

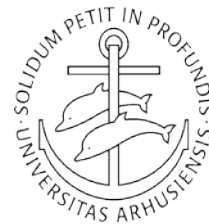
Colonic fermentation and absorption of short-chain fatty acids from whole grain cereal fractions

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Points to be addressed



- **Introduction**
- **The human colon – site for SCFA generation**
- **Factors influencing SCFA production**
- **Experimental models**
- **SCFA production and composition when fermenting wheat and rye fractions**
- **Biological actions of SCFA**
- **Summary**

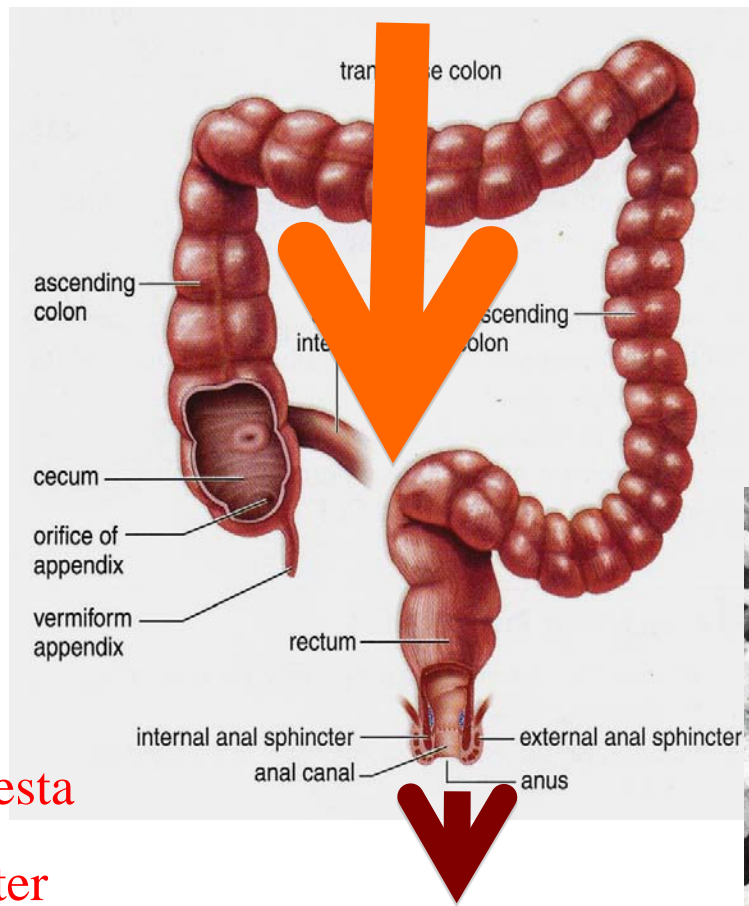




The human colon – site for SCFA production



Ileal flow



Dimension:

154 (113-207) cm
in length

1274 (731-2509)
cm² in area

Content:

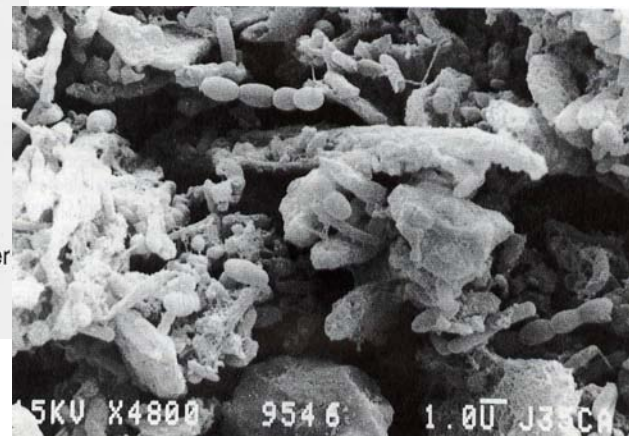
222 (58-904) g wet digesta

36 g DM and 186 g water

Bacteria:

10^{11} - 10^{12} per gram
biomass

5-6 genera account for 99
% of biomass





Gut lumen

Non-digested dietary components

Large intestinal microbiota

- Metabolic regulation
- Bacterial population

shift

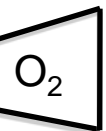
Gut environment

- Transit time
- pH,
- osmolarity

Gases

Host tissues

Host secretion



Metabolic cross-Secondary metabolites (e.g. bacteriocides)

Primary metabolites (organic acids + H₂, CO₂, CH₄)

