

“Human Microbiome Science: Vision for the Future”
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Gut Microbial Metabolism of Food Constituents: Modulating Human Dietary Exposures

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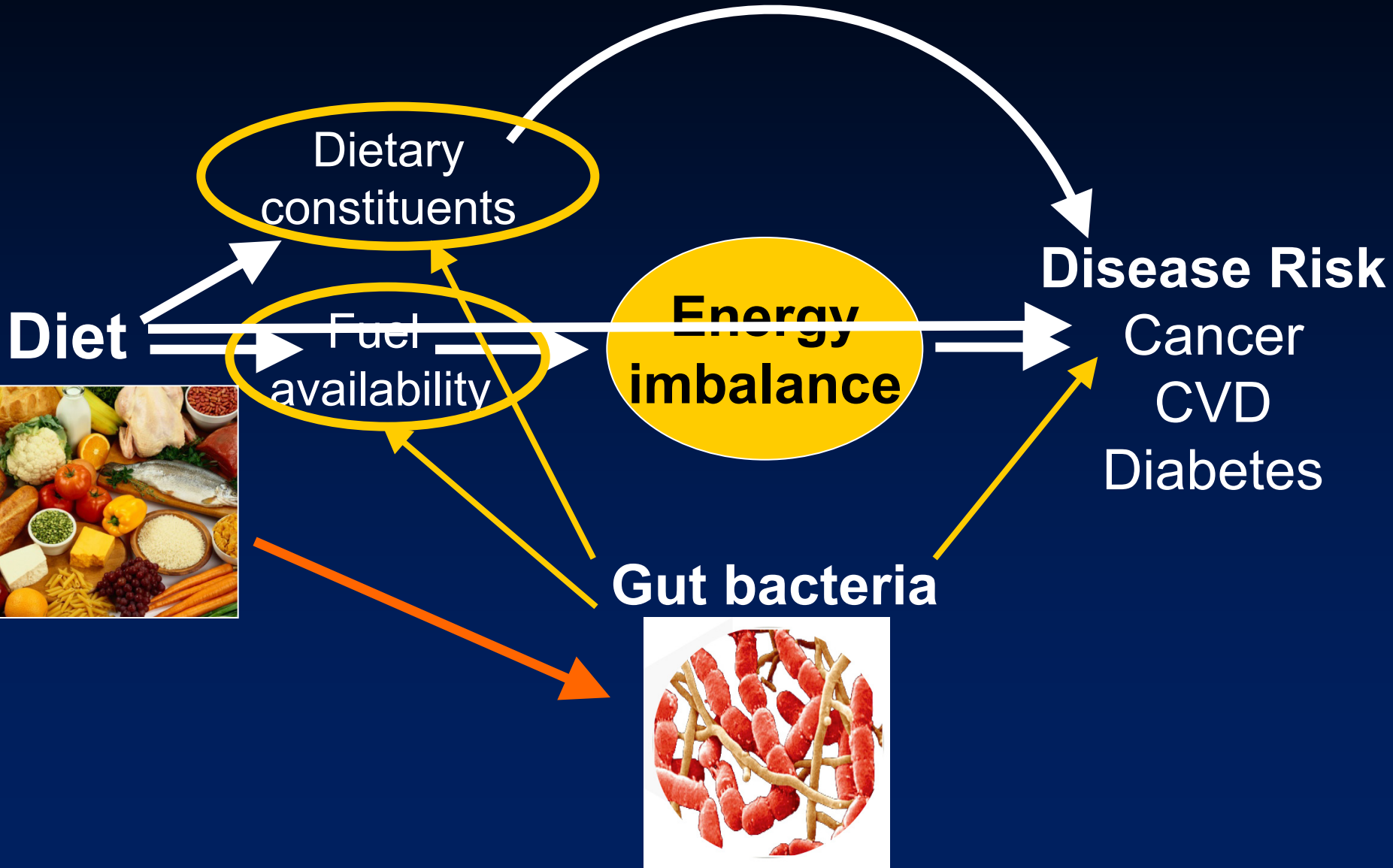
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Relationship of Diet and the Gut Microbiome to Health and Disease



Outline

- What are the gut microbes doing with our food?
- What is the effect of the gut microbiome on host dietary exposures?
- How might this influence disease risk?
- Gaps, needs, and challenges



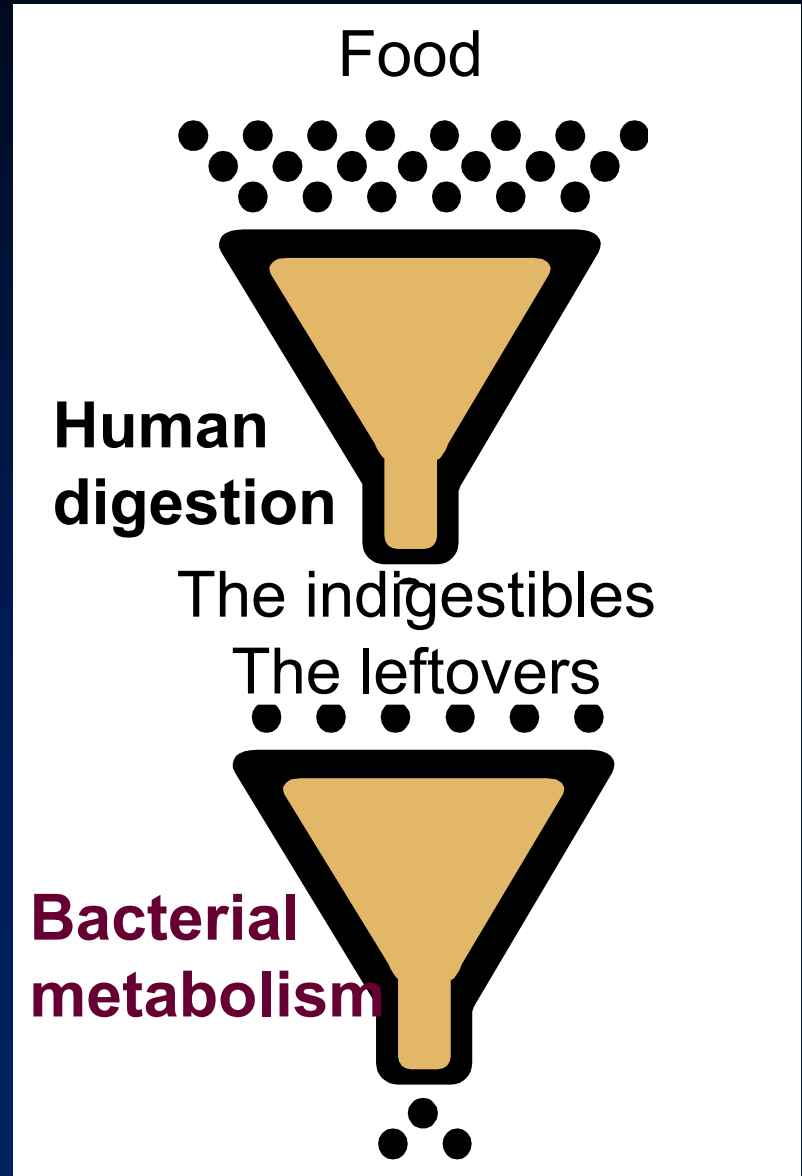
A collage of various food items including bread, pasta, fruits, vegetables, and meat. The items are arranged in a dense, overlapping manner, showcasing a wide variety of food sources. The background is a mix of colors from the different foods, creating a vibrant and textured appearance.

