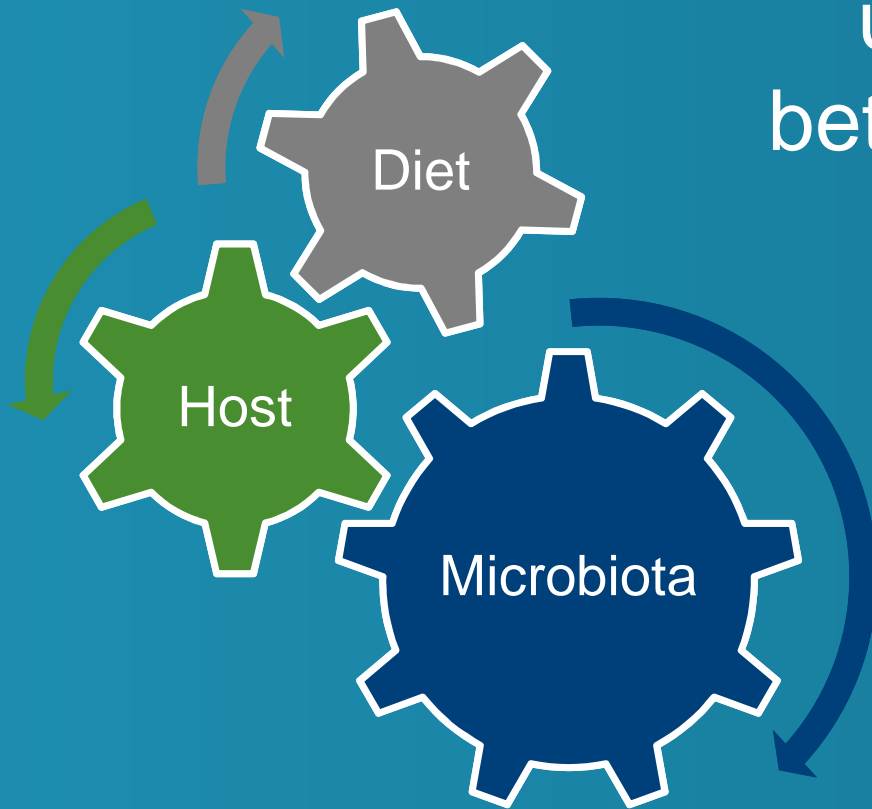


# How metabolomics can increase our understanding of the interaction between the diet, the microbiota and the host



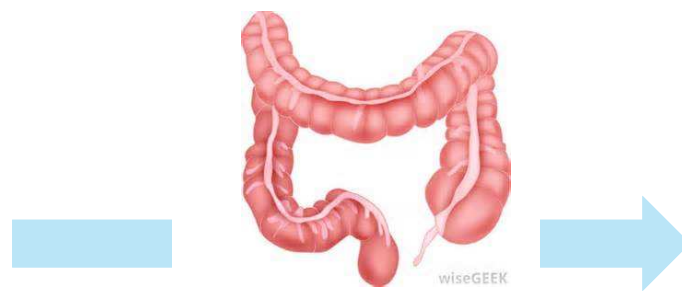
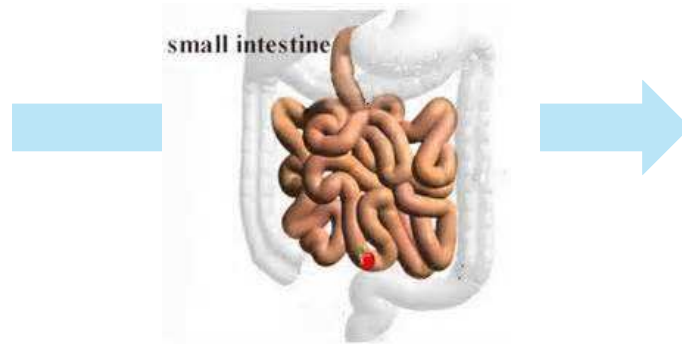
Kristin Verbeke

Translational Research in Gastrointestinal Disorders (TARGID) and  
Leuven Food Science and Nutrition Centre (LForCe)

KU Leuven, Belgium



# The human metabolome



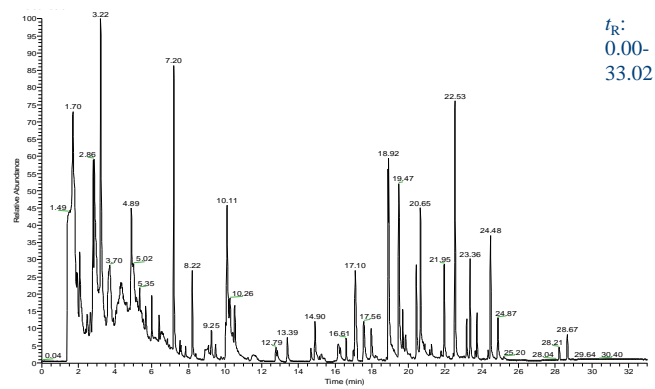
Endogenous  
metabolome

⇒ Highly complex and highly variable

# Targeted versus non-targeted analysis



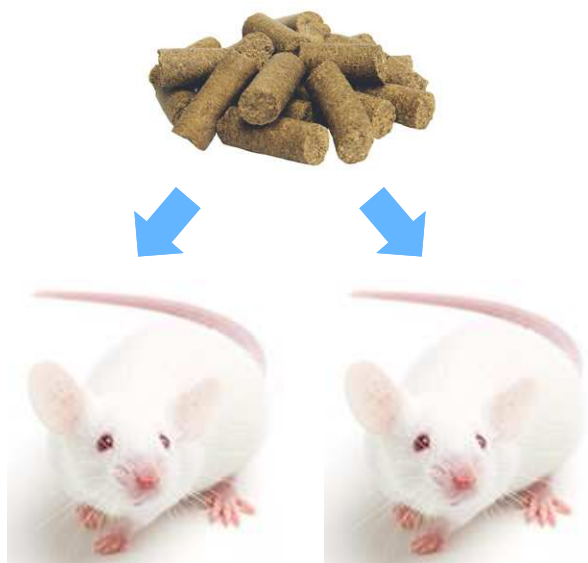
Hypothesis-driven



Data-driven

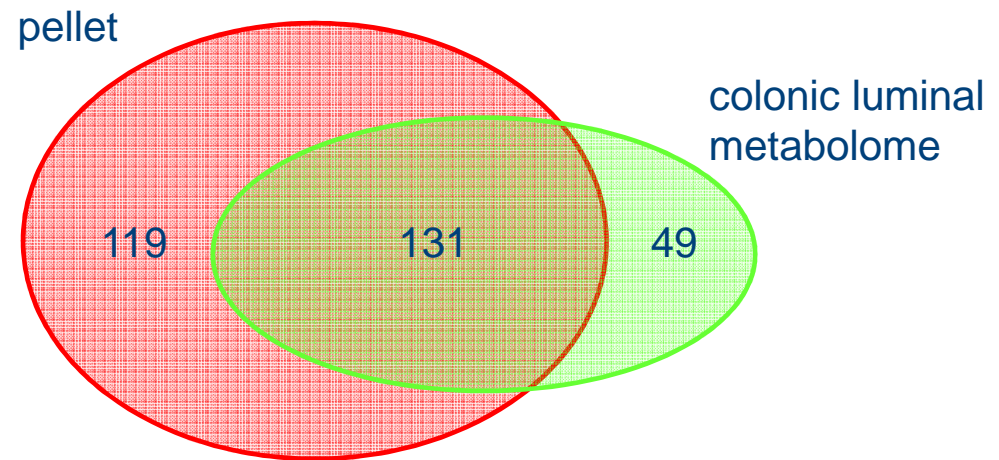
	1H-NMR	GC-MS	LC-MS
Sensitivity	+	+++	+++
Quantitative	+	+	+
robustness	+++	+	+
Sample preparation	no	yes	yes

