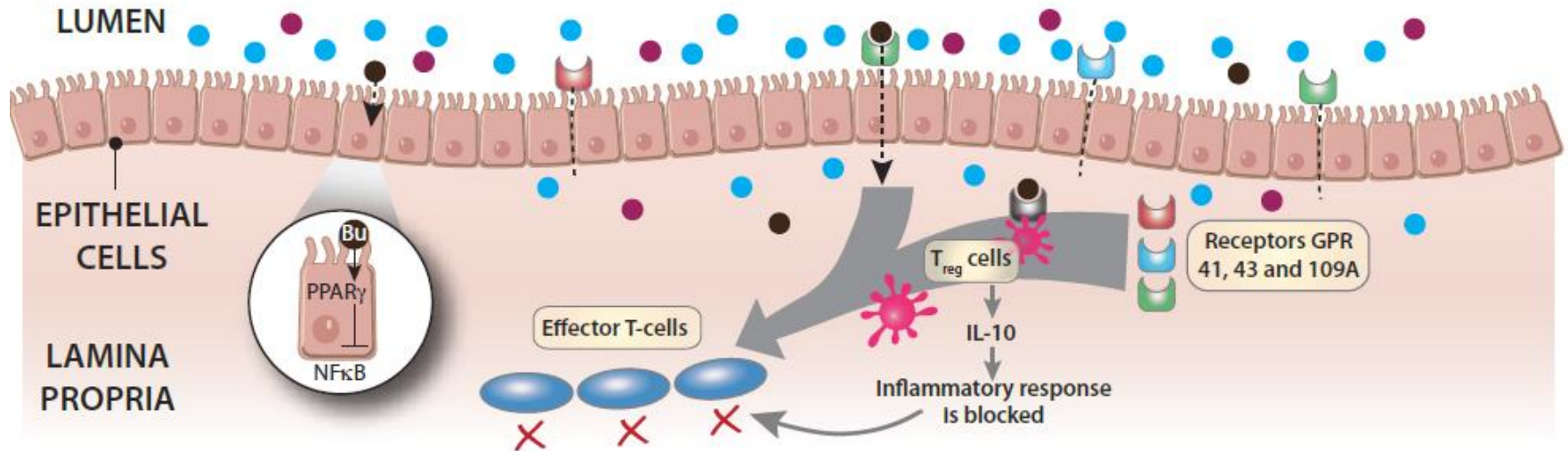
Pectin degraders

Bacteroides thetaiotaomicron Ac Su Pr
Faecalibacterium prausnitzii Bu

Peptide/amino acid utilisers

Bacteroides spp. Ac Su Pr
Clostridium bif fermentans Fo Ac

Cross feeding of break down products and metabolites. Main products detected in the colon are Pr Ac Bu