The human diet is complex.

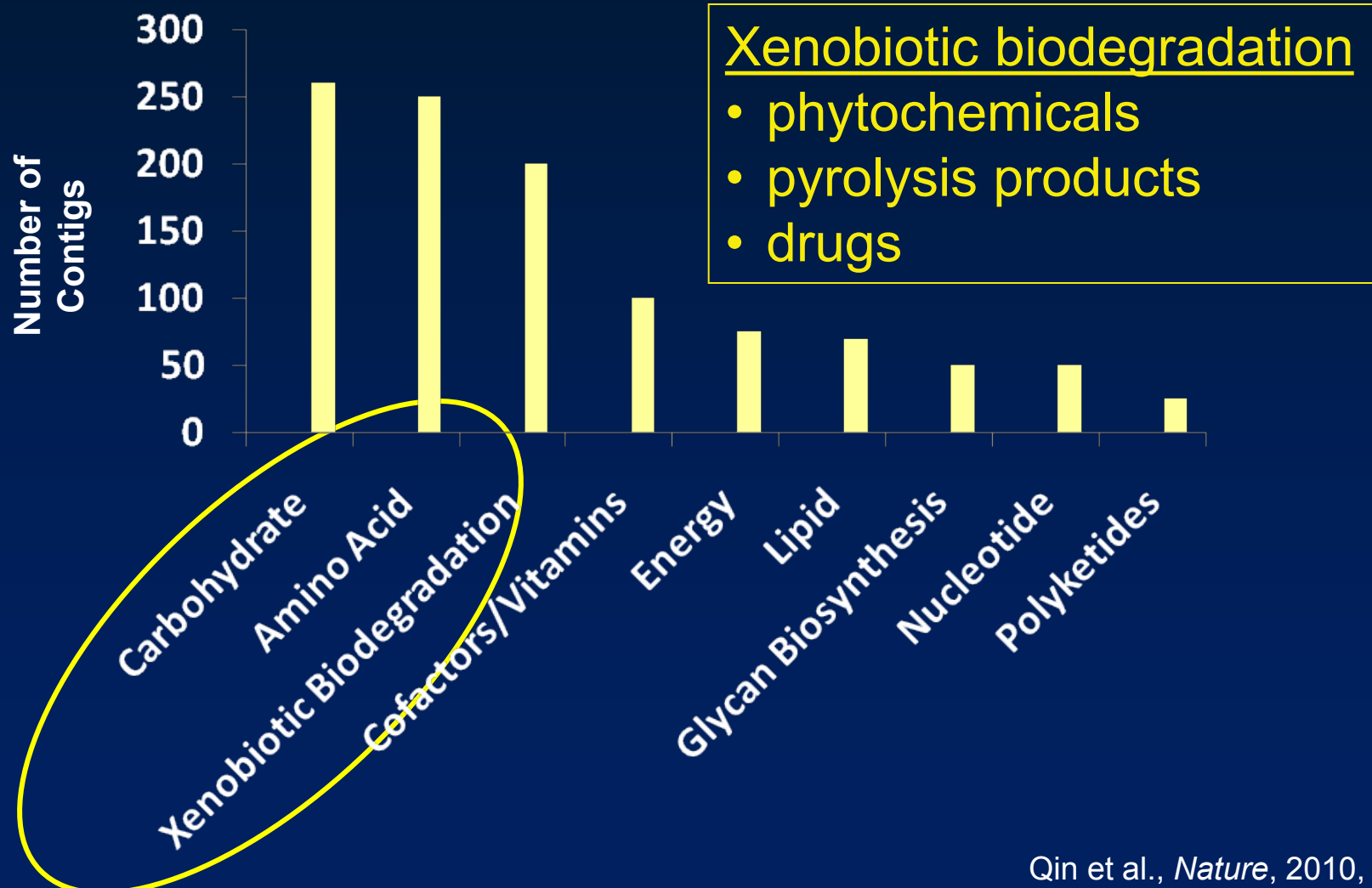
- 1000s of compounds
- Variety of methods of food preparation
 - Structure and particle size
 - Bioavailability to host

Gut Microbial Metabolism -- Designed to make the most of the situation

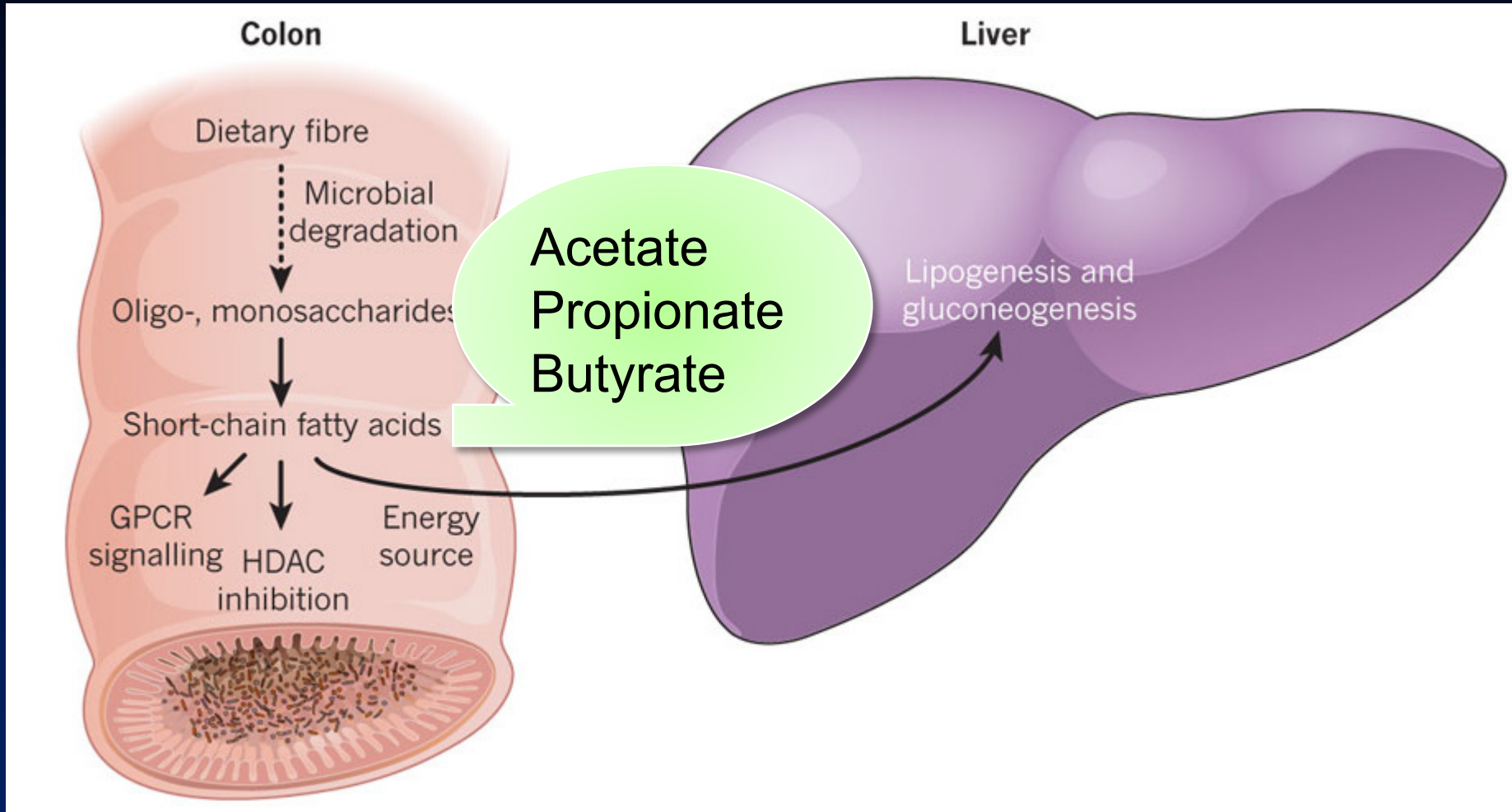
- Fermentation
- Reduction
 - nitrate, sulfate
- Esterification
- Aromatic fission
- Hydrolysis/deconjugation
 - glycosides
 - glucuronide conjugates



