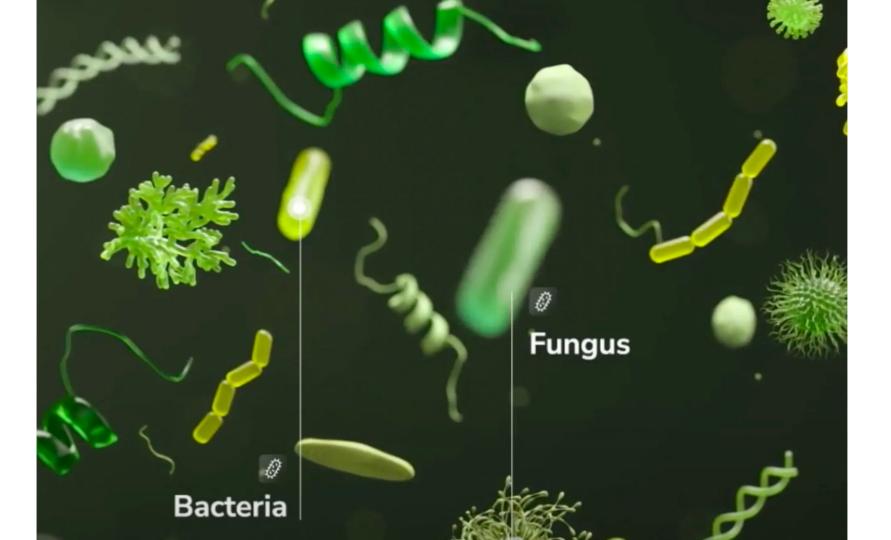
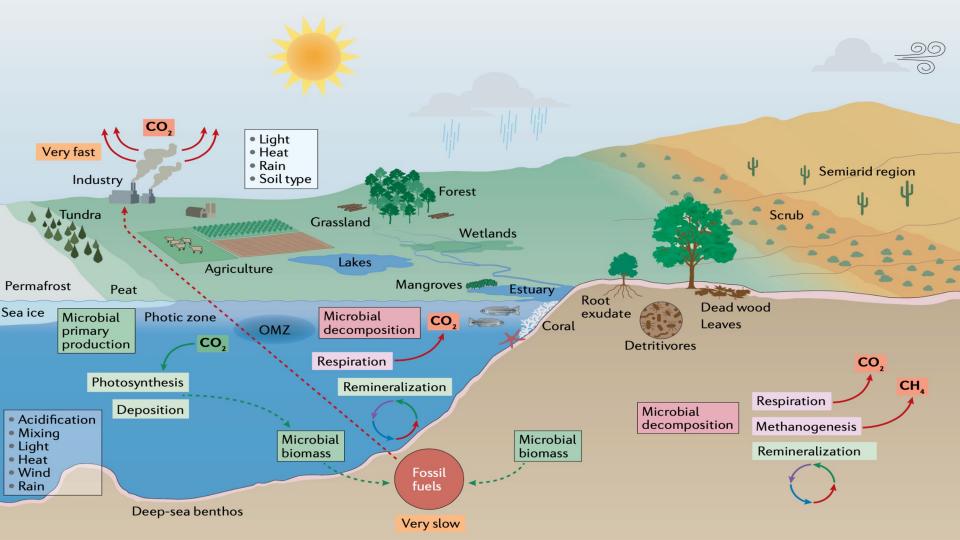
# Climate Change and Molecular Evolution

Malika Sharma and Sara Lawrence BIOL 4130 Feb 27, 2023 What is climate change?







# 3 Pillars of One Health

- Connection between humans, plants and animals - as well as microbes
- Changing relationships and connections to plants, animals and microbes

One Health is the idea that the health of people is connected to the health of animals and our shared environment.

> When we protect one, we help protect all.