# Impact of the diet and the microbiota on the fecal metabolome

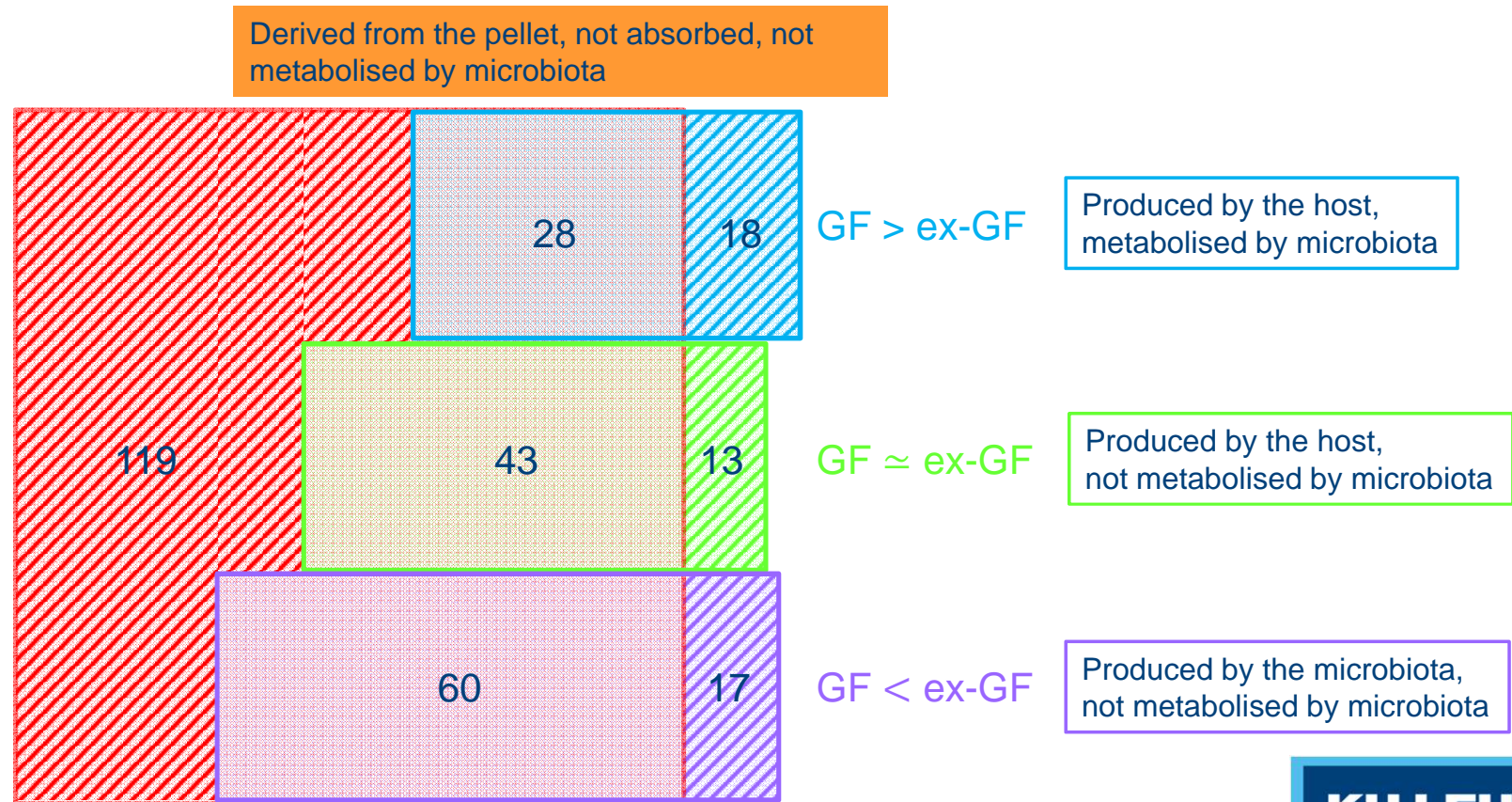


germfree mice

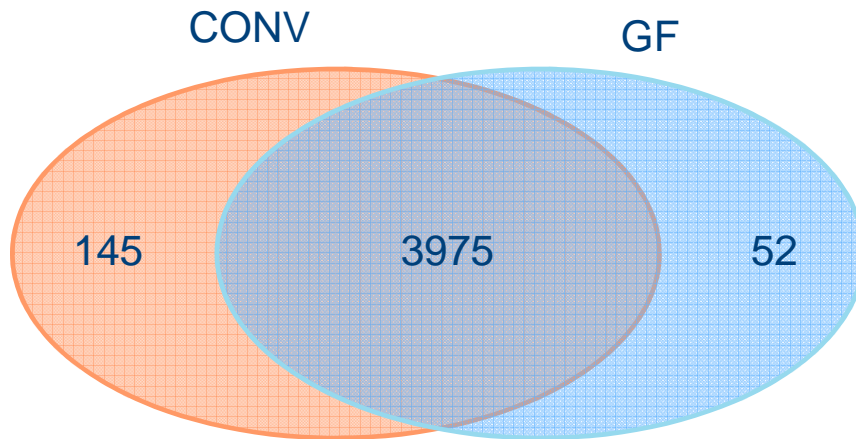
conventionalised mice



# Impact of the diet and the microbiota on the fecal metabolome



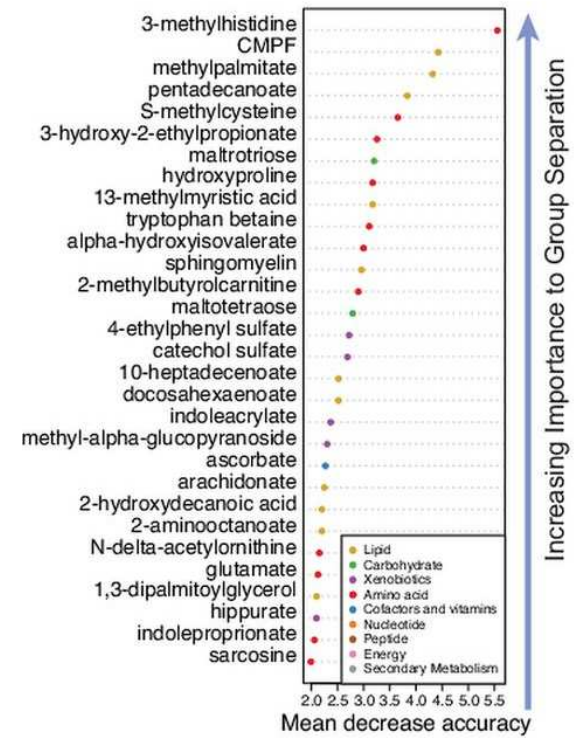
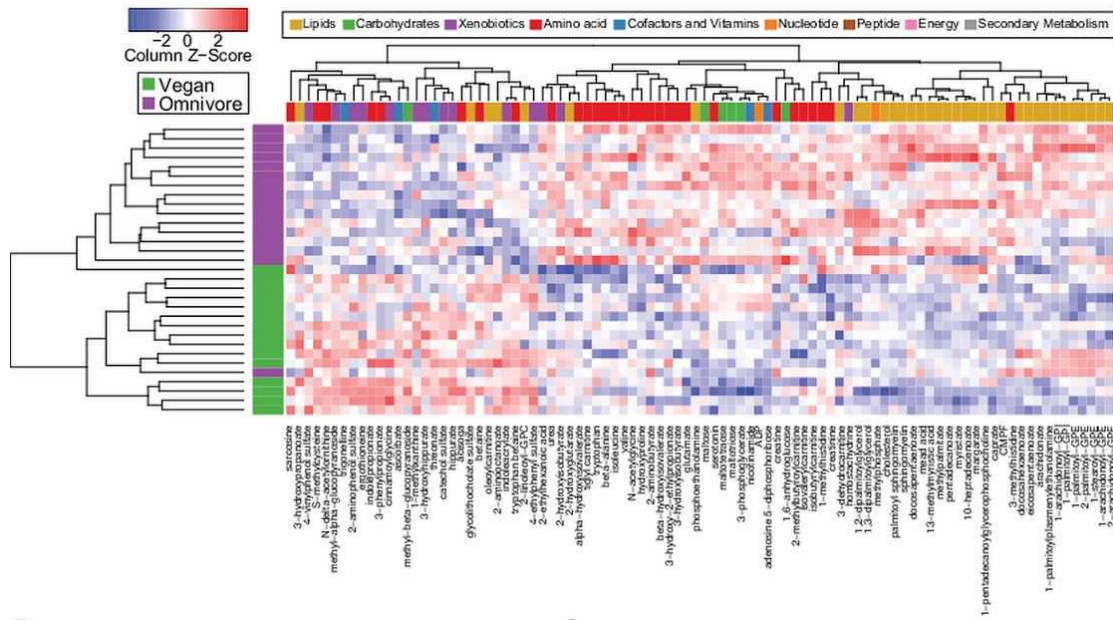
# Impact of gut microbiota on blood metabolites



Metabolite	Fold change	P value
<b>Indole derivatives</b>		
Tryptophan	1.7, GF	$8.42 \times 10^{-12}$
N-acetyltryptophan	2.4, GF	$3.56 \times 10^{-4}$
Indoxyl sulfate	conv-	$1.34 \times 10^{-7}$
Serotonin	2.8, conv	$1.27 \times 10^{-10}$
IPA	conv-	$7.69 \times 10^{-7}$
<b>Phenyl derivatives</b>		
Phenylalanine	1.05, GF	0.3
Tyrosine	1.44, GF	$1.14 \times 10^{-4}$
Hippuric acid	17.4, conv	$1.98 \times 10^{-9}$
Phenylacetylglucine	3.8, conv	$4.70 \times 10^{-8}$
Phenyl sulfate	conv-	$9.85 \times 10^{-7}$
p-Cresol sulfate	conv-	0.002
Phenylpropionylglycine	conv-	$3.07 \times 10^{-7}$
Cinnamoylglycine	conv-	$2.93 \times 10^{-7}$
<b>Flavones</b>		
Equol sulfate	conv-	$1.44 \times 10^{-5}$
Methyl equol sulfate	conv-	$2.18 \times 10^{-6}$
<b>Others</b>		
Urate	1.99, conv	$1.51 \times 10^{-6}$
Creatinine	1.08, conv	0.071
Dihydroxyquinoline glucuronide	conv-	$7.64 \times 10^{-6}$
12-Hydroxy-5Z,8Z,10E,14Z,17Z-eicosapentaenoic acid	4.0, conv	$8.20 \times 10^{-5}$
3-Carboxy-4-methyl-5-pentyl-2-furanpropionic acid glucuronide	3.4, conv	$1.37 \times 10^{-6}$