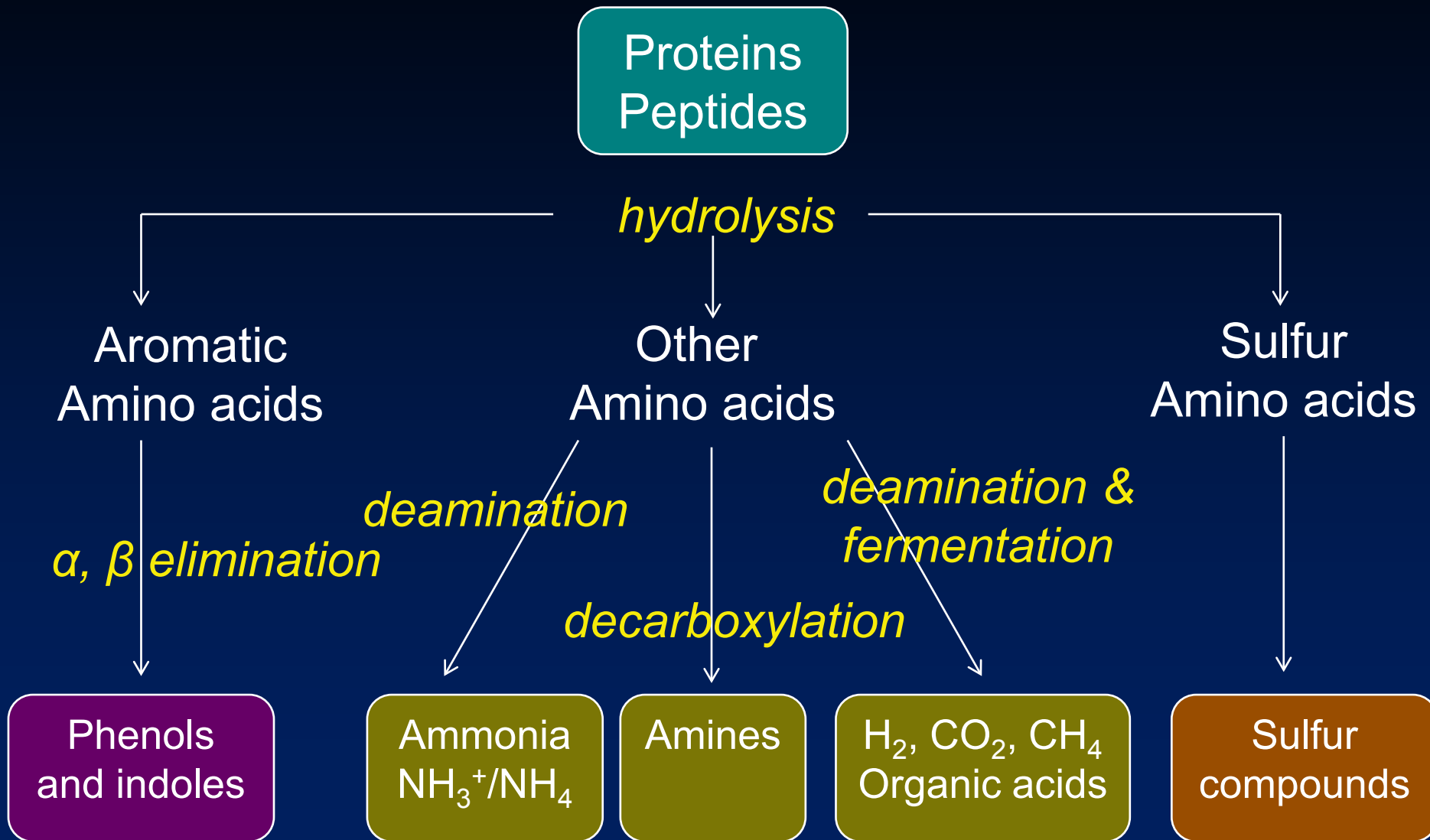
Distribution of Metabolic Pathways in the Gut Microbiome