feeding

shift

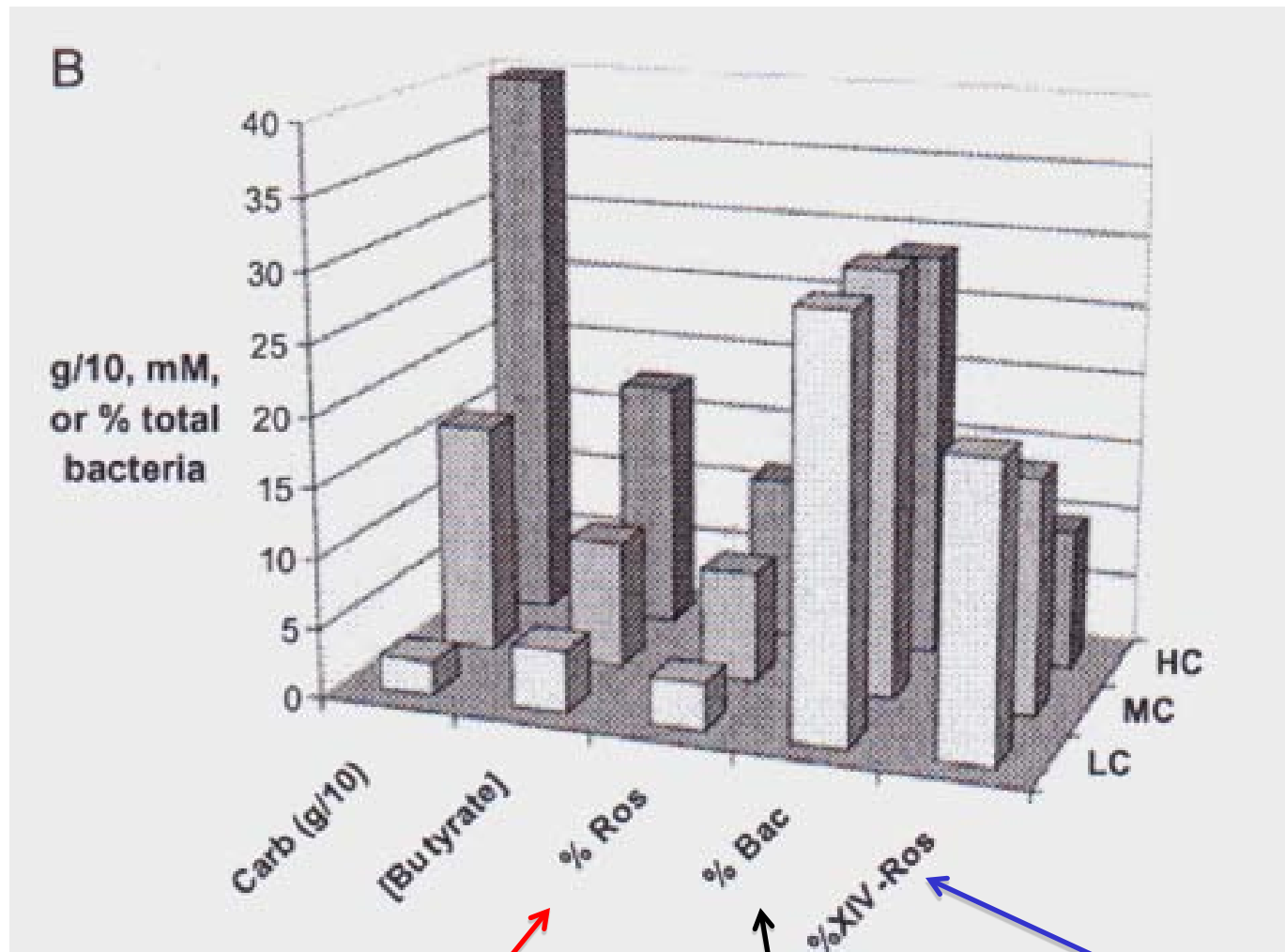
Excretion (faeces)



(Louis et al., 2007)



Influence of amount of carbohydrates for bacteria composition and butyrate formation