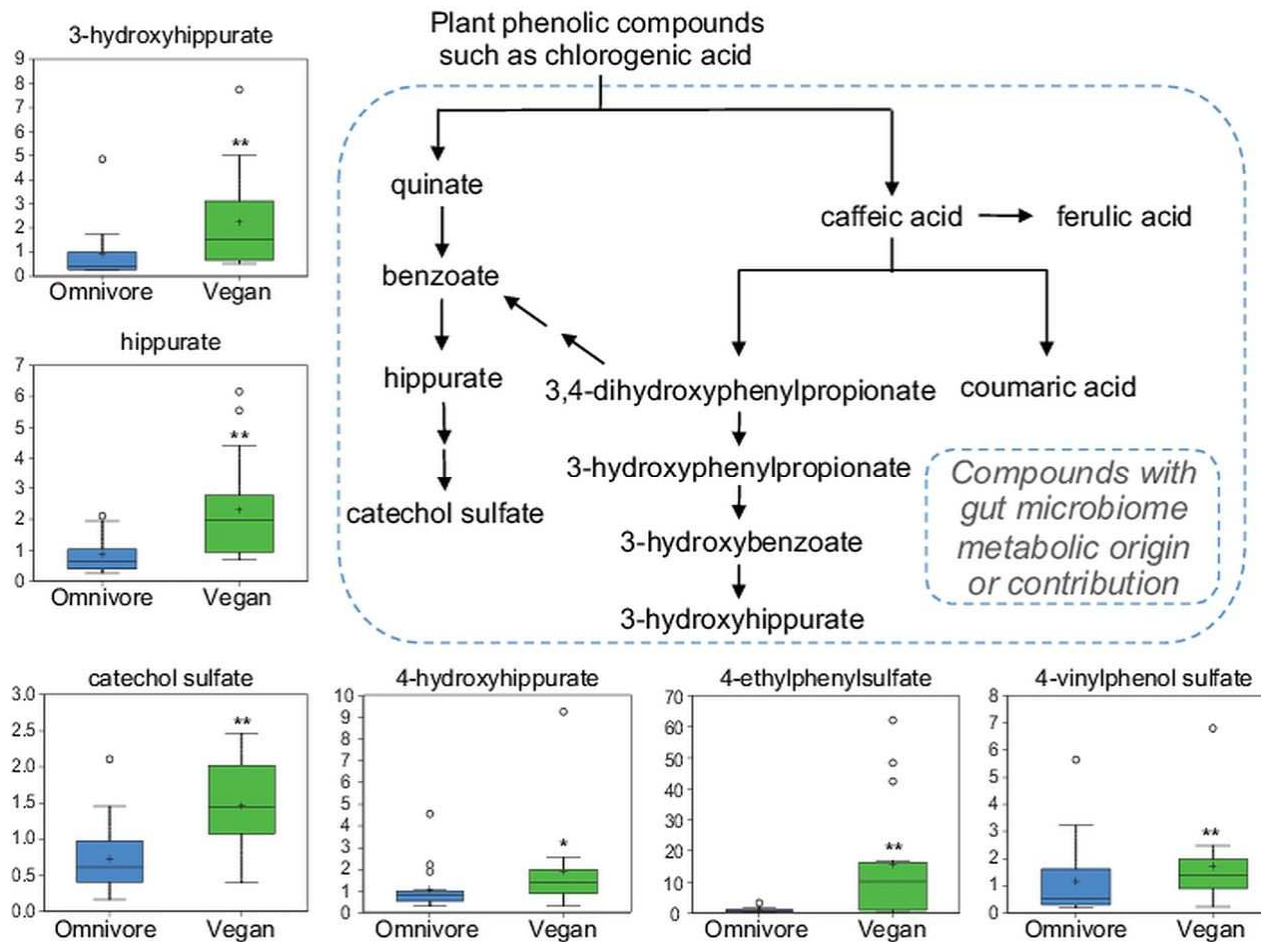
# Impact of diet on the plasma metabolome



- metabolome of omnivores particularly reflects the higher intake of meat and fat
- a few metabolites are microbial-human cometabolites

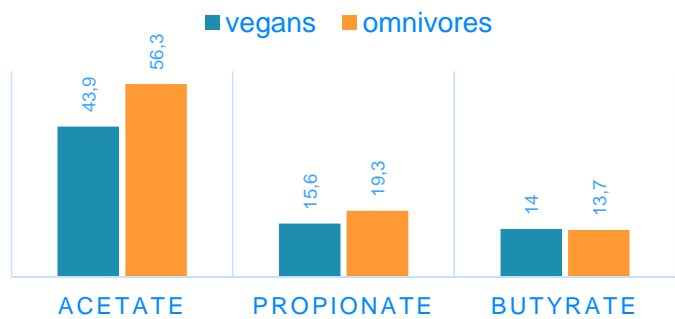
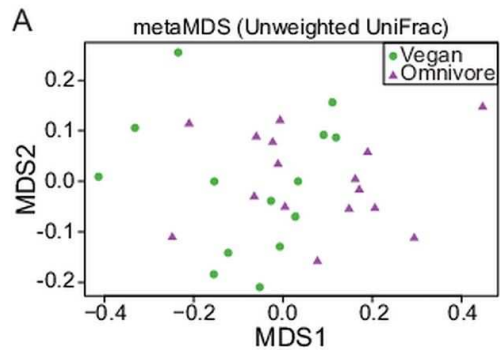


# Diet-dependent metabolites produced by the gut microbiota of vegans

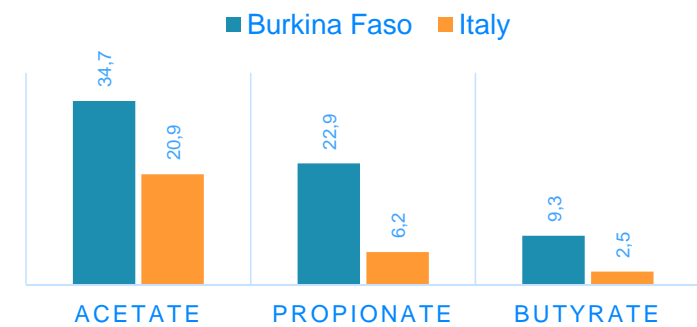
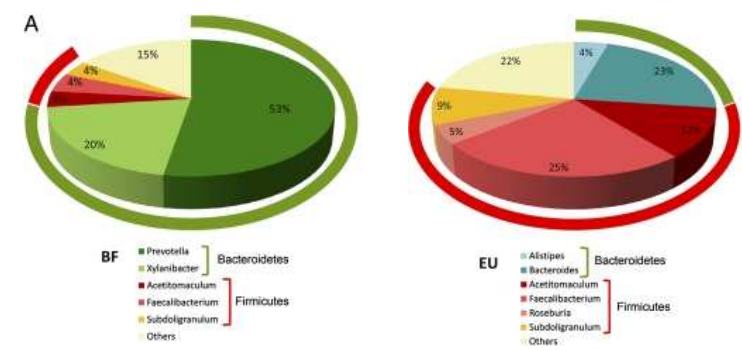


# Fecal short chain fatty acids

vegans and omnivores, both in western society

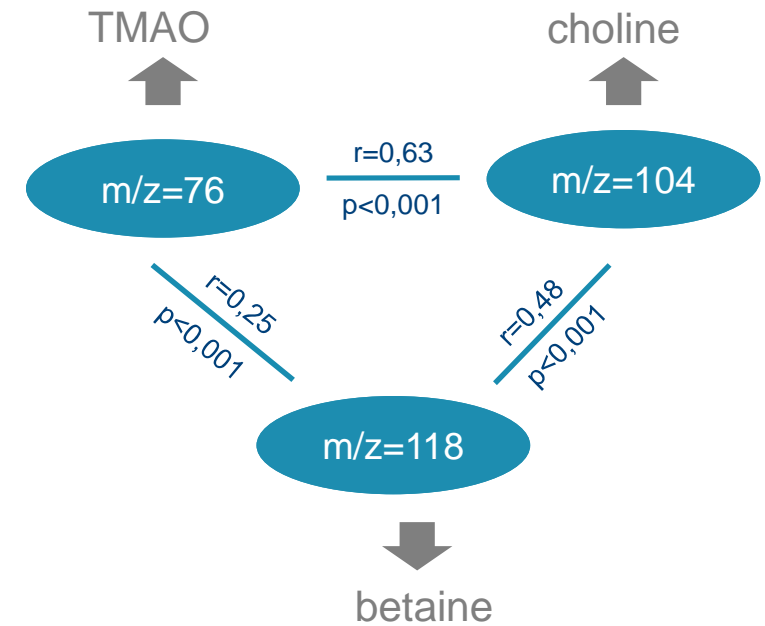
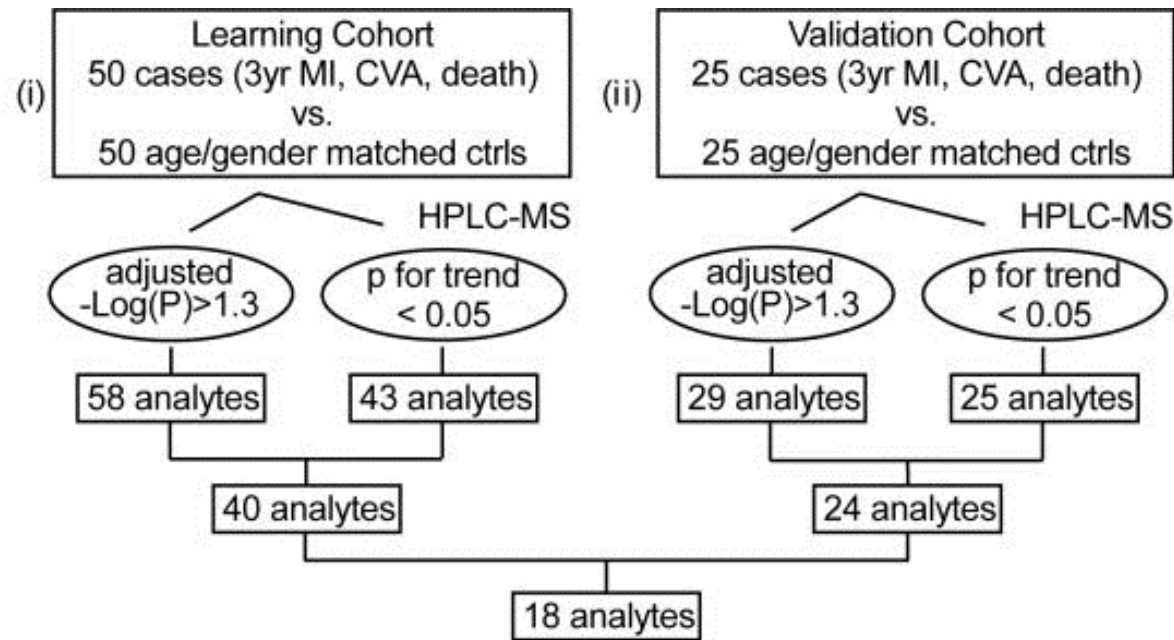