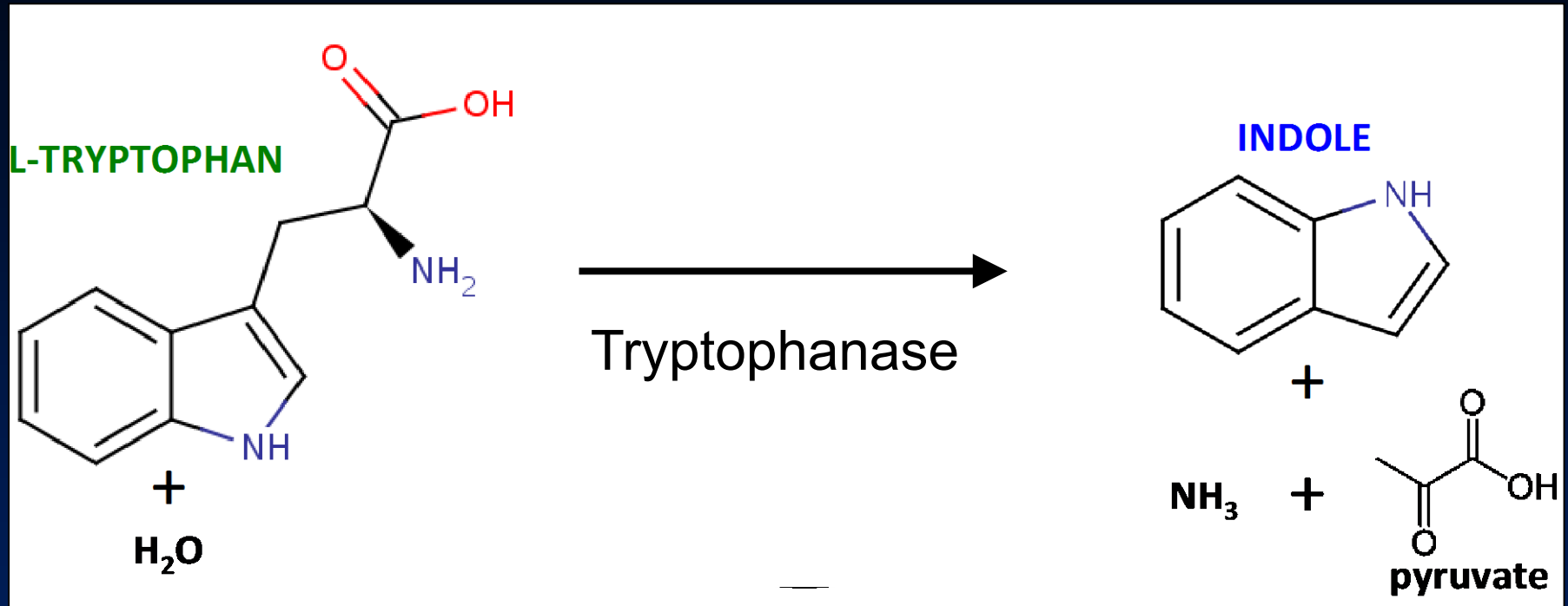
Fermentation of Carbohydrates



Microbial Metabolism of Proteins & Amino Acids



Aromatic Amino Acid Metabolism: Conversion of *L*-Tryptophan to Indole



- Concentration in human and rodent lumen – 0.1 to 4 mM
- Modulates expression of pro- and anti-inflammatory genes
- Strengthens epithelial cell barrier properties
- Decreases pathogen colonization

Sulfur Amino Acid Metabolism:

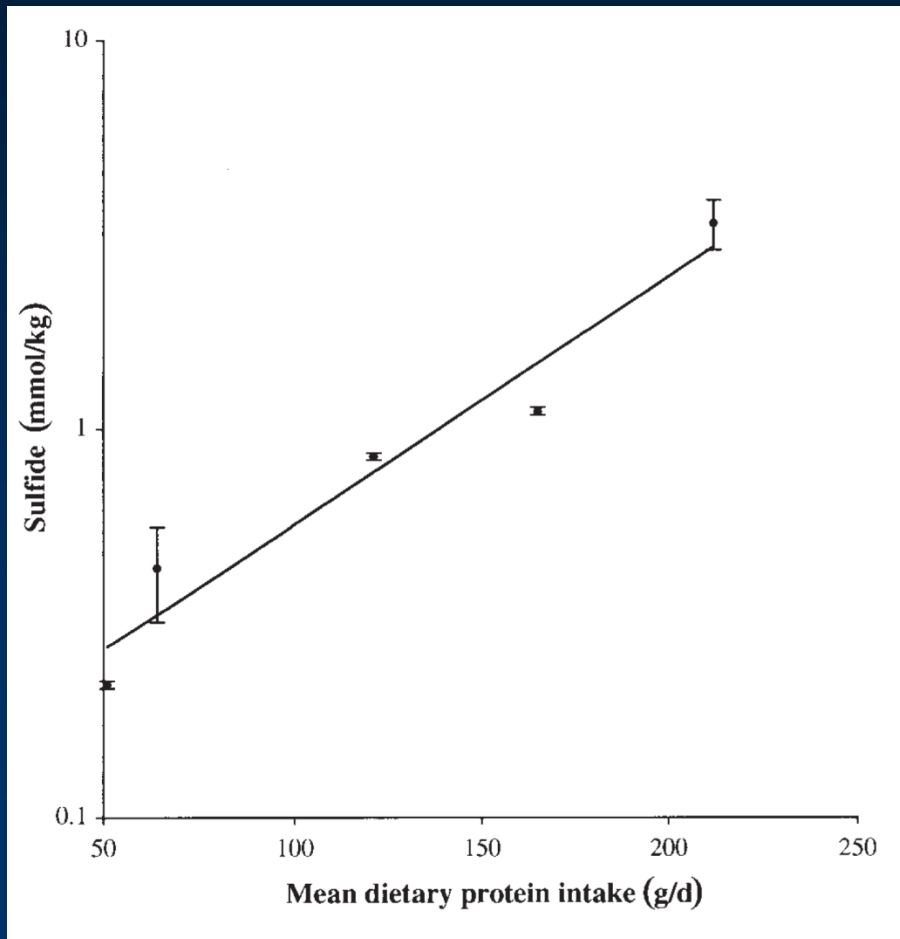
Generation of Hydrogen Sulfide (H₂S)

Produced by gut bacteria:

- Fermentation of sulfur-containing amino acids (methionine, cysteine, cystine, and taurine)
- Action of sulfate-reducing bacteria on inorganic sulfur (sulfate and sulfites)

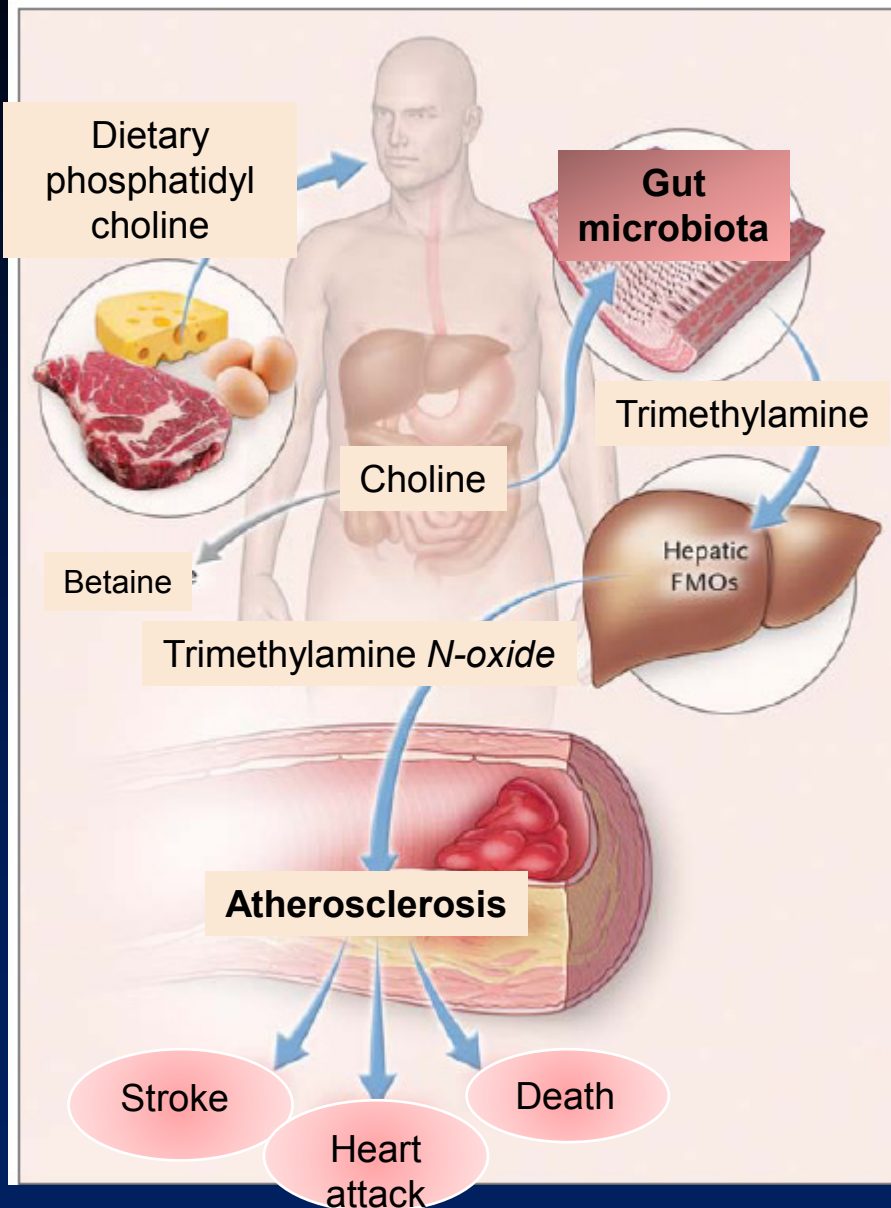
- Toxic to colonocytes both in vitro and in vivo
- Contributes to inflammation (UC and colon cancer)