### Why ONE HEALTH is Important

As Earth's population grows, our connection with animals and the environment changes:



closer together

Changes in climate People live and land use



travel and trade



Animals are more than just food

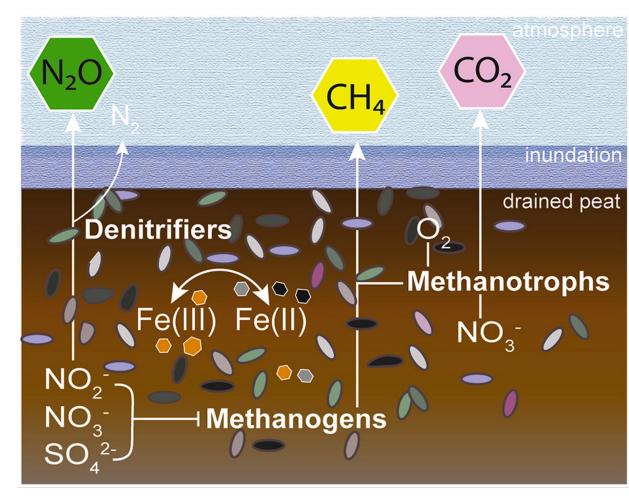
These factors make it easier for diseases to spread between animals and people.

A One Health approach tackles shared health threats by looking at all angles—human, animal, plant, and environmental



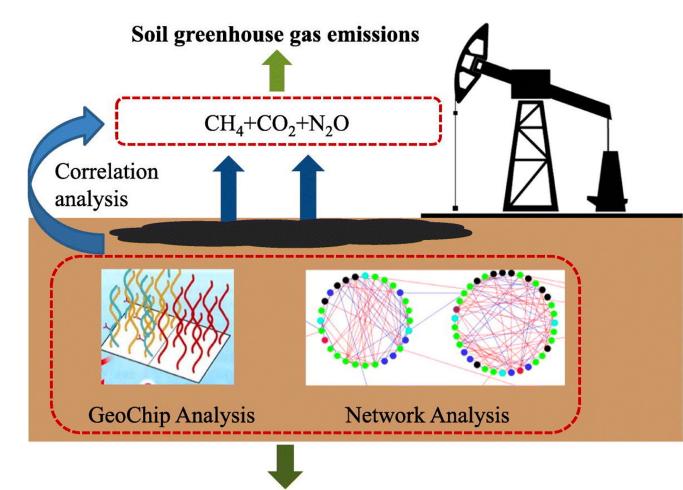
www.cdc.gov/onehealth

- Microbes can contribute to climate change through greenhouse gas emissions
- For example, the relationship between excess fertilizer and GHG



Source: https://doi.org/10.1016/j.soilbio.2020.107862

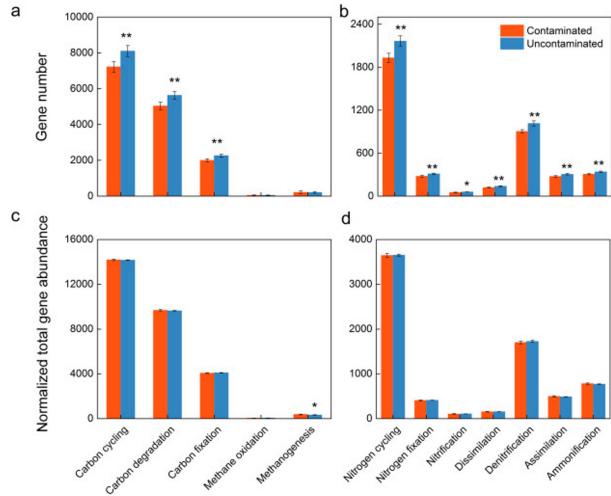
- Paper by Yang et. al
- Determination of microbial GHG emissions in oil contaminated areas vs. non-oil contaminated areas



Microbial functional gene patterns

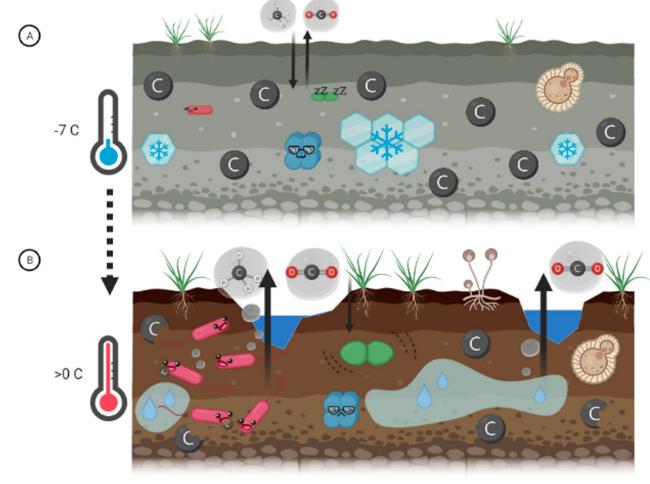
Source: https://doi.org/10.1016/j.scitotenv.2018.02.007