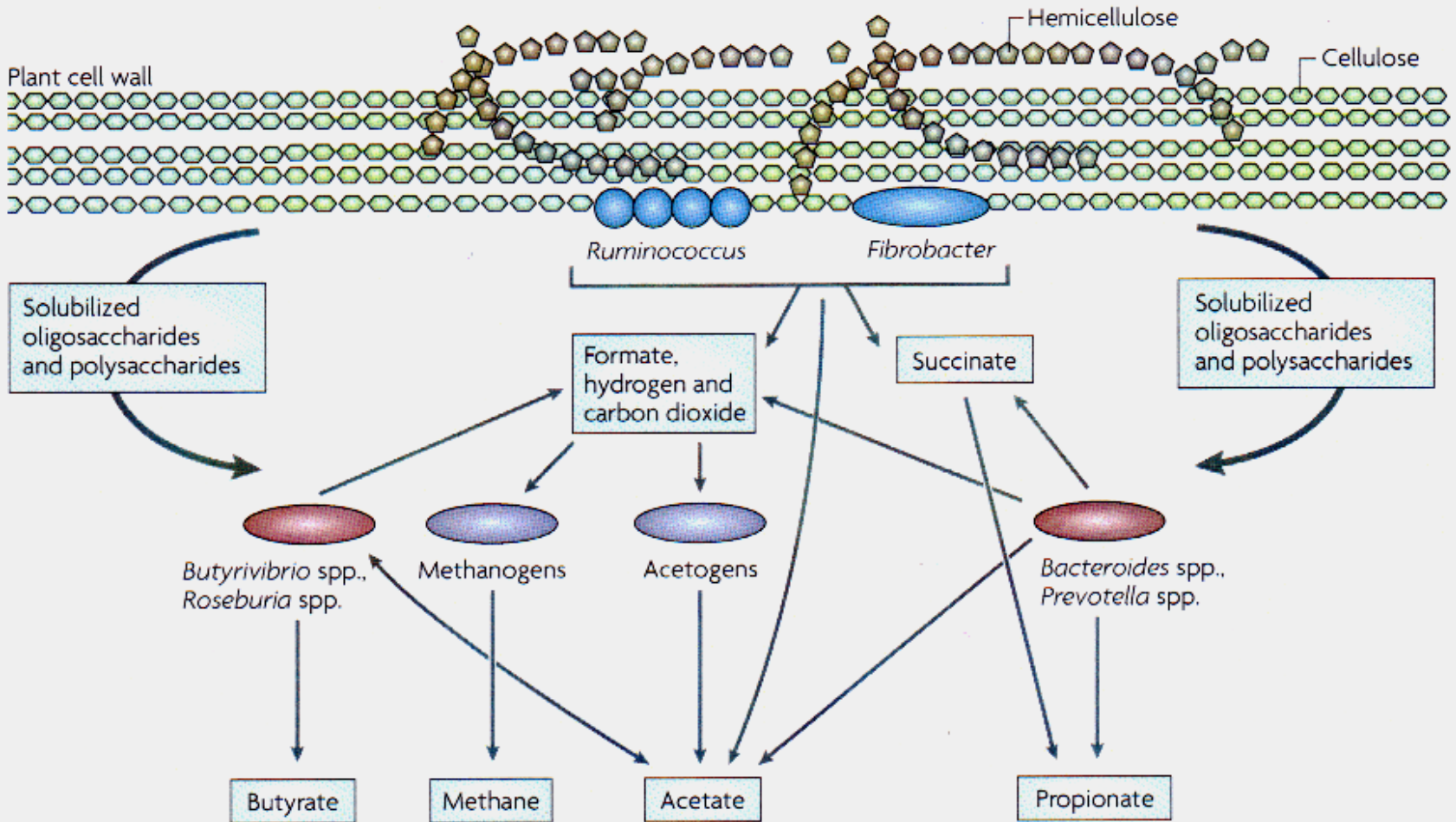
Roseburia/E. rectale group

Bacteroides group

Bacteria other than *Roseburia* group



Example of metabolic cross feeding

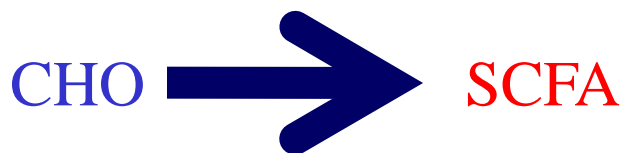
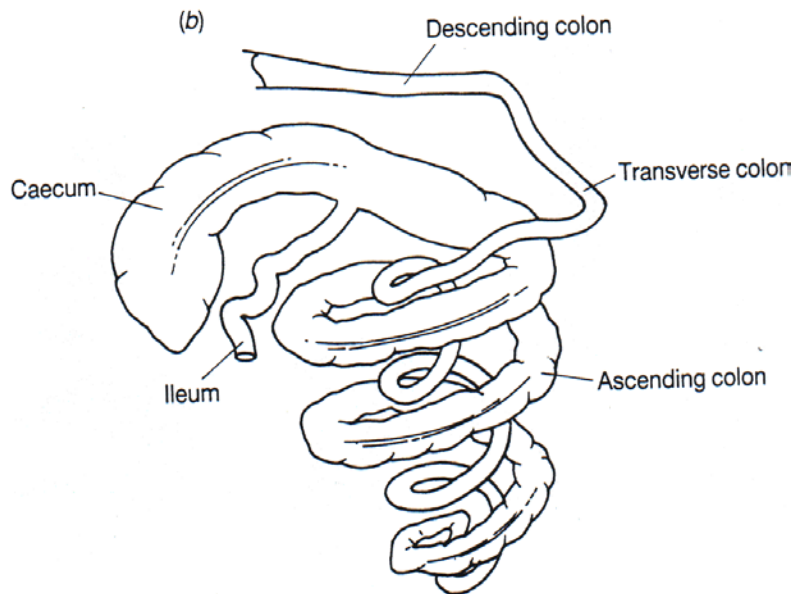
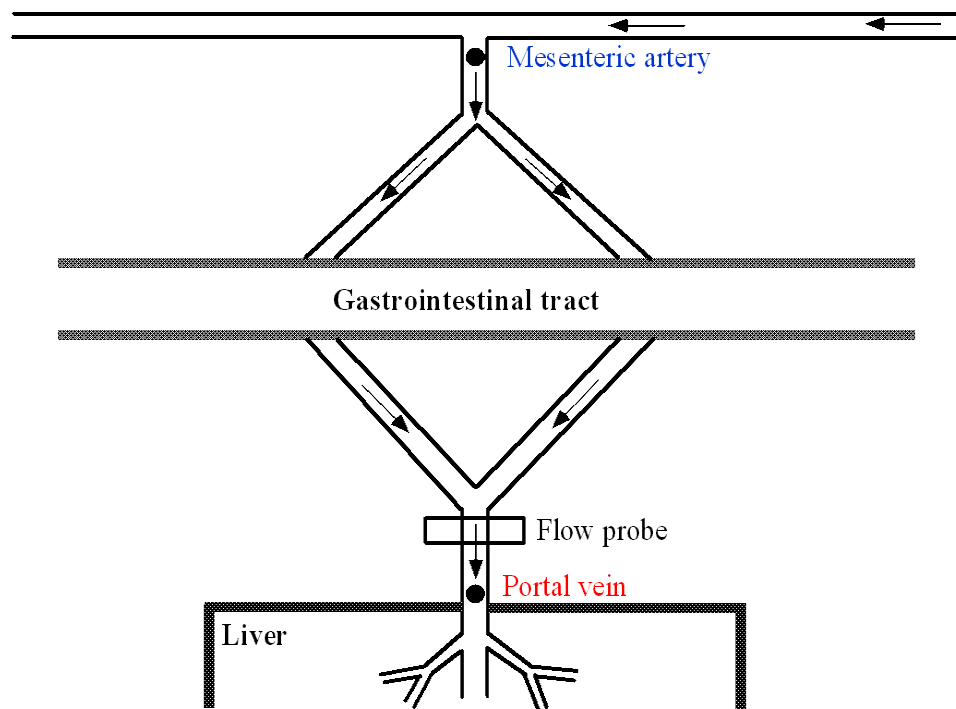