Fecal sulfide concentrations increase with increased protein intake in a controlled feeding study



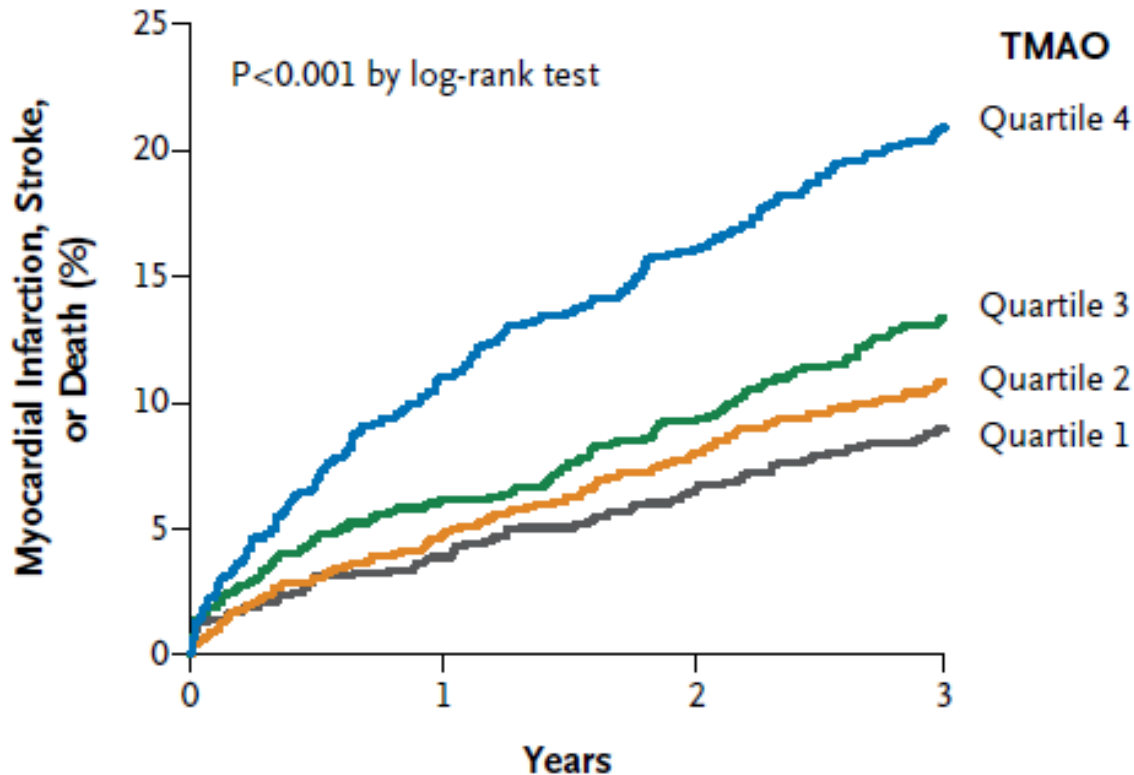
- 5 male volunteers
- Randomized cross-over study of 5 protein doses for 10 days each:
- 0 – 600 g meat /d
- Measured fecal sulfide excretion

Conversion of Choline to Trimethylamine



- Microbial metabolism important in production of TMAO.
- Levels of TMAO and choline and betaine increased after a phosphatidylcholine challenge (2 eggs and [d9]-phosphatidylcholine).
- Plasma TMAO suppressed after antibiotics and reappeared after antibiotic withdrawal.

Major Adverse Cardiovascular Events Increase by Quartile of Plasma TMAO



- 4007 adults undergoing elective diagnostic cardiac catheterization
- 3-y F/U for major adverse CVD events.
- Increased plasma TMAO associated with increased risk of CVD event.

