Microbial community response to environmental conditions & the “Microbiomes in Transition “MinT” Initiative

JANET K. JANSSON, PI
We live in a changing world largely governed by microbial processes, and the consequences of changes in microbiomes and their functions are largely unknown.

- **Examples of environmental ecosystems in transition caused by climate change:**
  - Coastal ecosystems – rising seawater levels and changes in salinity
  - Arctic – rising temperatures and permafrost thaw
  - West coast – increased drought and fire frequency

- **Examples of external influences that cause transitions in human microbiome:**
  - Chemical and drug exposure
  - Diet
  - Disease

Gilbert et al., Nature 2016 535:94-103
MinT Team & Research Focus
**Approach: Multi-omics pipeline will facilitate determination of impacts of perturbations on microbiomes**

Impact of climate change on environmental microbiomes

Impacts of environmental exposures, diet & disease on human gut microbiome

**Examples of information:**
Microbial community composition comparisons

**Importance of environmental variables**

Draft Genomes of novel uncultivated microbes

Biochemical pathways

**Microbiome (microbial community)**

**Metagenome (total genes)**

**Meta-Transcriptome (expressed genes)**

**Meta-Proteome (protein products)**

**Meta-Metabolome (metabolites)**

Examples of information:
Microbial community composition comparisons

Importance of environmental variables

Draft Genomes of novel uncultivated microbes

Biochemical pathways
MinT is Tackling Tough Challenges

To understand microbiome function across different “omics” levels

- Developing extraction protocols for biomolecules from complex soil and human/mouse stool samples
- Developing & optimizing multi-omics approaches to determine microbial community composition and function
- Developing new databases for omics data
- Using omics data to develop models
- Developing statistical approaches for interpretation and analysis of omics data.
Permafrost is an Example of an Ecosystem in Transition Due to Climate Change

Microbial response to climate change is critical, but feedback mechanisms are uncertain

Climate models vary greatly in prediction of long-term impacts of elevated atmospheric CO$_2$ on terrestrial carbon (C) pools.

Vast portion of terrestrial C (980 Gtons) is sequestered in permafrost (as much as currently in Earth’s atmosphere and vegetation).

Question to address: How will microbes respond when permafrost transitions from frozen to thaw, and what will be the feedback to climate?
What is the impact of natural thaw?

Jenni Hultman

Thaw Gradient

Permafrost
Active layer
Thermokarst bog
Multi-omics reveals natural response of permafrost microbiome to thaw

Hultman et al., Nature. 2015
Coordinated shifts in permafrost microbiome and metabolome after thaw

New measurement capabilities being developed through MinT are aimed at mechanistic understanding of climate change impacts

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James Stegen and Eric Bottos
Molecular transformation networks show connections

- Well connected nodes define the subnetworks
- Phosphorylation transformations link the subnetworks

Number of edges increases from green to red
Complex interplay between built environment, host genetics and diet on mouse gut microbiome & metabolome

Nature Microbiology
In press

UNC
30 CC strains

BE 1
16 strains
BE 2
14 strains
BE3
(LBNL)
30 strains co-housed

Fecal samples
microbiome
metabolome

2wk
microbiome

4wk
microbiome

6wk
microbiome

8wk
microbiome
metabolome

Bacteroidales
Burdorobacterales
Clostridiales
Coriobacteriales
Desulfobulboccales
Erysipelotrichales
RF32
Verrucomicrobiales

D-Xylose
D-Galactose
Urea
L-Serine
L-Lysine
L-Homoserine

L-Phenylalanine
Xanthine
Hyposinamine

D-Glucose
Glycera

Lactobacillaceae

Prox1
Ctnma3
Igf2bp2
Trx2
St8ga11
MHC locus
Multi-omics enables genomes to phenomes revolution
Save the Date!

Multi-omics for Microbiomes Conference
August 1-3, 2017
Pacific Northwest National Laboratory, Richland, WA

This conference brings together scientists who develop and apply multi-omics approaches to understand complex microbial communities, bioinformaticians who integrate omics data, and users who apply omics tools for their experimentation. The 3-day event includes presentations, a session on imaging biosystems, and a tour of EMSL, a national scientific user facility funded and sponsored by the U.S. Department of Energy’s Office of Biological & Environmental Research.

In collaboration with PNNL’s Microbiomes in Transition (MinT) Initiative, which integrates multidisciplinary research to develop multiscale models that enable a mechanistic understanding of microbiome function and response to perturbation.


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