The principles in the experimental models



The catheterised pig model



Net absorption

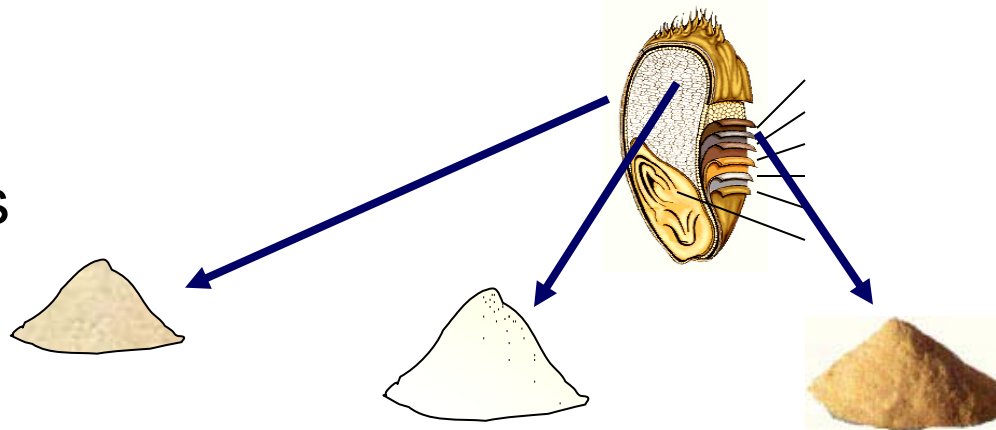
$$q = (C_p - C_a) F (dt)$$

$$Q = \sum_{t_0}^{t_n} q$$





Fractions



Wheat fractions from Buhler & MRI

Tiger

- Whole grain flour
- 100 % flour after peeling
- 100 % flour after pearling
- Standard white flour
- Aleurone 1
- Aleurone 2
- Bran
- Fine bran
- Fine bran <200 μ
- Peeling
- Pearling

Crousty

- Whole grain flour
- Standard white flour
- Bran

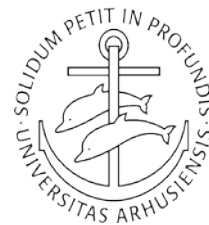
Rye fractions from Raisio:

- Whole grain flour, ash 1.8-2 %
- Flour, ash 0,65-0,75
- Flour, ash 0,8-0,9 &
- Rye flour, ash 3-3,5 %
- Rye bran, ash 6-7 %





Composition of experimental diets

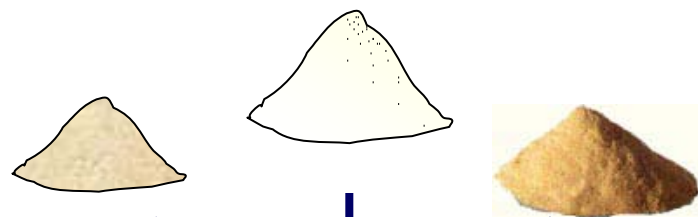


	Mean	SD	Range
Whole grain cereals and fractions	415	336	108-757
Vitacel	34	29	0-79
Corn starch	281	228	0-548
Casein	132	81	34-111
.....			
Non-starch polysaccharides	82	7	
Cellulose	20	14	6-56
Arabinoxylans	45	9	25-63
Klason lignin	15	5	
Dietary fibre	97	9	

