

Introduction to Gut Microbiota



Tine Rask Licht Senior Scientist, Research Manager National Food Institute, Technical University of Denmark Email: <u>trli@food.dtu.dk</u> Phone: +45 72 34 71 86

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The Bacteria in our Intestines

• Who are they? - They outnumber us!

- What are they doing? – And what is their impact on our health?
- What determines the bacterial composition?
 - The intestinal ecosystem
- How do we study them? – Methods for gut microbiota analysis



Intestinal microbiota



10¹⁴ bacteria more than 500 different species

Most of these are not cultured

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Diversity of predominant gut species





Zoetendahl, Vaughan & de Vos, 2007, Molecular Microbiology 59:1639-50

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Impact of gut microbes on host health



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• Immune system

- Maturation/maintenance
- Allergy
- IBD/IBS (Crohn's, Ulcerative Colitis)

Competitive exclusion of pathogens

- Colonization resistance
- Competition for nutrients
- Competition for adhesion sites
- Production of SCFA and antipathogenic substances (Lactic Acid Bacteria)

Host nutrition utilization

- Growth promotion
- Obesity
- Cancer
- Cardiovascular diseases

The Good, the Bad and the Ugly...



The good

- Fermentative bacteria
- Short Chain Fatty Acids, Low pH
- Immune balancing

The bad

- Putrefactive, proteolytic
- Ammonia, amins, indole, toxic enzymes

• The ugly

- Pathogenic, infective, toxigenic



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Fermentation in the colon





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From: Guarner and Malagelada, 2003 Lancet 361:512-519

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The Good: Butyrate formation





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Figure 2. production of carcinogens and tumour promoters by the colonic microflora

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Some facts about the microbiota of the human gut

- It is surprisingly stable
- Variation between individuals is much larger than variations over time
- Thus we all have our own'poopprint'





What determines the microbiota of an individual?

• First colonizers

- Difference between children born by cesarian and children born through the birth channel

Host gene pool

 Identical twins often have highy similar microbiotas

• Diet

 For adults little but probably important influence

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Cross feeding interactions







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The intestine considered as a chemostat (Rolf Freter, 1983)

dB/dt = kB - uB
(B: bacterial population; k: growth rate; u:excretion rate)

- k is a function of nutrient availability
- u is approximately constant
- If B is constant, then k=u



Freter:



- Two bacterial strains competing for the same limiting nutrient can co-exist in the intestine only if one has specific adhesion sites available.
- Populations limited by the same nutritional compound will typically be closely related.
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Methods for investigation of microbial composition in complex populations

• Selective cultivation

Poor discrimination and shows only the 'tip of the iceberg'

- Many oxygen sensitive organisms

16S PCR-based methods

 DGGE (Denaturing Gradient Gel Electrophoresis)
T-RFLP (Terminal Restriction Fragment Length Polymorphism)

• Genomic-based appraoches

- Microarrays (e.g. 16S based)
- Metagenomic sequencing

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Secondary structure of

procaryotic 16S rRNA

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16S rRNA-based phylogenetic tree

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Figure S8

Phylogenetic tree of the 16S rKNAs corresponding to the represented in the MscS protein phylogenetic tree. (Psymi et al., 2001)

Example: Analysis of composition of intestinal microbiota by DGGE of PCR-amplified ribosomal rRNA genes





Example: Microarray analysis



- Typically 16S gene based (phylogenetic array)
- However, could also target other genes or their expression
- Data handling and analysis is essential

...And that's THE END!









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