Dietary Bioactive Phytochemicals



Phenolics

Phenolic acids
Stilbenes
Curcuminoids
Chalcones
Lignans
Flavonoids
Isoflavones

Terpenoids

Phenolic terpenes
Carotenoids
Saponins
Phytosterols

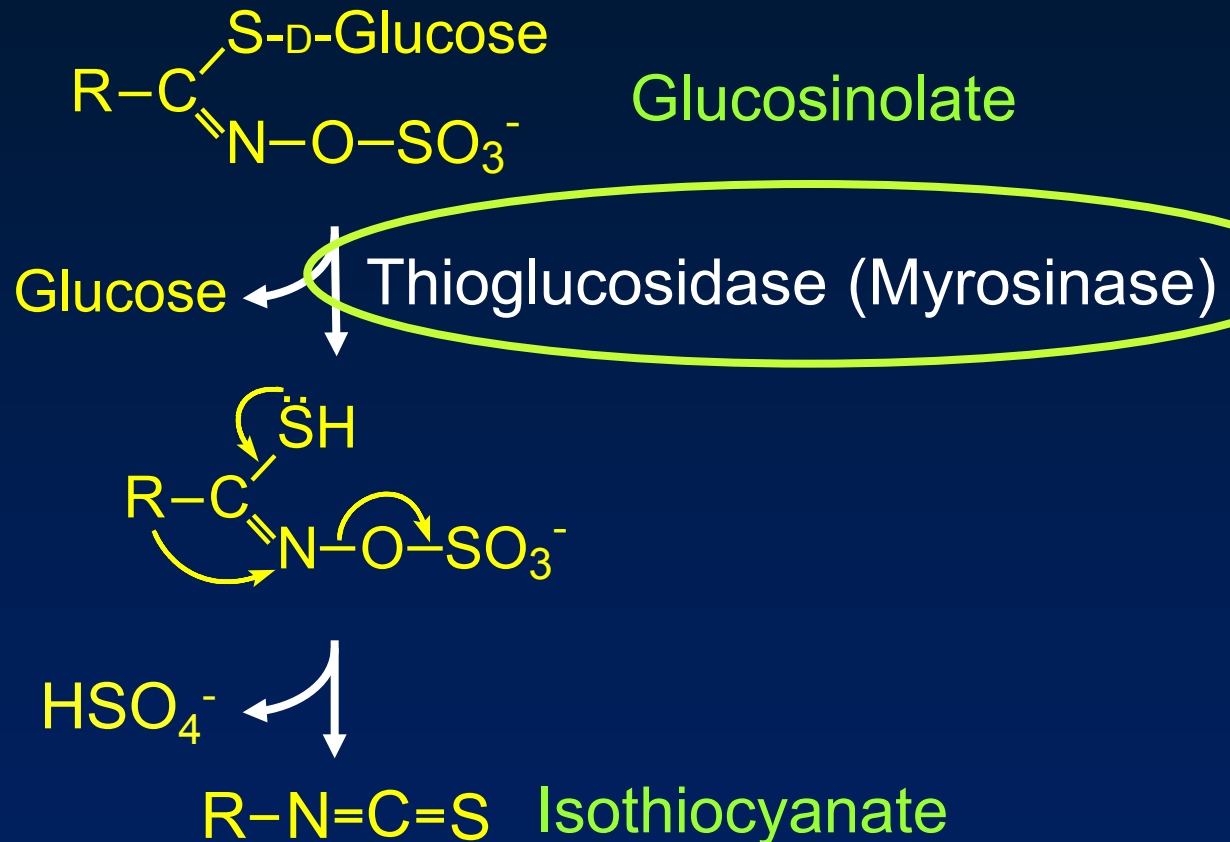
Organosulfurs

Thiosulfinates

N-containing compounds

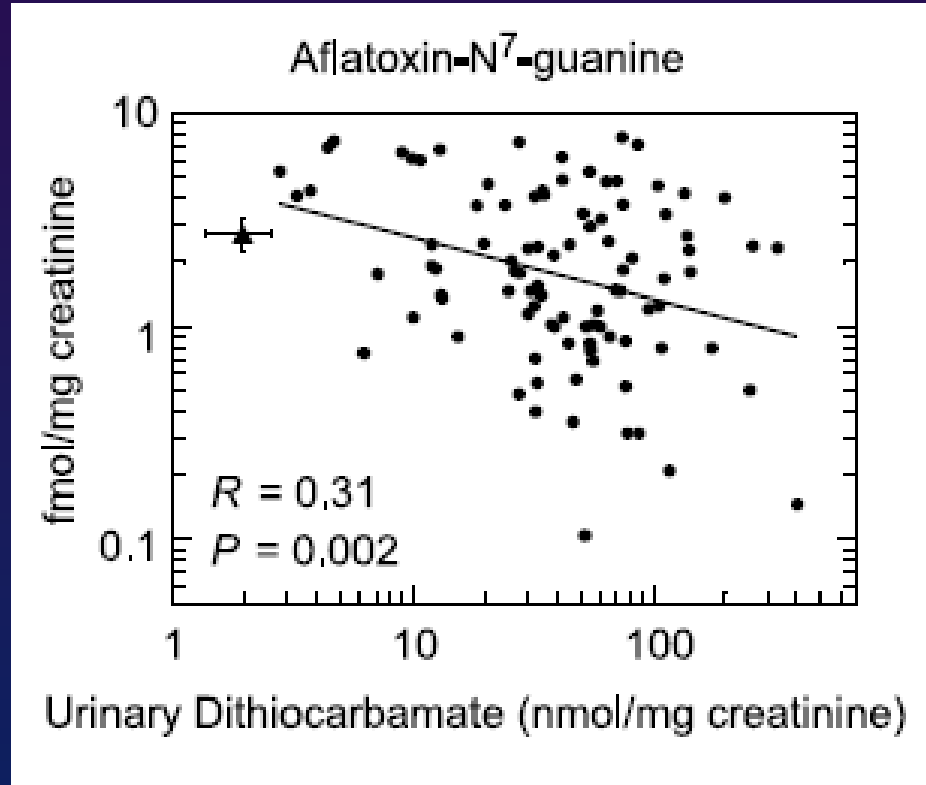
Glucosinolates
Indoles

Isothiocyanates from Glucosinolates in Cruciferous Vegetables

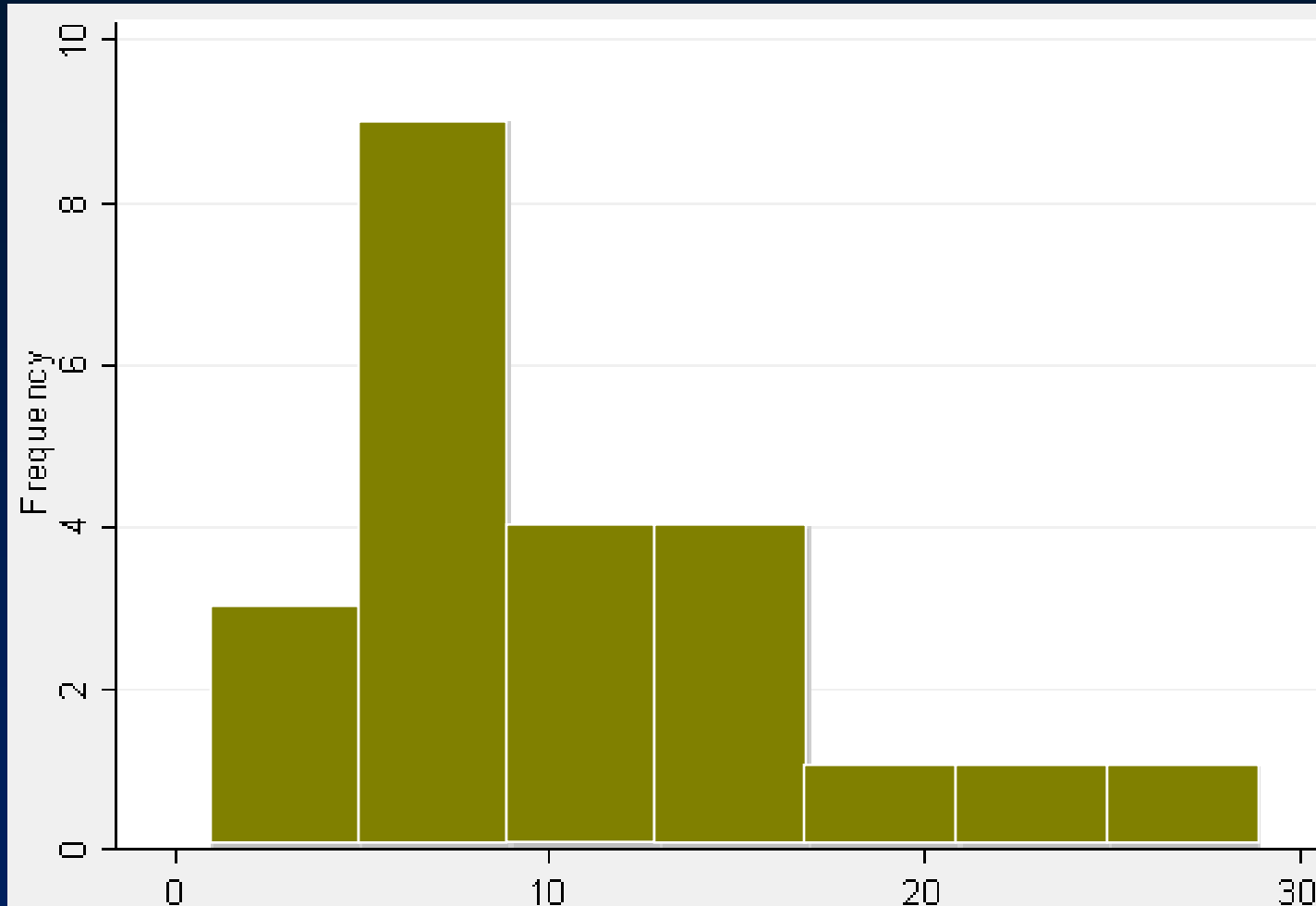


Inverse association between urinary ITC excretion and aflatoxin-DNA adducts – Interindividual variation in ITC bioavailability

- N=200, Qidong, China