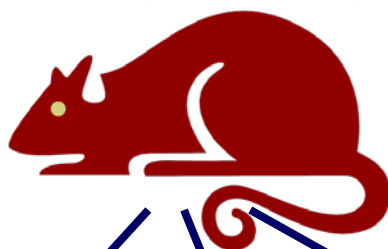




Experimental setup



Iso-DF, protein and fat diets based on wheat and rye fractions



Rat as biological filter

Tissue samples

Blood from vena cava and the portal vein

Digesta from caecum





Relationship between caecal pool size and estimated absorption



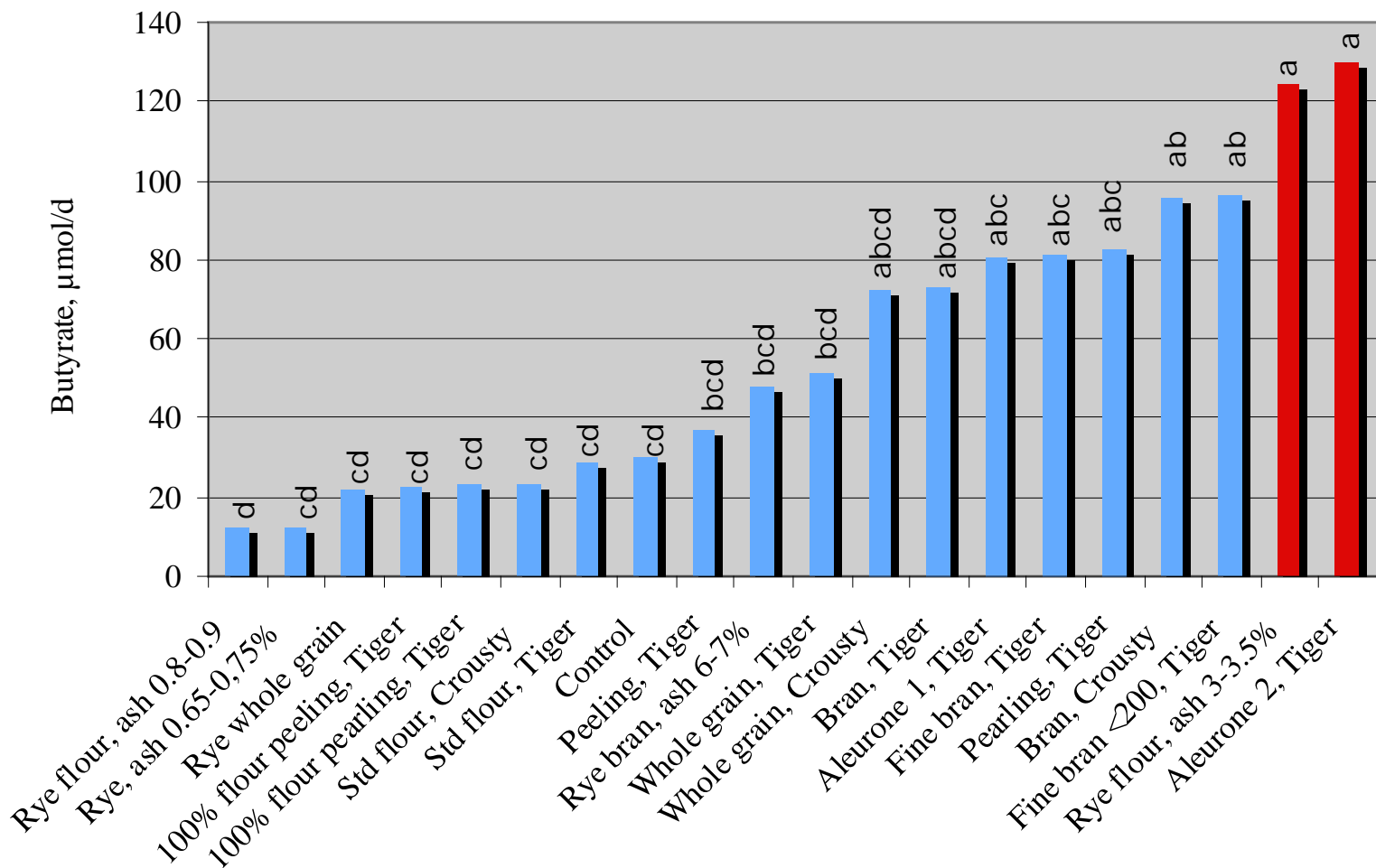
		R²	P-value
Short-chain fatty acids	P.V. = 120 + 0.73xCae	0.20	<0.0001
Acetate	P.V. = 115 + 0.53xCae	0.11	<0.004
Propionate	P.V. = 13 + 0.72xCae	0.44	<0.0001
Butyrate	P.V. = -2.9 + 1.13xCae	0.71	<0.0001