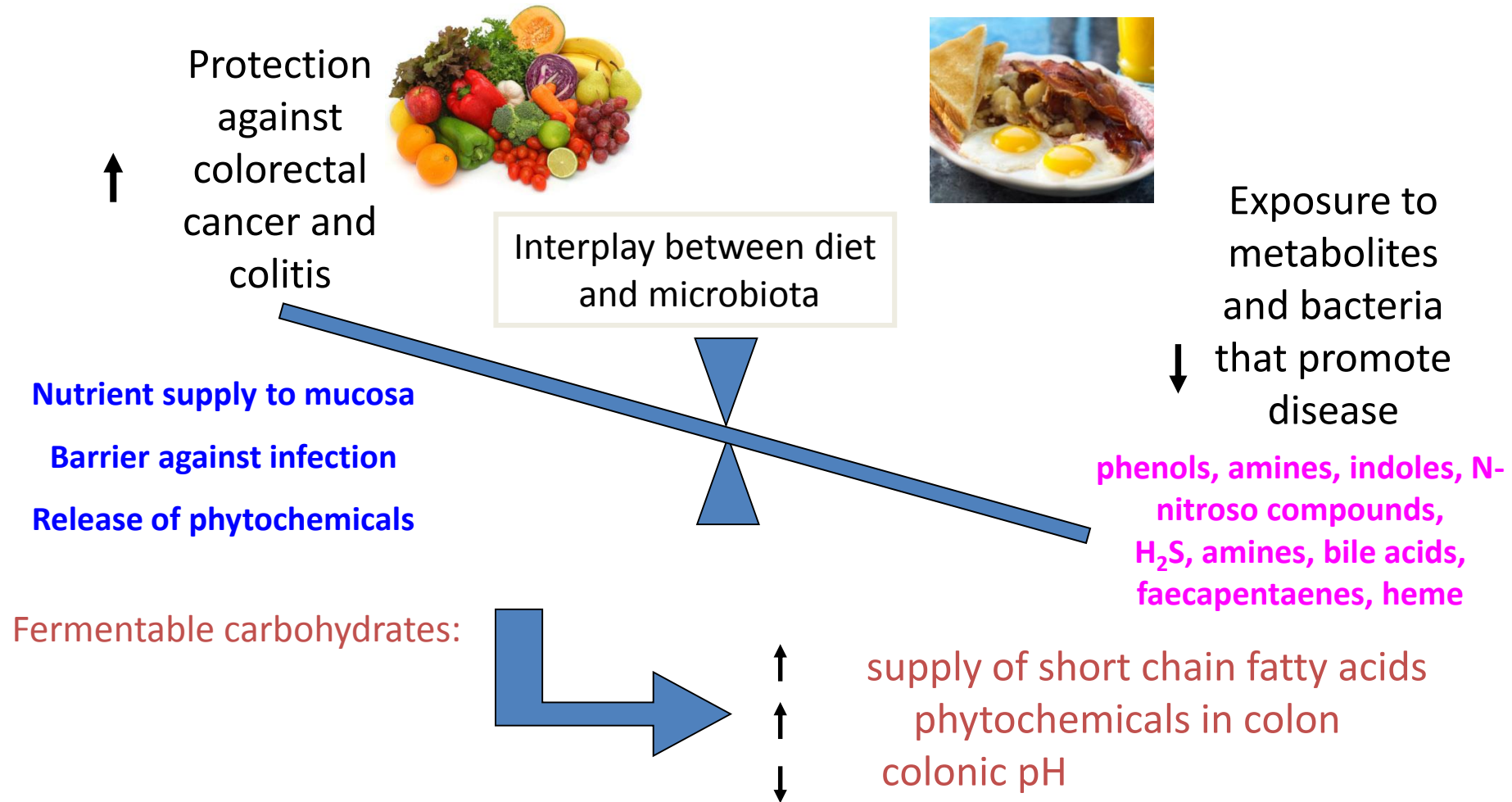


Conclusions

- **Long-term dietary patterns have significant impacts on both intestinal microbiota composition and activity**
 - Fibre consumption appears to be a major driver
- **Microbiota composition and activity are strongly correlated with markers of host health/disease**
 - Mechanistic studies now starting to emerge that link diet/microbiota/health
- **Specific bacterial groups/species respond strongly to dietary change, but there is inter-individual variation in the groups that respond**
- **Many gut bacteria appear to be nutritionally specialised; these species are likely to show the greatest responses to dietary manipulation**
 - ‘Keystone’ species may determine the ability to ferment insoluble substrates
- **Implications for therapeutic dietary intervention:**
 - The response may depend on the underlying microbiota composition of a given individual
 - Need continued and improved characterisation of the microbiota in order to predict responses to dietary manipulation



Interplay between diet and microbiota on gut health



Acknowledgements

Rowett Institute of Nutrition and Health/University of Aberdeen

Microbiology Group

Harry Flint
Sylvia Duncan
Gillian Donachie
Petra Louis
Jennifer Ince
Lucy Webster
Xiaolei Ze
Aurore Bergerat
Freda McIntosh
Karen Scott
Jenny Martin



David Brown (*Analytical Chem*)
Wendy Russell (*Mol Nutr*)
Alex Johnstone (*OMH*)
Gerald Loble (*OMH*)
Sylvia Stephen (*HNU*)
Grietje Holtrop (*BioSS*)

University of Aberdeen
Keith Dobney



Pathogen Genomics Group

Julian Parkhill
Paul Scott

Bacterial Pathogenesis Group

Trevor Lawley
Mark Stares

Core Sequencing Teams

Carol Churcher
David Harris
Richard Rance

All other members of the Sanger Institute's sequencing teams

University of Modena and Reggio Emilia
Maddalena Rossi
Andrea Quartieri



University of Adelaide

Alan Cooper
Christina Adler
Laura Weyrich
John Kaidonis
Wolfgang Haak
Corey Bradshaw
Grant Townsend



University of Warsaw
Arkadiusz Soltysiak



Johannes Gutenberg University of Mainz
Kurt Alt



St. George's, University of London
Phil Cooper



U. Maryland
Colin Stine
Mihai Pop



Funding Sources:

wellcometrust



The Scottish Government
Riaghaltas na h-Alba