- Different expression of genes related to carbon and nitrogen cycling in contaminated vs.
   uncontaminated areas
- Adaptation and evolution of microbes to human caused change in environment
  - Potentially leading to even more harmful results



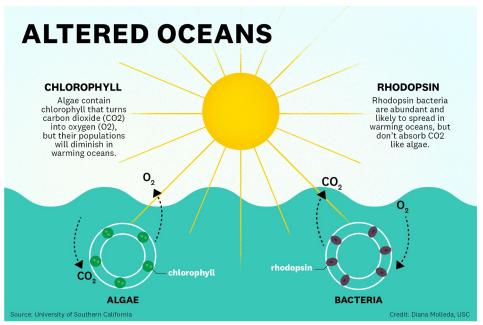
Source: https://doi.org/10.1016/j.scitotenv.2018.02.007

- Effect of climate change on microbes found in permafrost
  - Increased temperatures lead to increased release of GHGs from active microbes
- potential release of unknown microbes



Source:https://blogs.egu.eu/divisions/cr/2021/10/22/its-getting-hot-in-here-ancient-microbes-in-thawing-permafrost/

# Which microbes are THRIVING?



Source: University of Southern California Credit: Diana Molleda,

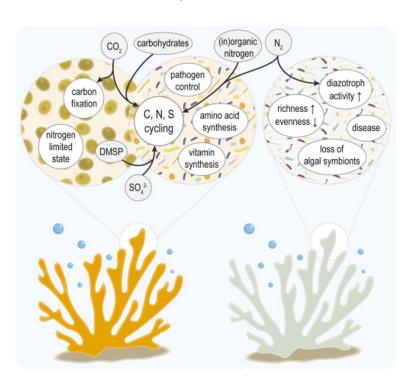
Source: https://news.usc.edu/159287/marine-bacteria-earth-warming-climate-usc-research/



Source: https://phys.org/news/2023-02-fungi-bacteria-binging-soil.amp

## Which microbes are DYING?

- Potential extinction of highly specialized microbes or microbes with necessary mutualistic relationships





Source: https://news.cgtn.com/news/2019-12-12/Why-do-legumes-have-nodules-on-their-roots--MmxlxHWkda/index.html

Source: https://doi.org/10.1016/j.isci.2020.100972

## Which microbes are UNAFFECTED?

Metagenome

mappability

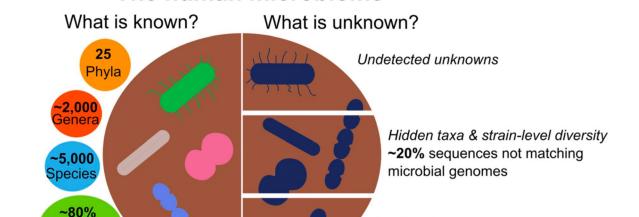
316

million

The human microbiome

Is it possible for any microbes to be unaffected by climate change?

 Could microbes in isolated environments eg. human body, be unaffected?



Functional unknowns

functional databases

~40%\* genes without a match in

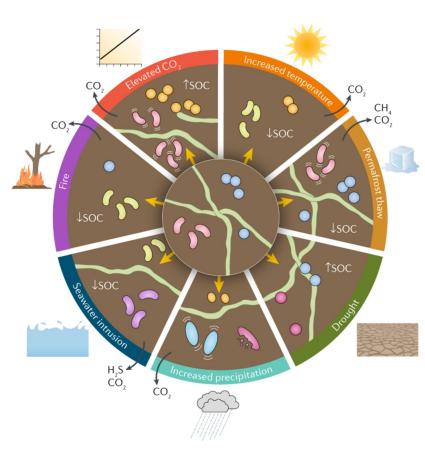
Source: https://www.gutmicrobiotaforhealth.com/the-knowns-and-unknowns-of-the-human-microbiome/

## Physiology adaptation of microbes

Short generation time allows for rapid evolution and changes in their physiology. Climate change forces microbes to evolve in ways that suits their fitness and survivability best.

