

The Gut Microbiome: Contributions to Variation in Response to Plant-Food Bioactives

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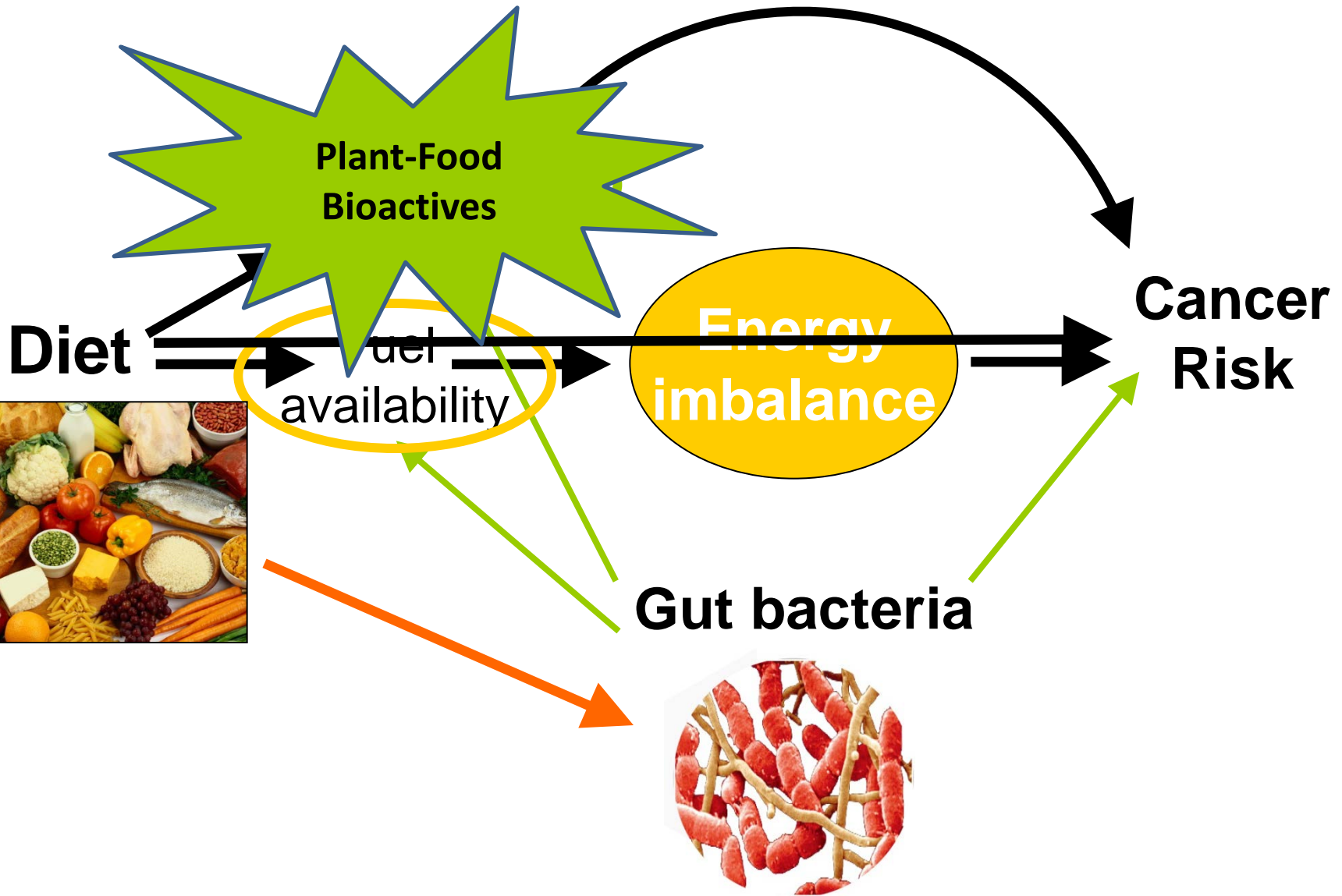
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Human Gut Microbiome

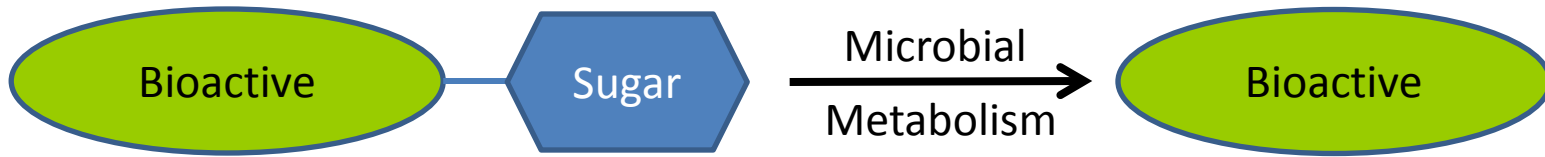
- Collective genomes of the gut microbial community.
- ~ 10-100 trillion microorganisms in GI tract (10 times more than human cells in the body).
- ~500-800 species.
- 100 x more genes than human genome.
- Important symbiosis between human host and microorganisms.



Relationship of Diet and the Gut Microbiome to Cancer Risk



Microbial Metabolism of Plant-Food Bioactives



Cruciferous vegetables

- Glucosinolates → isothiocyanates



Soy food isoflavones

- Daidzein → equol and ODMA



High-fiber foods

- Plant lignans → enterolactone & enterodiol

What are we finding?



Cruciferous vegetables

- Fecal bacterial glucoraphanin degradation higher in high-ITC excreters.

Li et al., Br J Nutr, 2011



Soy food isoflavones

- Obese adults more likely to be ODMA-nonproducer phenotype.

Frankenfeld et al., Eur J Clin Nutr, 2014



High-fiber foods

- Gut bacterial composition in high ENL excreters is different than low ENL excreters.

Hullar et al, Cancer Epidemiol Biomarkers Prev, 2015

Where is this taking us?

Characterize gut microbial-diet metabolism phenotypes

- *Identify associations between gut microbiome and gut microbial metabolism of plant-food bioactives*

Improve understanding of effects of bioactives on cancer risk

- *Using observational and intervention studies*
- *Stratification by microbiome differences or phenotypes*

Personalized/precision nutrition for disease prevention

- *Subgroups who may benefit more or be harmed by particular bioactives*

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