agrarian society vs western society



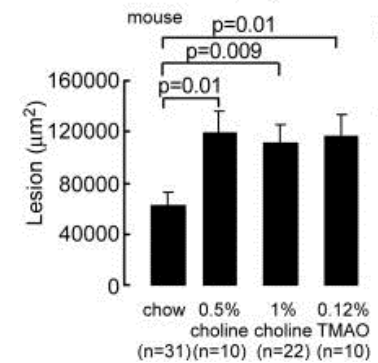
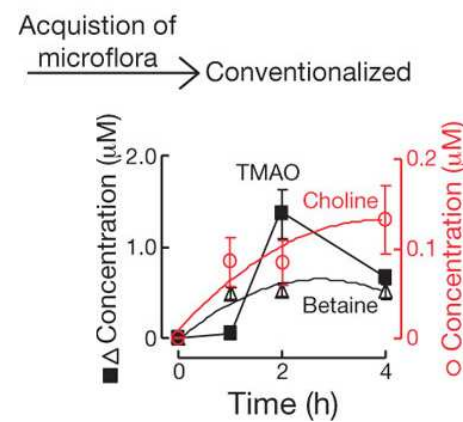
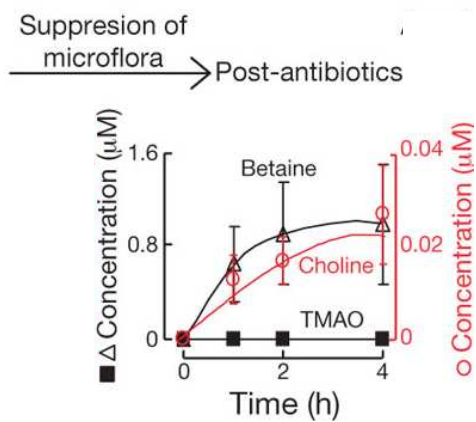
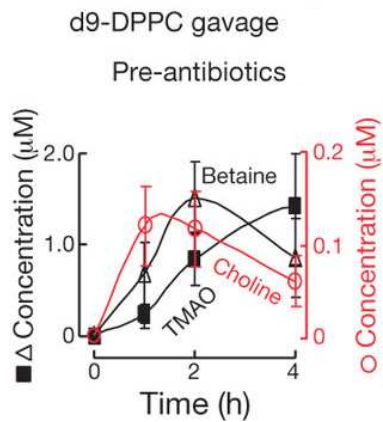
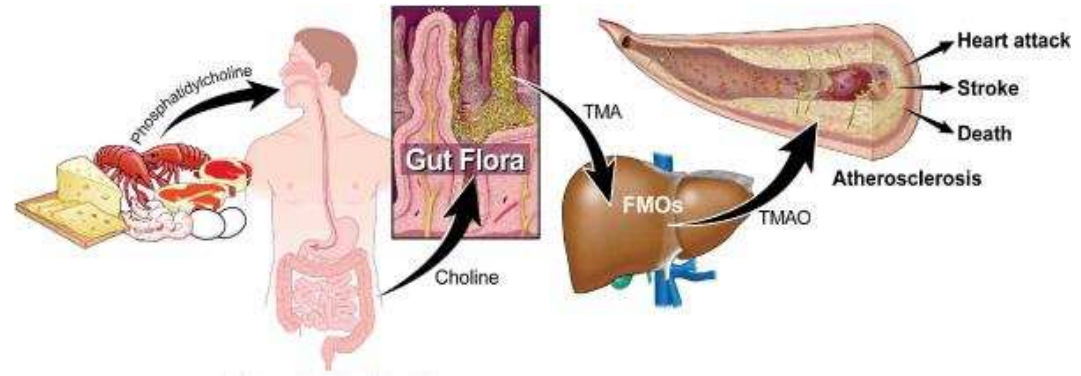
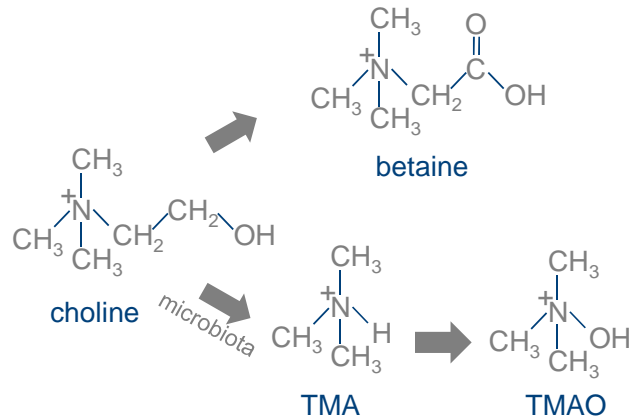
⇒ The production of gut bacteria-derived metabolites from dietary substrates is constrained by the composition of the gut microbiota

# Identification of TMAO as a risk factor for cardiovascular disease



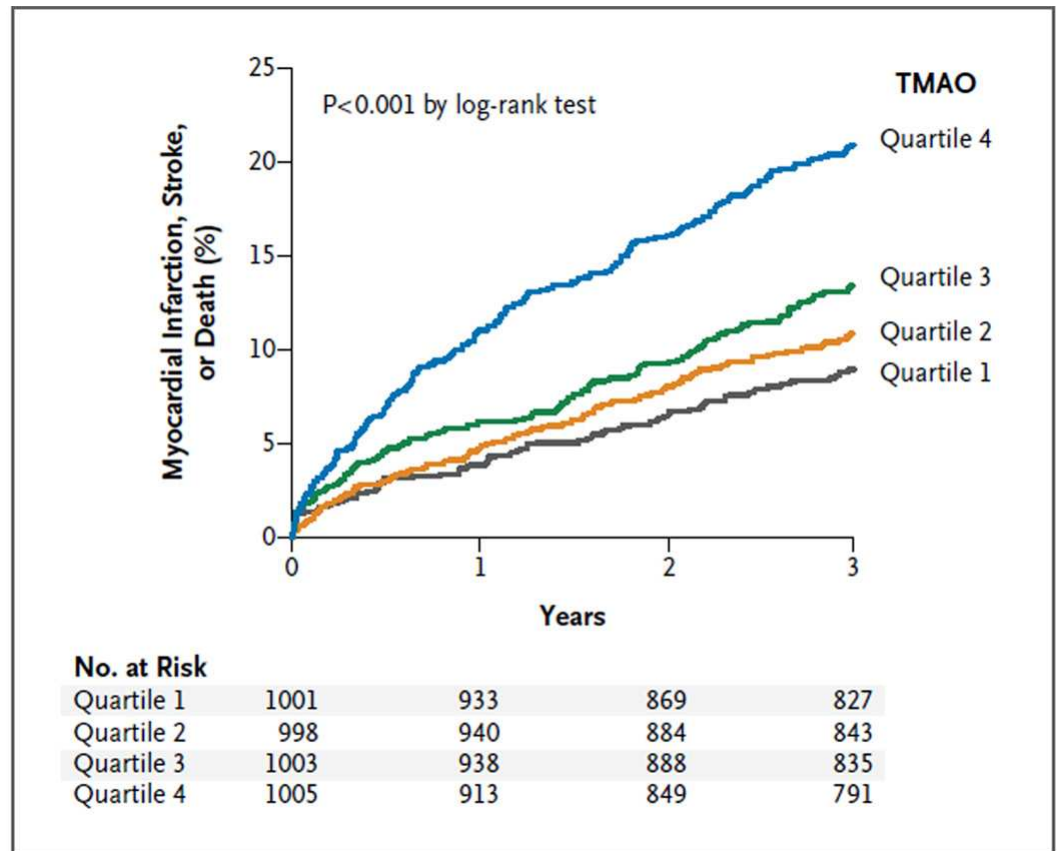
⇒ correlation suggests common biochemical pathway