- Randomized, parallel arm, 2-week trial
- 400 μmol glucoraphanin/d vs. placebo
- Urinary ITC recovery 1-45% of dose

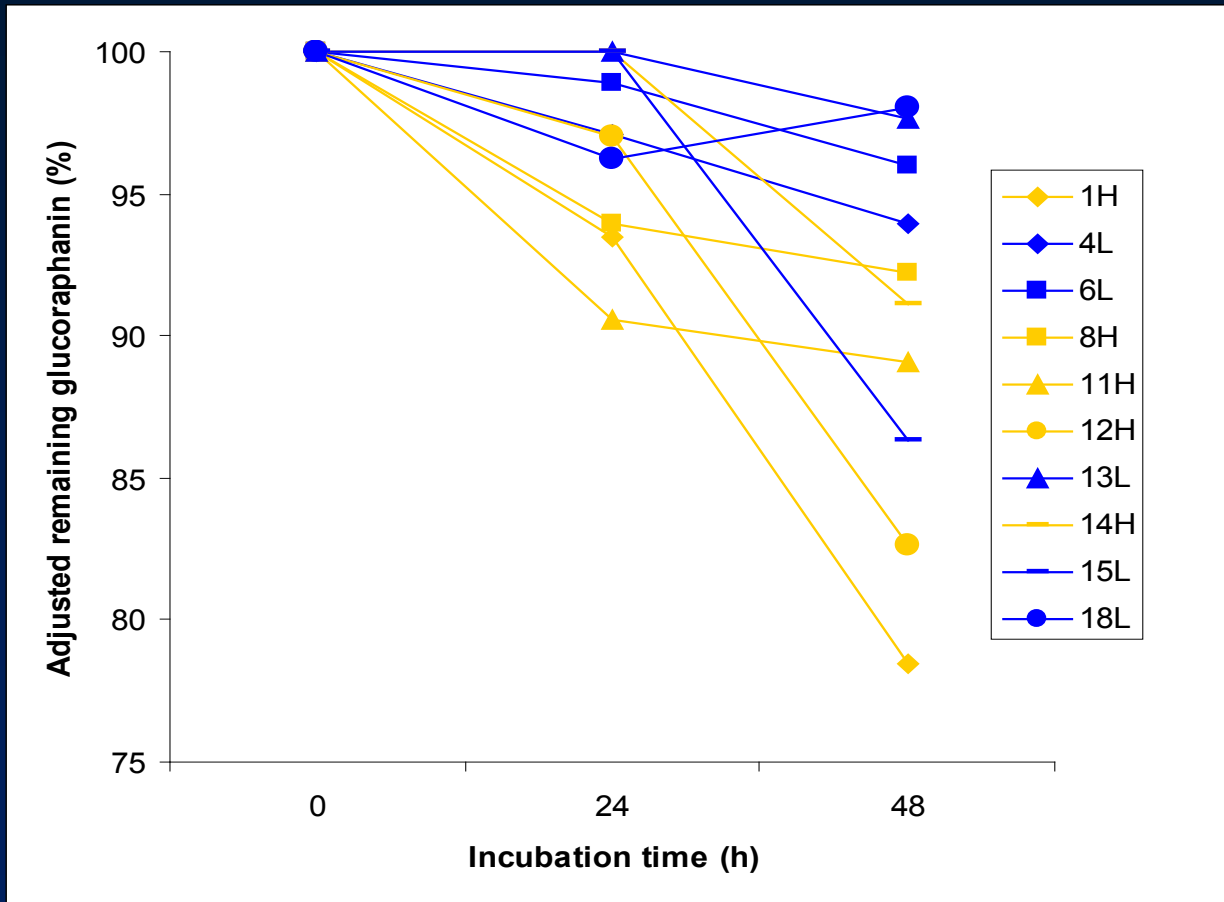


Isothiocyanate Recovery in Urine Ranged from 1 to 28% with 200 g Cooked Broccoli



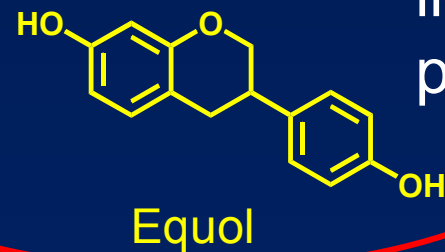
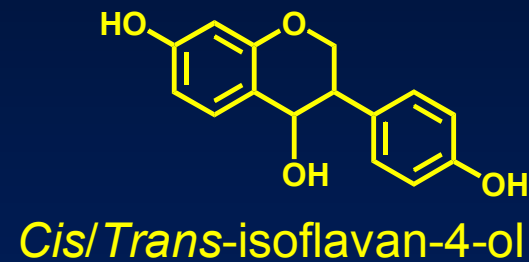
% ITC excreted in urine after 200 g broccoli

Fecal Bacterial Degradation of Glucosinolates In Vitro Differs by ITC-Excreter Status



- Low- and high-ITC excretors identified with standardized broccoli meal
- Fecal bacteria incubated with glucoraphanin for 48 h