P.V., portal vein; Cae, caecum



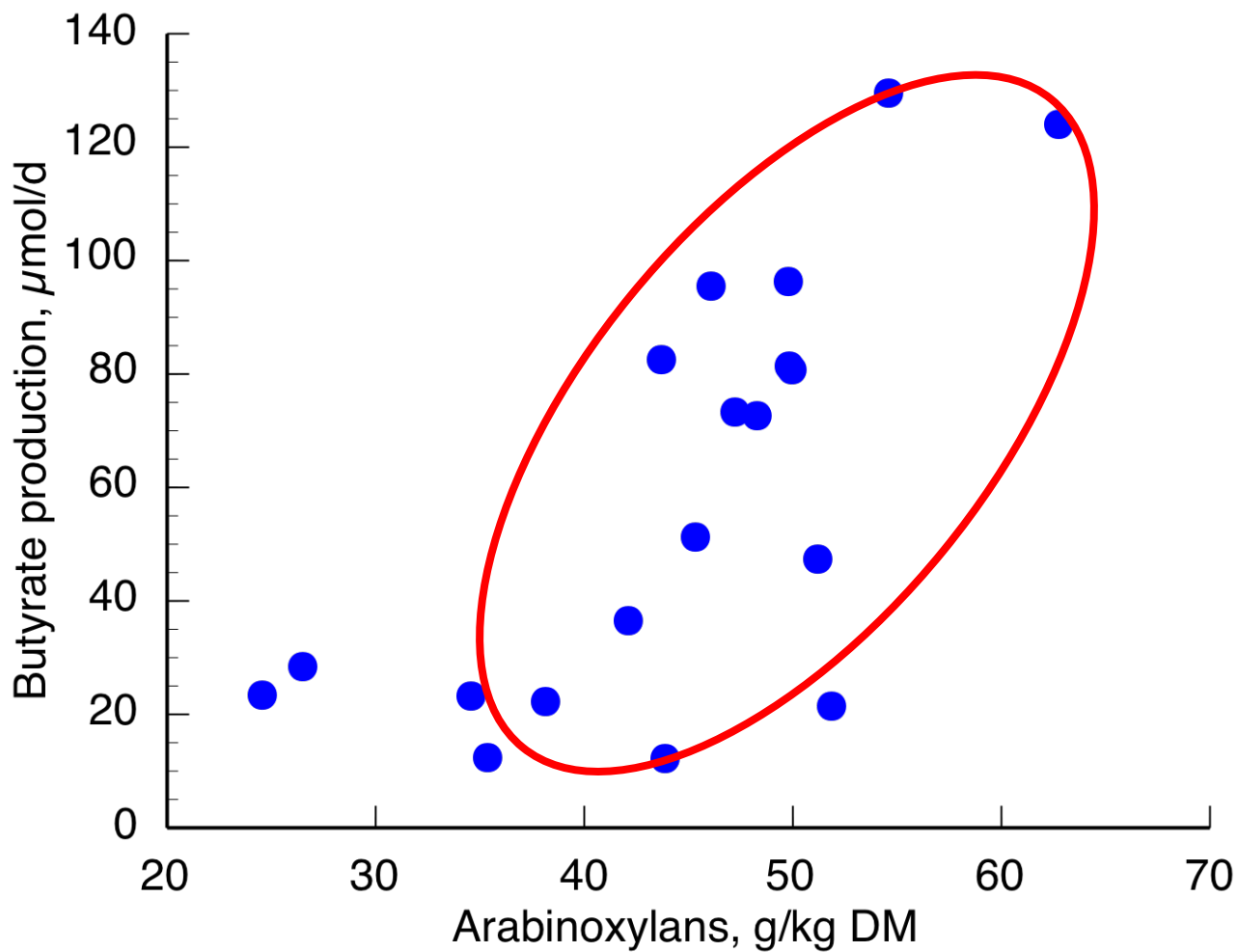


Butyrate production



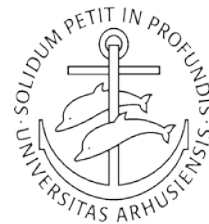


Correlation between arabinoxylans and butyrate production





Experimental diet – pig study

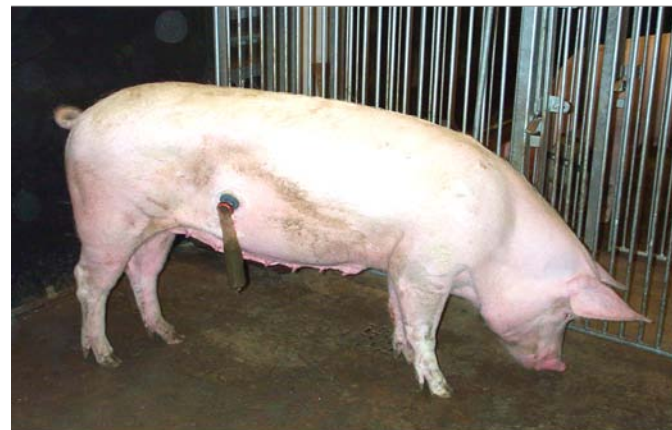
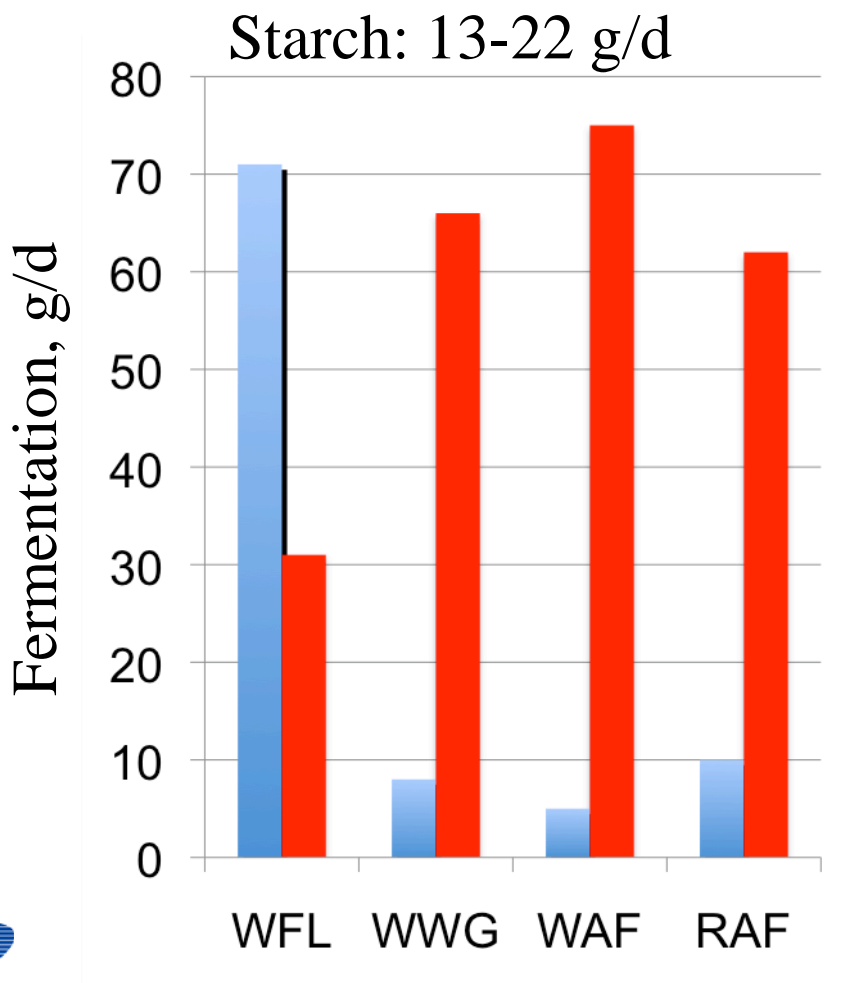


	WFL	WWG	WAF	RAF
Carbohydrates	641	631	588	626
NSP	115	103	103	94
Cellulose	66	17	14	12
β -glucan	1 (0)	4 (0.1)	8 (0.3)	9 (2)
AX	27 (11)	64 (18)	64 (10)	51 (21)
Klason lignin	10	22	23	26
Dietary fibre	125 (14)	124 (23)	125 (13)	120 (29)





Fermentation of cellulose and AX in the large intestine and short-chain fatty acid profile

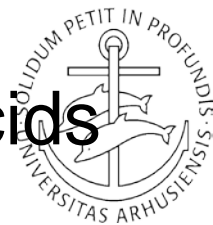


	Percent	
Diet	Acetate	Butyrate
WFL	70	5,4 ^b
WWG	66	9,6 ^a
WAF	60	13,7 ^a
RAF	64	10,3 ^a