# TMAO and cardiovascular disease risk



## Confirmation in humans

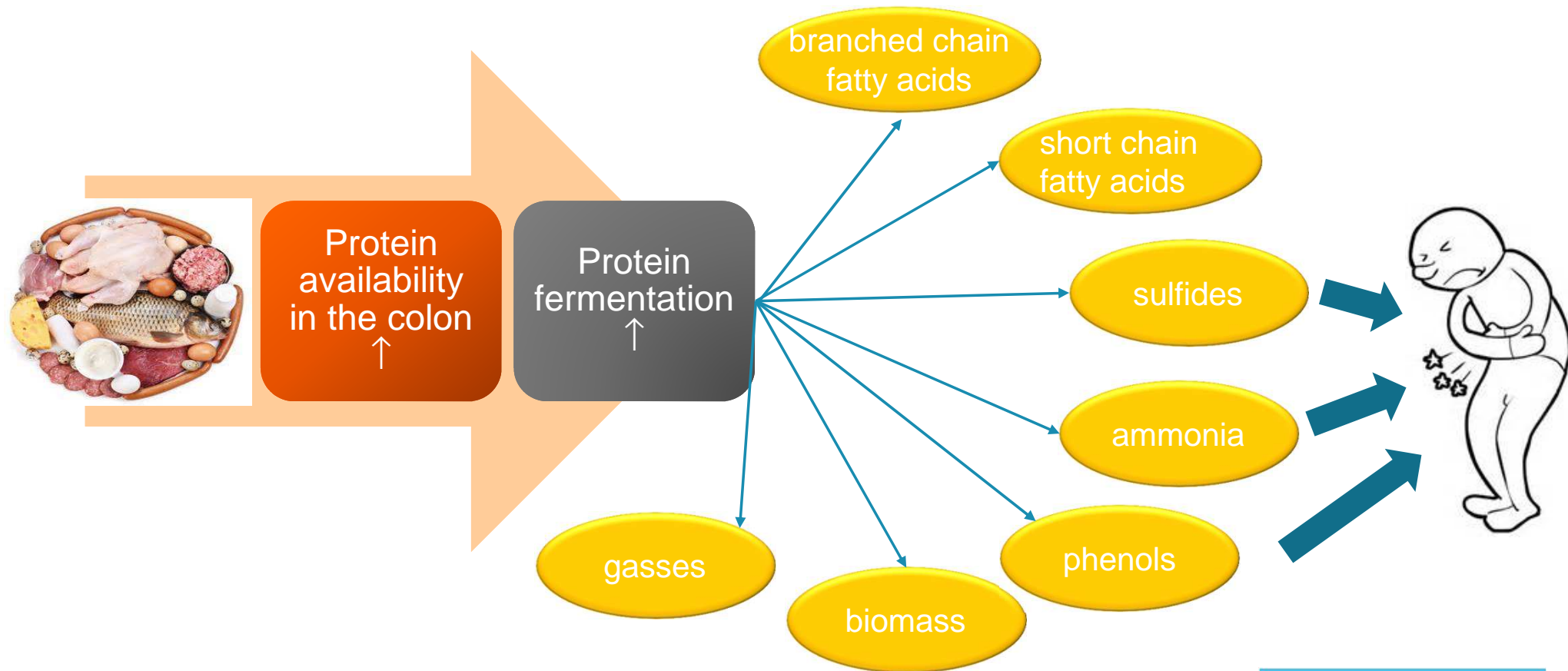
- 4007 patients with no evidence of coronary syndrome
- Undergoing diagnostic cardiac catheterisation
- Follow-up for 3 years
- Quantification of plasma TMAO



## High protein diets

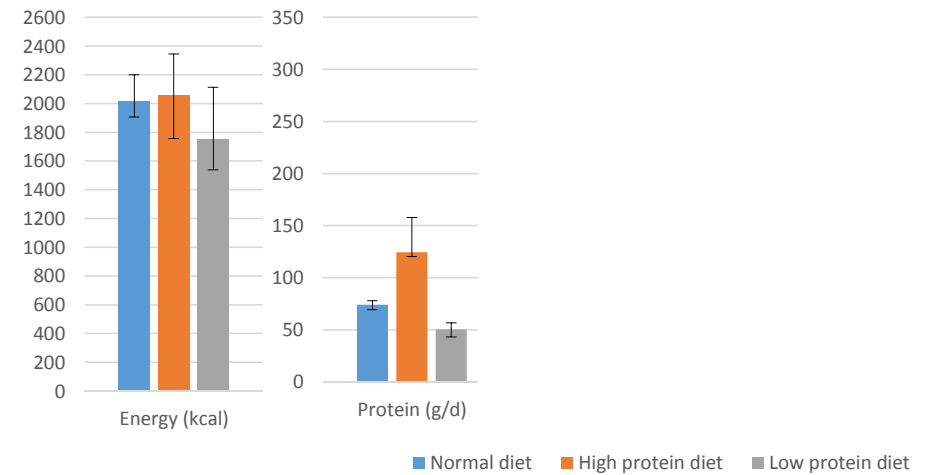
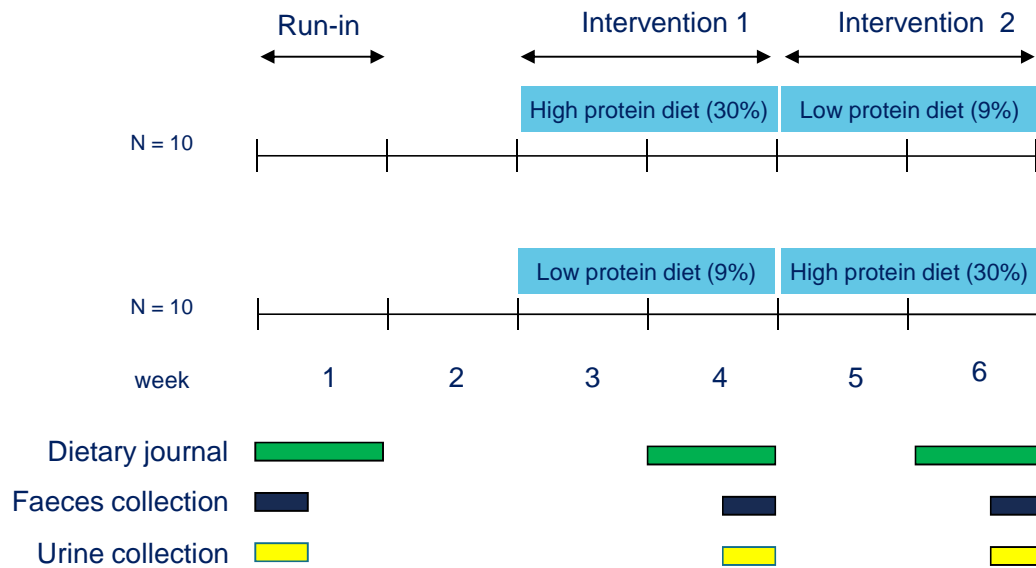
- highly popular because of increased weight loss (at least on short term)
- concerns about safety
  - cardiovascular risk?
  - kidney function?
  - bone health?
- what about gut health?

# The impact of high protein diets on gut health



# The impact of high protein diets on fecal metabolite patterns

## Isocaloric high protein diet

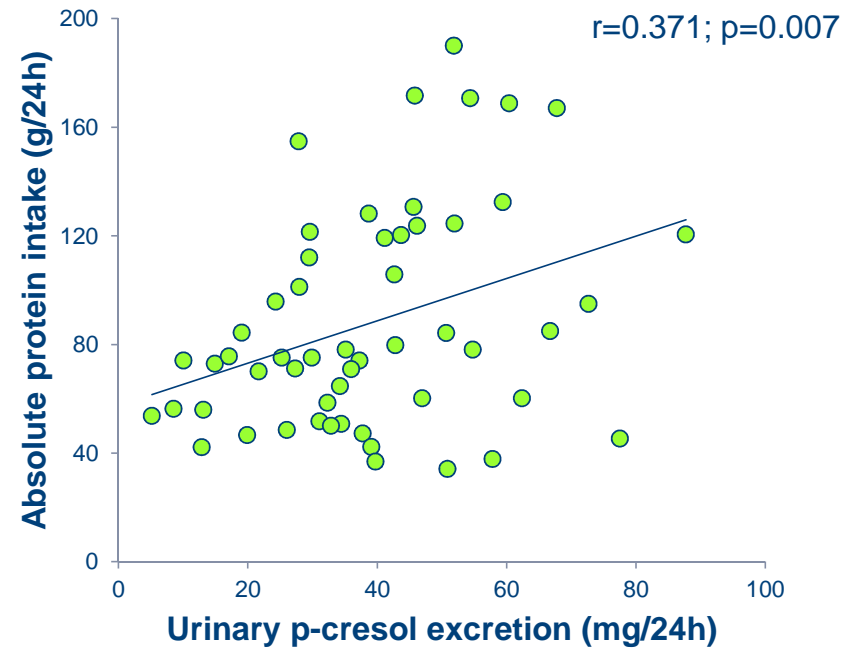
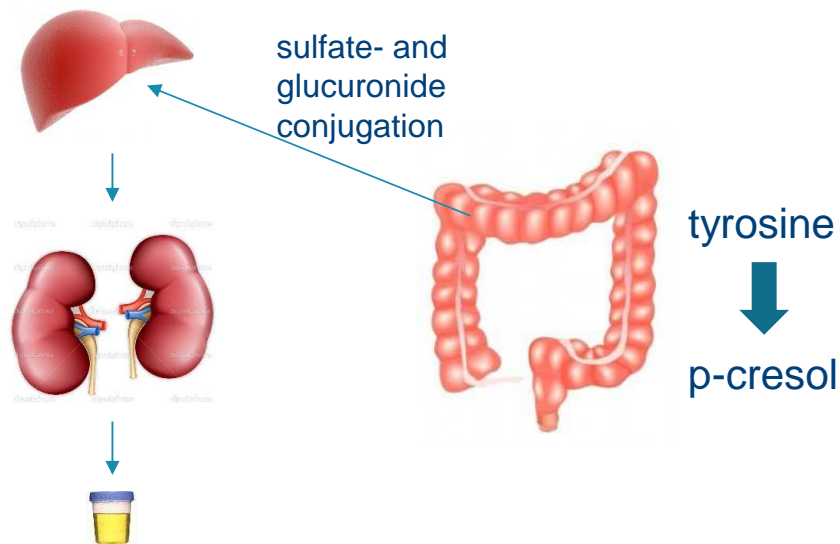