Ex: tundra microbial communities change in the soil layer of permafrost after warming.





# Tools we can use to study microbial evolution

Recent advances in meta-omic technology has allowed us to better understand microbial evolution

Eg. use of 16S rRNA sequencing to study changes in microbial composition



### **Gene Marker Analysis**

Technology Platform: Next Generation Sequencing Common Software: QIIME, Mothur, VEGAN, phyloseq, DADA2

Pros: Cost-effective, analytical pipelines widely accepted

Cons: Lacks clear functional information, potential errors in differentiation of taxa



### Shotgun Metagenomics

Technology Platform: Next Generation Sequencing

Common Software: IDBA-UD, SPAdes, MEGAHIT, MetaPhlAn2, MG-RAST, HUMAnN2

Pros: Captures all microbial genomes present within a sample

Cons: Expensive, computationally demanding, no consensus on analytical pipelines



#### Metabolomic

Technology Platform: LC/GC-MS

Pros: allows for profiling of the metabolites microbiota produce, semi-quantitative

Cons: Origin of metabolite unknown



### Metaproteomics

Technology Platform: LC/GC-MS

Pros: Allows for identification and quantification of the proteins within a sample Cons: Origin of protein unknown



### Metatranscriptomics

Technology Platform: Next Generation Sequencing

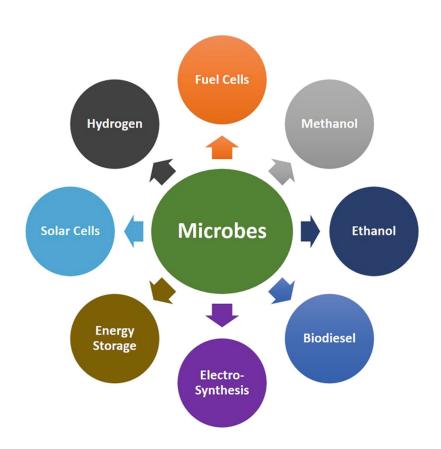
Common Software: SOAPdenovo

Pros: Allow assessments of gene expression

Cons: Protein expression may depend on translation and post-translational modifications

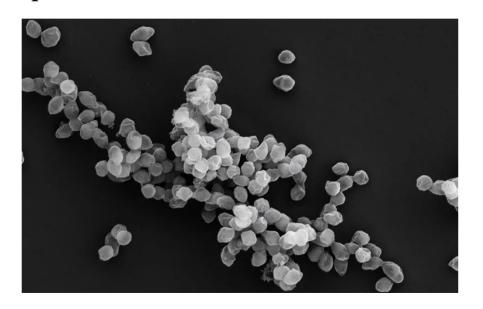
Source: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7598837/

## How can we learn from them?



# Mitigation

Eg. Ruminating animals produce methane when digesting food. Baby kangaroo feces, when used in tandem with a known methane inhibitor, was shown to **reduce** methane production

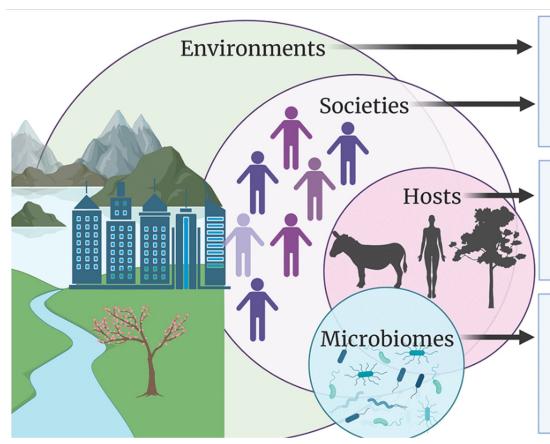




https://www.news9live.com/science/microbes-from-baby-kangaroos-can-reduce-methane-emissions-from-cows-au941-2053742

Eg. Photoferrotrophs steal electricity from iron and can absorb carbon dioxide on a large scale

## What can we do?



Understand the context

surrounding the microbiome samples: biological, social, and environmental factors as well as constraints.

Engage in discussion with resident and previously displaced groups to understand context and obtain informed consent.

Collaborate with

impacted groups to inform design, understand context, share information, and maximize beneficial impacts.

Source: https://doi.org/10.1128/msystems.01240-21

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