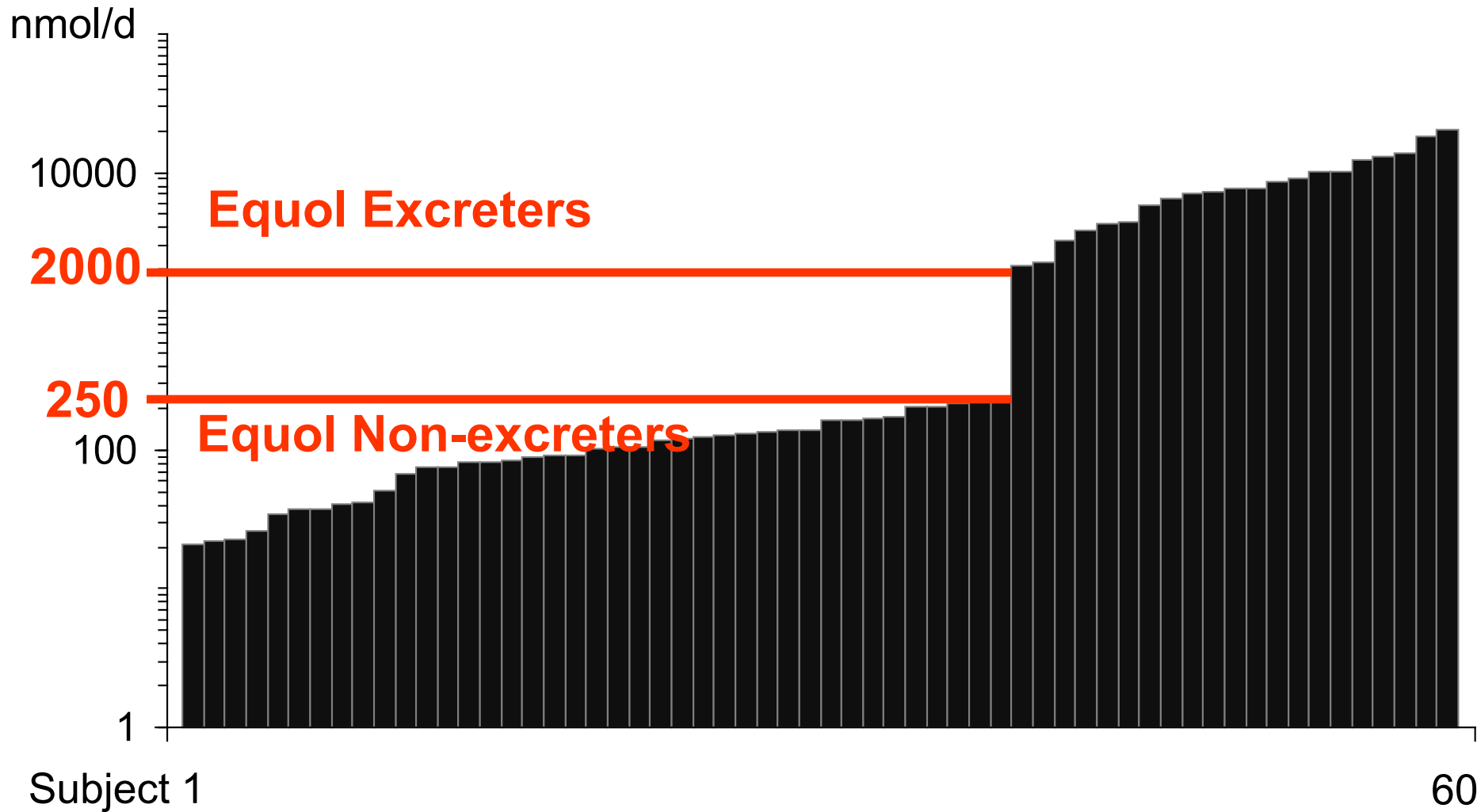
Microbial Production of Equol and ODMA



80-90% of individuals produce

20-60% of individuals produce

Urinary Equol Excretion with Soy Challenge



Soy Interventions

Equol-Producing Capacity Associated with:

- Greater lengthening of menstrual cycle follicular phase.
Cassidy et al., Am J Clin Nutr 60:333, 1994.
- Lower estrone, estrone-sulfate, testosterone, DHEA, DHEA-sulfate, androstenedione, and cortisol, and higher SHBG and mid-luteal phase progesterone
Duncan et al., Cancer Epi Biomark Prev 9:581, 2000.
- Improved bone mineral density in post-menopausal women.
Lydeking-Olsen et al, Eur J Nutr 43: 246, 2004.
- Differential gene expression in peripheral lymphocytes of equol producers and non-producers.
Niculescu et al, J Nutr Biochem 18:380, 2007.

Equol-Producing Capacity and Health: Observational Studies

- Positively associated with 2-OH/16 α OHE1 ratios in premenopausal and postmenopausal women.

Atkinson et al, *J Steroid Biochem Mol Biol* 86:71, 2003

Frankenfeld et al, *J Steroid Biochem Mol Biol* 88:399, 2004

- Mammographic density 39% lower in equol producers.

Frankenfeld et al, *Cancer Epidemiol Biomarkers Prev* 13:1156, 2004

- Plasma equol concentrations inversely associated with prostate cancer risk in Japanese men.

Akaza et al., *Jpn J Clin Oncol* 32:296, 2002

- Significant interaction between soy intake and equol-producer status in predicting breast density in postmenopausal women.

Fuhrman et al., *Cancer Epidemiol Biomarkers Prev* 17:33, 2008

What Human Gut Microbes Produce S-(-)Equol?

Daidzin ► Daidzein ► Dihydrodaidzein ► Equol

Daidzein ► Equol

- *Adlercreutzia equofaciens*
- *Bacteroides ovatus*
- *Bifidobacterium*
- *Eggerthella* sp YY7918
- *Enterococcus faecium*
- *Fingoldia magna*
- *Lactobacillus mucosae*
- *Lactococcus garvieae*
- *Ruminococcus productus*
- *Slackia* sp HE 8
- *Streptococcus intermedius*
- *Veillonella* sp

Daidzin ► Dihydrodaidzein

- *Clostridium-like bacterium*

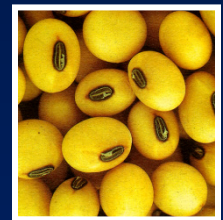
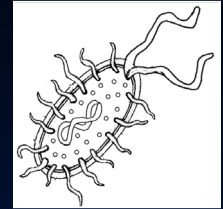
Dihydrodaidzein ► Equol

- *Eggerthella* sp Julong 732

Microbial Metabolism of Dietary Components

Summary

- Gut microbial metabolism modifies a variety of dietary components.
- Differences in gut microbial community capacity to handle substrates is detectable as metabolic phenotypes.
- Diet as consumed is not necessarily that experienced by the host.
- The gut microbiome needs to be considered in context of host diet to understand its impact on metabolism and disease risk.



Gaps, Needs and Challenges: More Specific to Nutrition

- **Challenge:** Testing causality of gut microbiome's contribution to health and disease in humans.
- **Need:**
 - Prospective cohorts with repeated measures of exposure (i.e., diet, etc) and samples for gut microbiome characterization.
 - Well-controlled dietary interventions to understand inter-individual variation in bacterial metabolic phenotypes in the context of diet.
 - Accurate model systems of human dietary metabolism and associated microbiota.

Gaps, Needs and Challenges: Broader Considerations

- To facilitate transdisciplinary research to allow for integrated breadth and depth of knowledge.
- Methods of assessing composite functionality of the gut microbiome and integration of the structure and function of microbial systems.
- Computational methods to integrate high-dimensional microbiome and metabolome data.

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