# High protein diets increase colonic protein fermentation

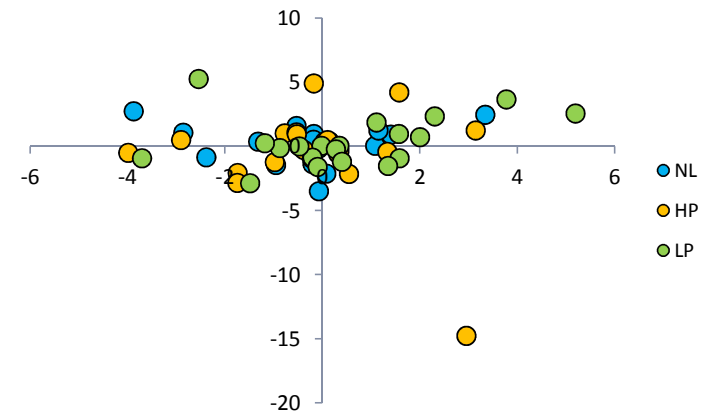
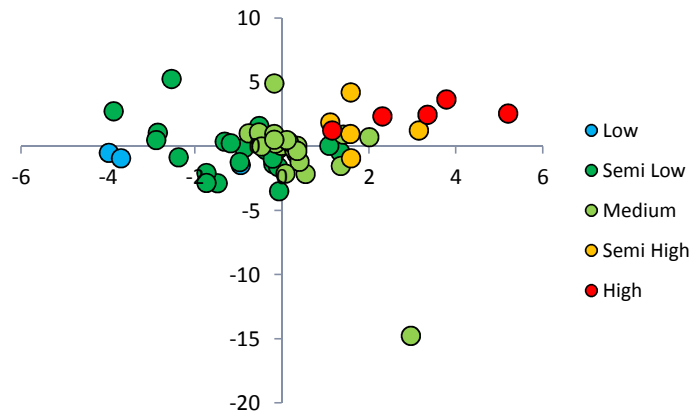
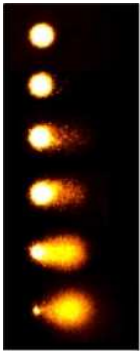
Urinary p-cresol excretion:

- Unique bacterial metabolite of tyrosine
- biomarker for protein fermentation

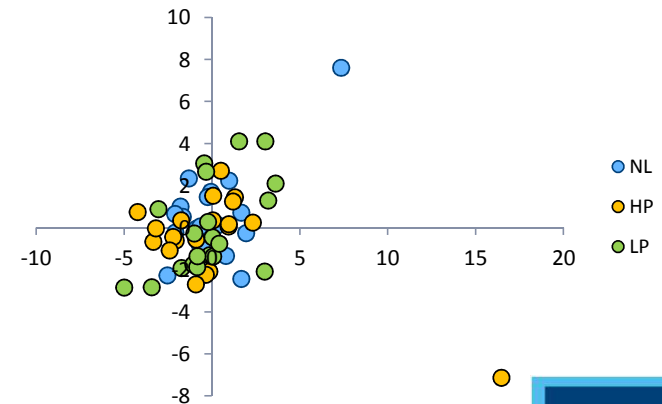
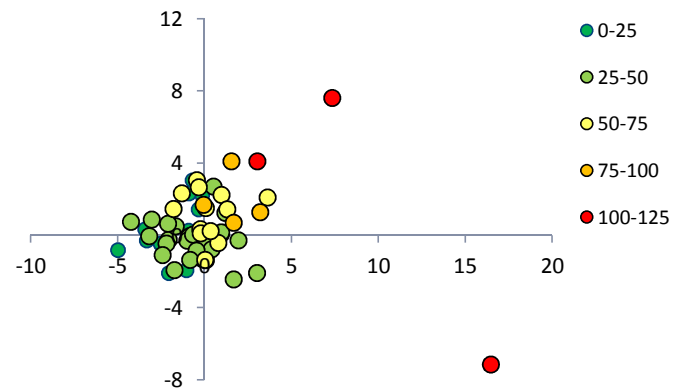


# Impact of protein intake on fecal water toxicity

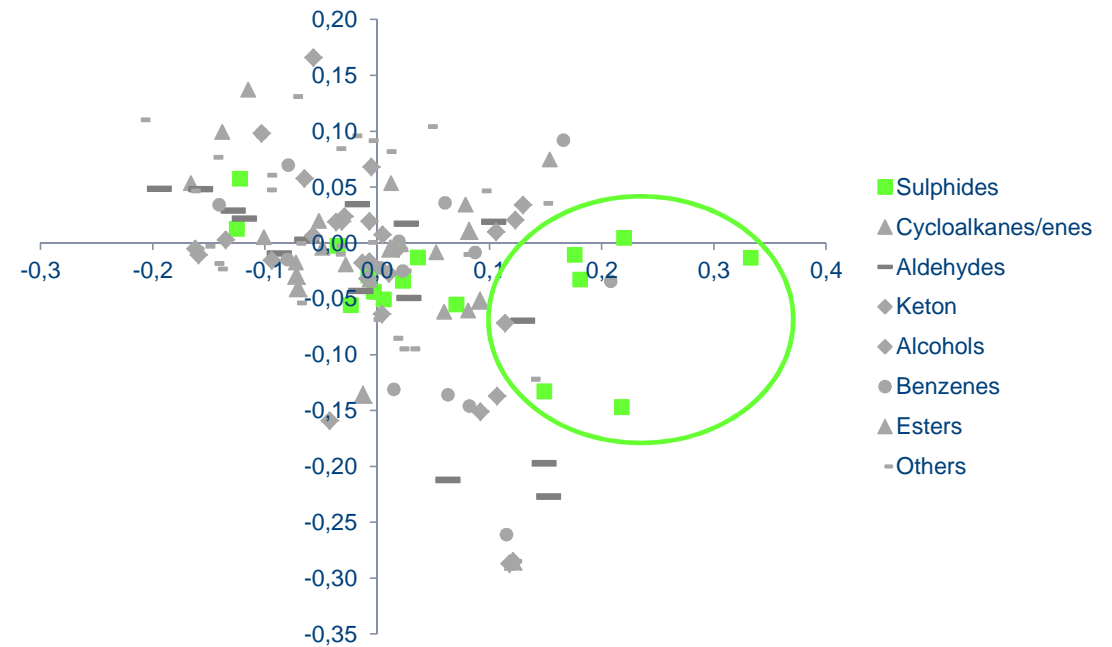
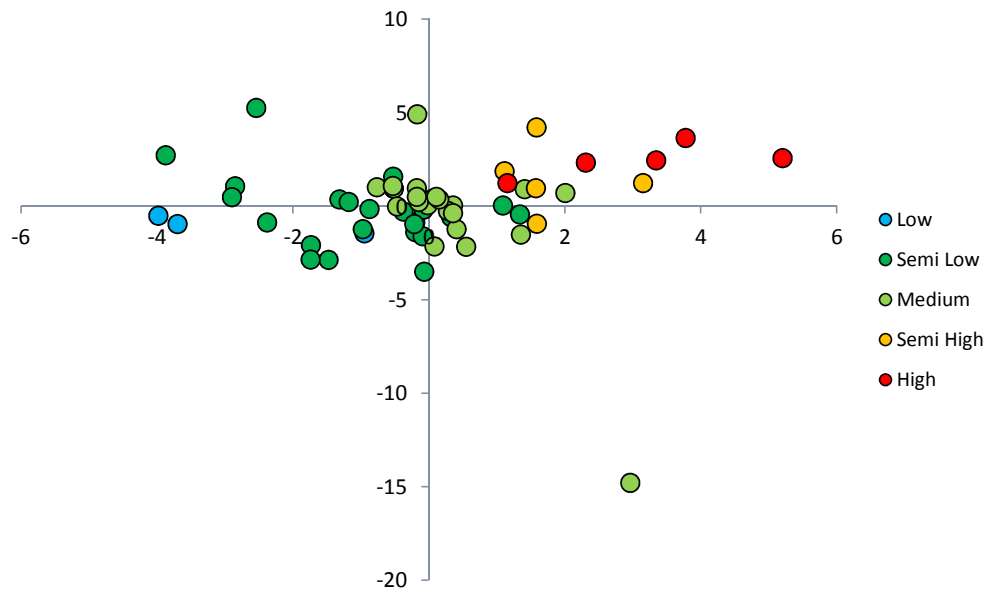
## genotoxicity