Absorption (mmol/h) of short-chain fatty acids

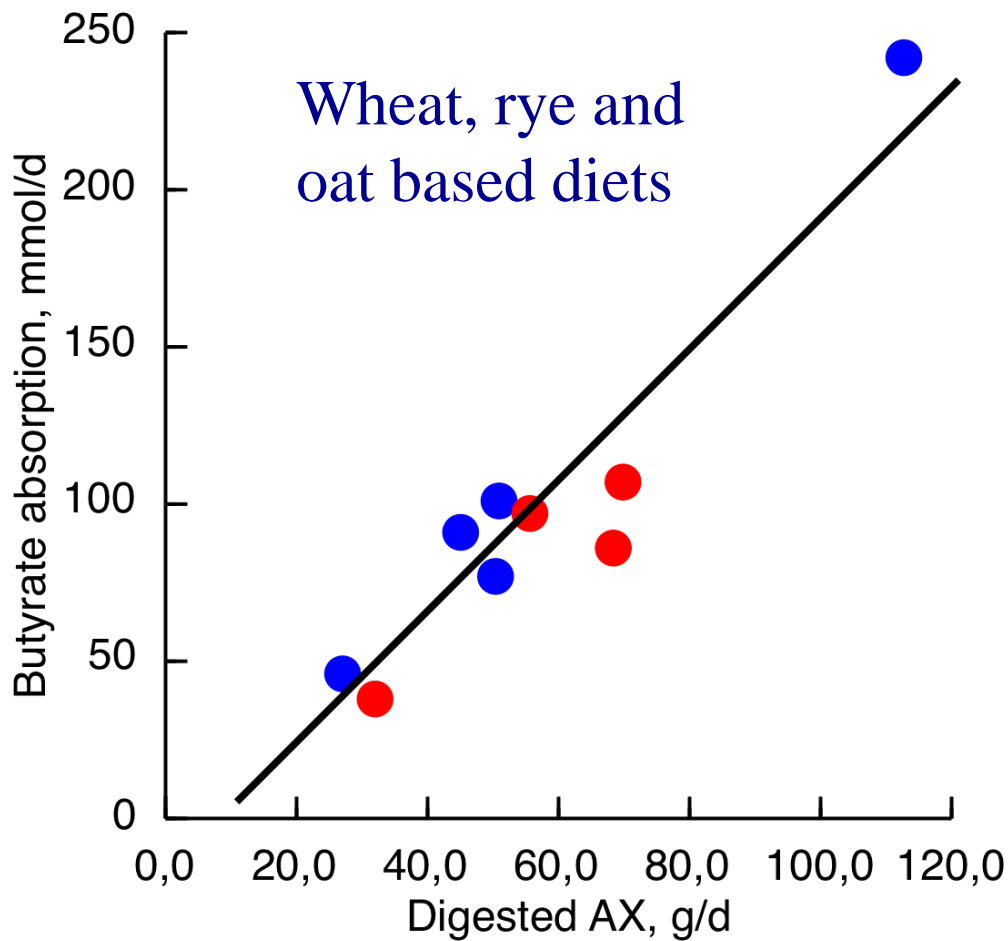


	WFL	WWG	WAF	RAF	P-value
SCFA	34	36	41	40	0.59
Acetate	23	22	23	21	0.96
Propionate	7.5 ^b	8.4 ^{ab}	12.0 ^a	12.0 ^a	0.007
Propionate, %	22.2 ^b	25.0 ^{ab}	29.0 ^a	30.0 ^a	0.0002
Butyrate	1.6 ^b	3.6 ^a	4.4 ^a	4.0 ^a	0.0001
Butyrate, %	4.9 ^b	9.6 ^a	10.9 ^a	9.8 ^a	<0.0001



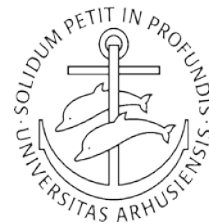


Relationship between AX degradation and butyrate absorption in different cereal diets





Possible mechanisms



- **Little evidence of direct stimulation of butyrate producing microorganisms by arabinoxylans**
- **More likely is therefore:**
 - ✘ Arabinoxylans are broken down small molecules by versatile polysaccharide-degrading bacteria, i.e. bacteroides and non-pathogenic clostridia
 - ✘ Cross-feeding to butyrate producing bacteria, i.e. *Roseburia spp.*, *Eubacterium rectale* and *Faecalibacterium prausnitzii*
 - ✘ Influence of the pH – high butyrate at pH 5.5 low butyrate at pH 6.5



Biological actions of short-chain fatty acids



- **Local in the gut**

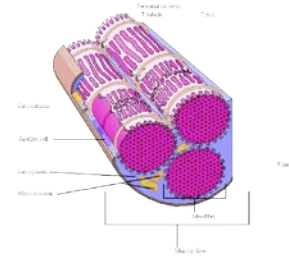
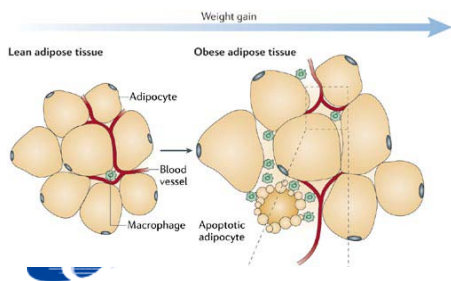
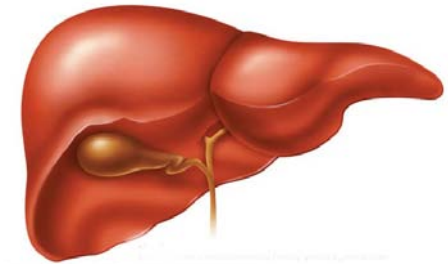
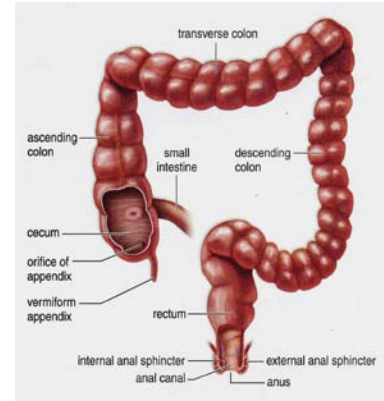
- ✗ Colonic defence barrier & intestinal epithelial permeability
- ✗ Oxidative stress
- ✗ Inflammation
- ✗ Colon carcinogenesis
- ✗ Gut hormones

- **Liver**

- ✗ Lipoprotein metabolism

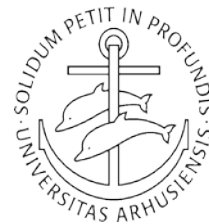
- **Peripheral**

- ✗ Adipose tissues (insulin sensitivity)
- ✗ Muscles (energy)





Conclusions



- **Short chain fatty acids are produced by microbial fermentation in the large intestine**
- **The production of SCFA is influenced by amount and types of substrate, microbial composition, pH, host factors etc.**
- **Arabinoxylans from wheat and rye enhances butyrate formation**
- **There is growing evidence that SCFA and butyrate in particular have a number of biological actions in the large intestine, the liver and the peripheral tissues**





Acknowledgement



- **The EU 6th framework programme 'HEALTHGRAIN' (FP6-514008) for the funding**
- **The companies and institutes, i.e Buhler, MRI and Raisio for delivering the fractions**
- **Colleagues at the Department for technical assistance**