## cytotoxicity

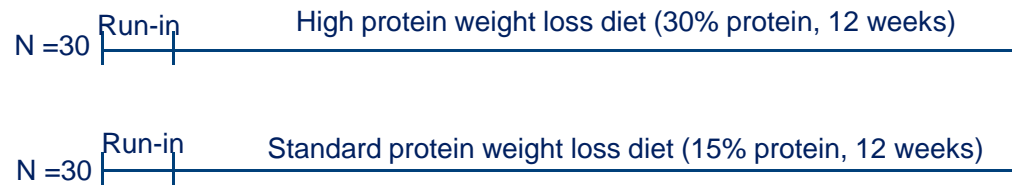


# High genotoxic samples are associated with sulfides



# Impact of a high protein diet with caloric restriction on fecal metabolites

\*



Energy requirement

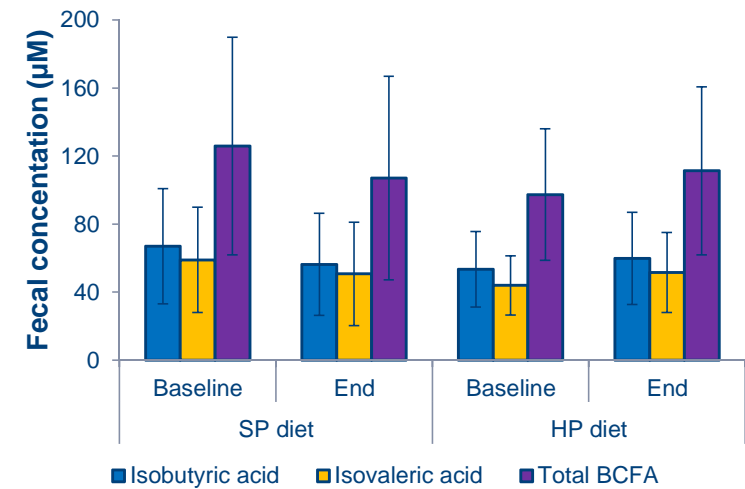


Fecal sample

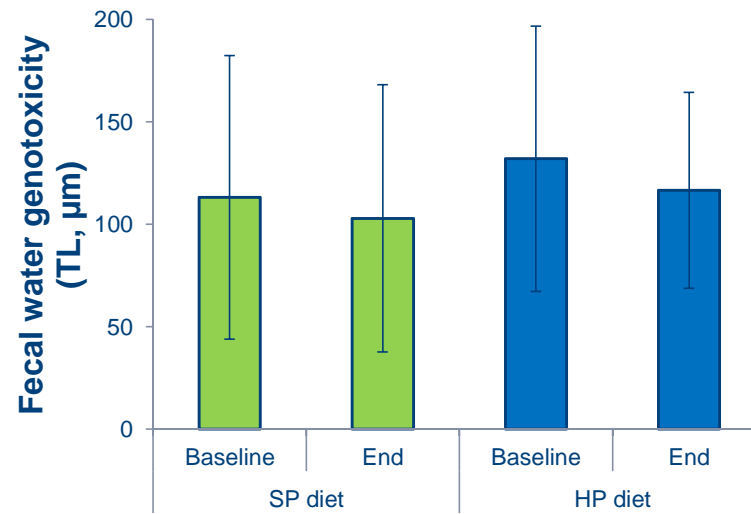
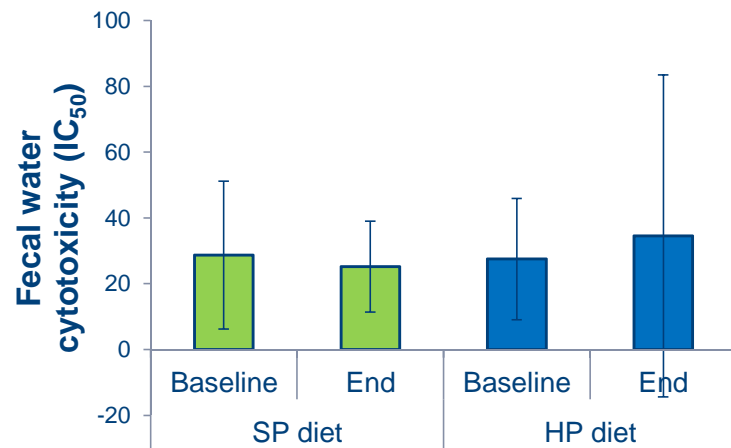


Dietary intake

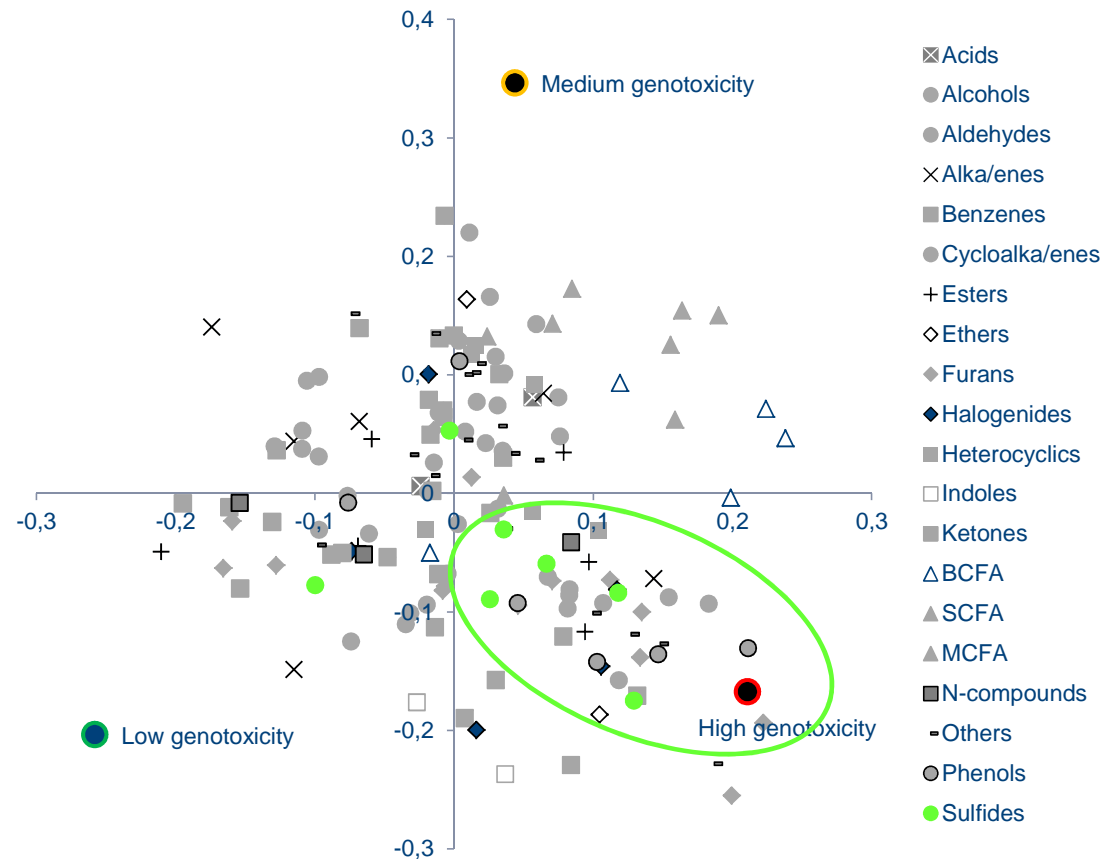
	Run-in	HP weight loss diet	SP weight loss diet
<b>Energy intake</b>	Isocaloric		
<b>Protein (%)</b>	15	30	15
<b>Carbohydrates (%)</b>	55	40	55
<b>Fat (%)</b>	30	30	30



## Fecal water toxicity was not affected by the diets



# Sulfides are associated with high genotoxic samples



# Role of sulfate-reducing bacteria (SRB) in fecal water genotoxicity

S-containing AZ  
(cysteine, methionine)

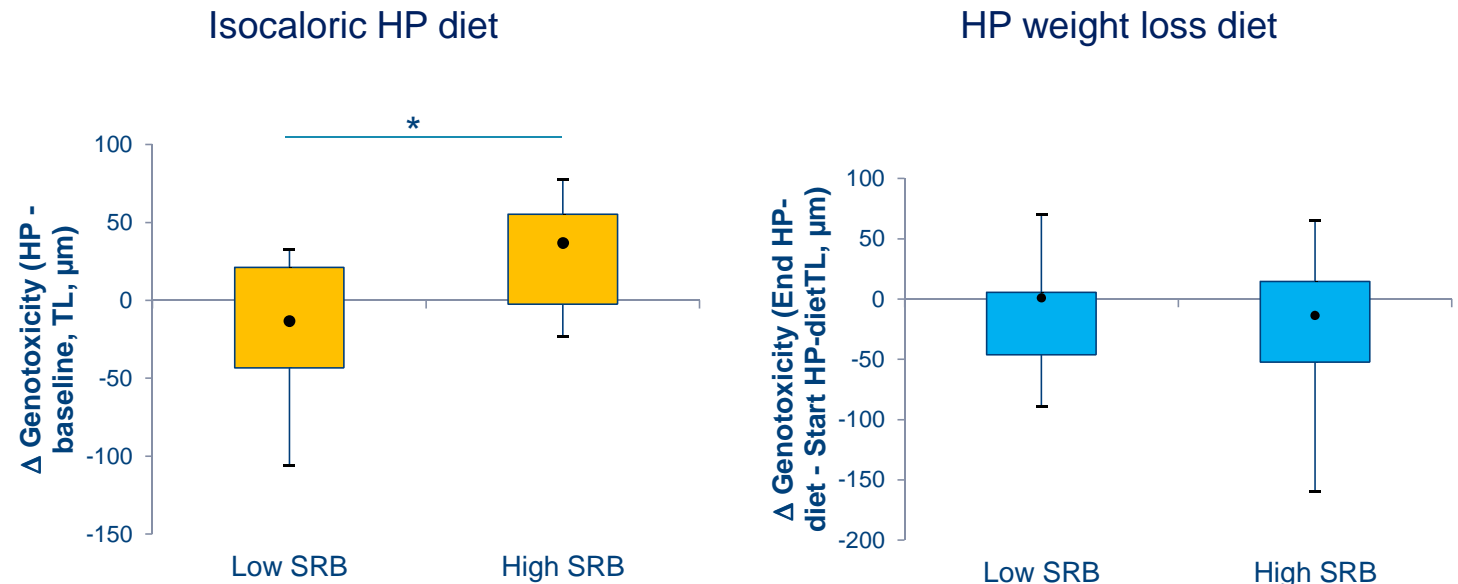
Inorganic sulfur



Sulfate

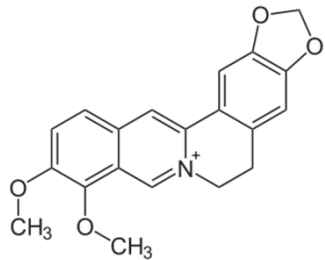


H<sub>2</sub>S



- ⇒ baseline number of SRB predisposes to increased fecal water toxicity only after an isocaloric high protein diet
- ⇒ minimal absolute protein intake seems required

# The lipid-lowering effect of orally administered berberine



*Coptis chinensis*

- Antimicrobial activity against bacteria, viruses, fungi, protozoans and helminths
- Lipid-lowering effect

BUT

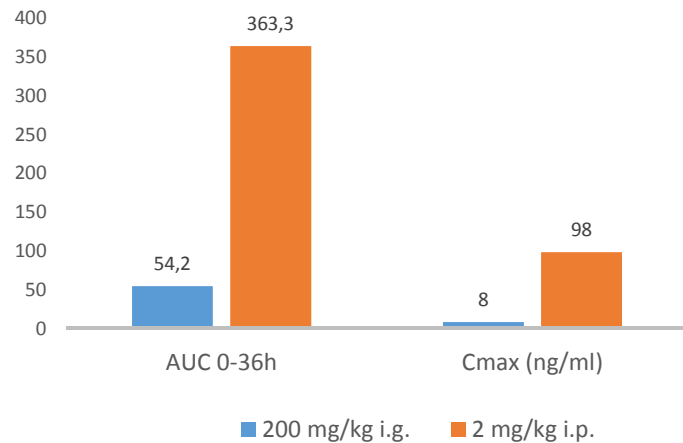
- Poorly absorbed from the gut  $\Rightarrow$  levels in blood and tissues far below effective concentrations used in cell culture studies



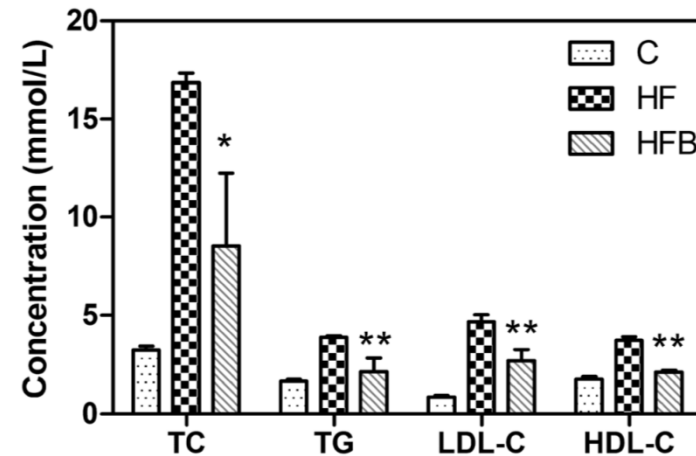
- Accumulation of berberine in the gut may affect the microbiota



# The lipid-lowering effect of orally administered berberine

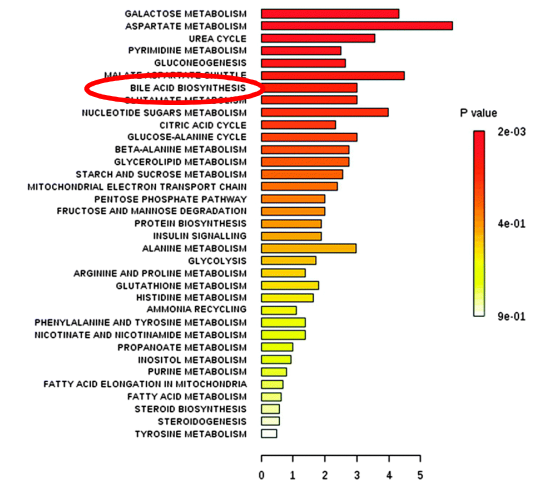
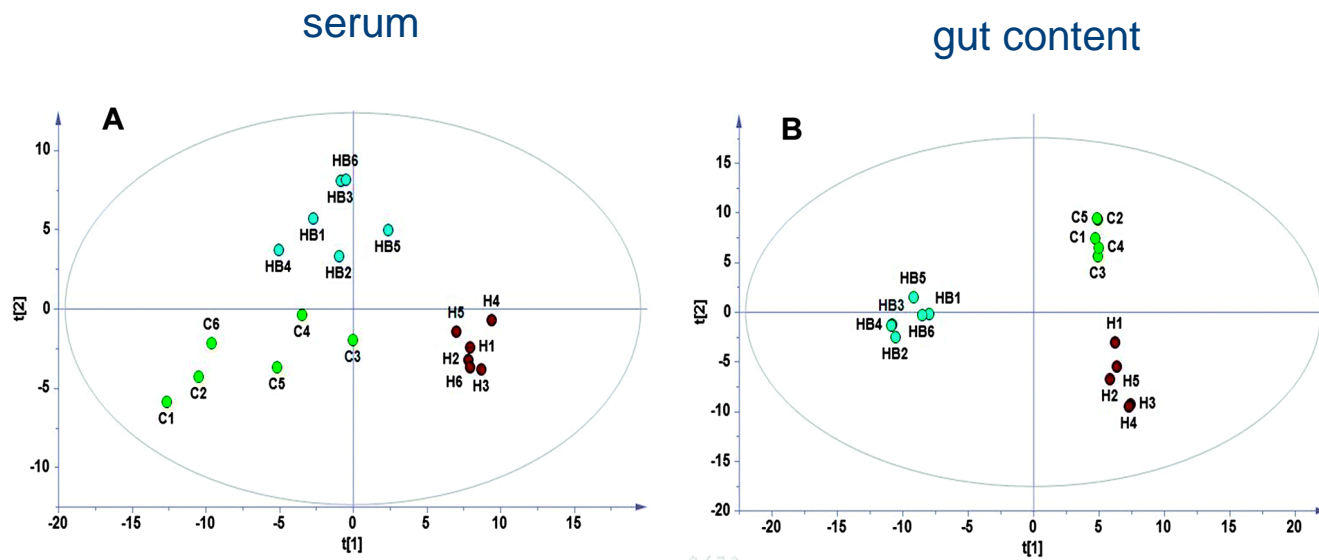


Control diet (C)  
High fat diet (HF)  
High fat diet + berberine (HFB)

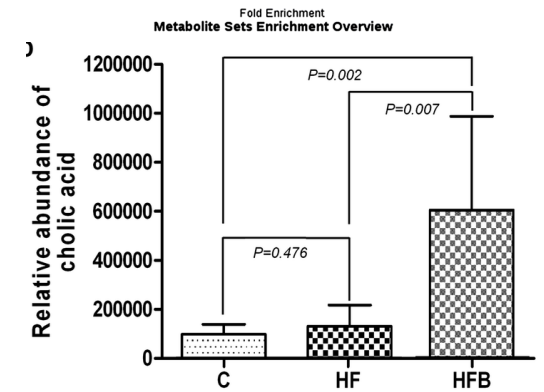


⇒ Metabolomic analysis of serum and cecal samples

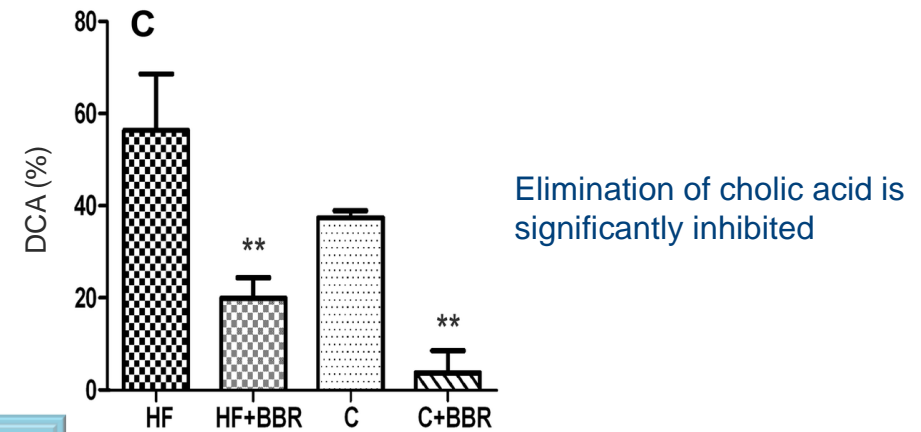
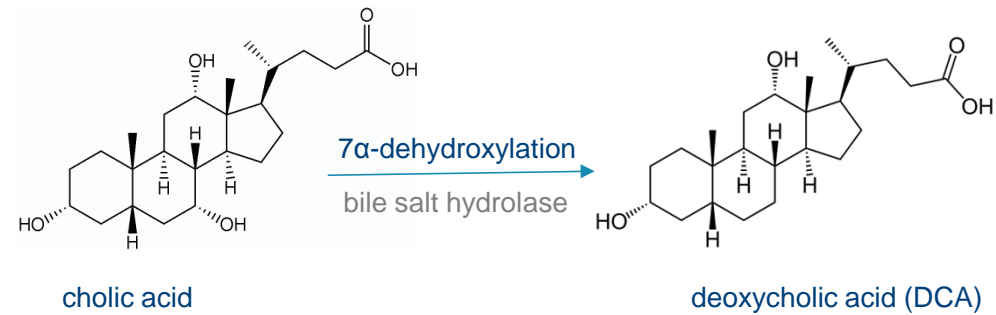
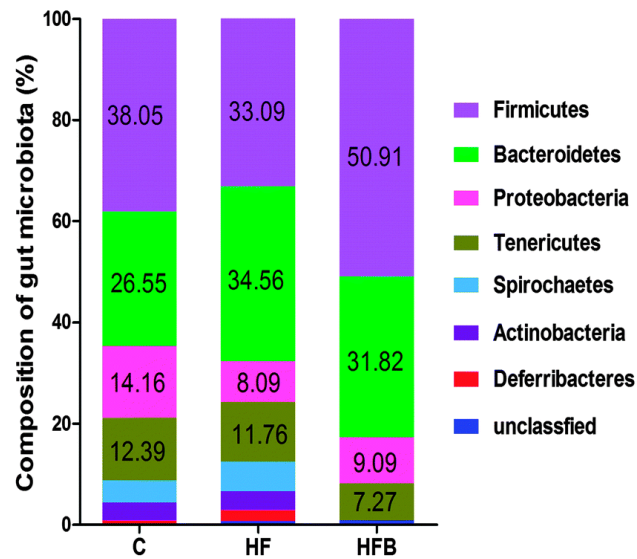
# Effect of berberine on the metabolites in serum and gut content



⇒ Metabolic impact analysis: significant impact on metabolism of cholesterol and/or biosynthesis of bile acids



# Effect of berberine on microbiota composition and activity



lipid lowering effect of berberine was attributed to increased bile acid synthesis and inhibition of its degradation by the microbiota

## Conclusions

- metabolomics holds much promise to increase our understanding of physiological processes
- Impact of the diet on the metabolome is more pronounced in animals than in humans
- main goal is to generate hypotheses about metabolic mechanisms
  - ⇒ need further validation in targeted studies