The Human Microbiome in Health and Disease



David A. Relman, Stanford University
The Forum for Medical Affairs
Annual Educational Program
November 9, 2014

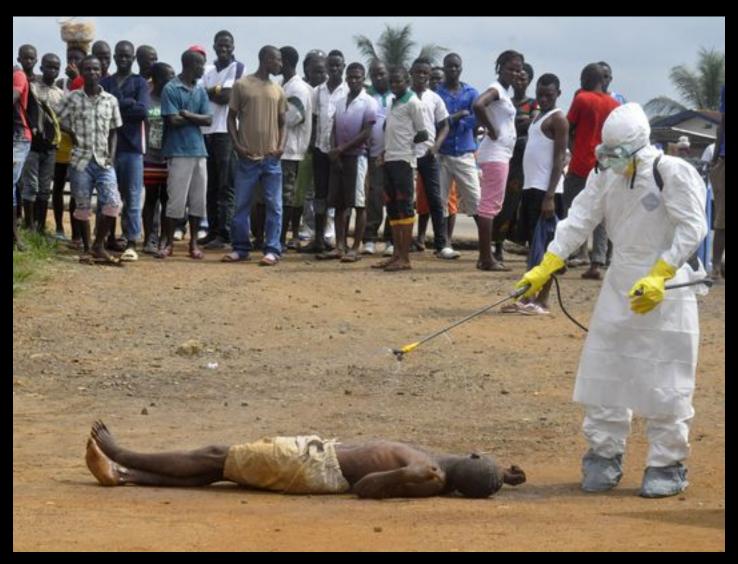
Topics



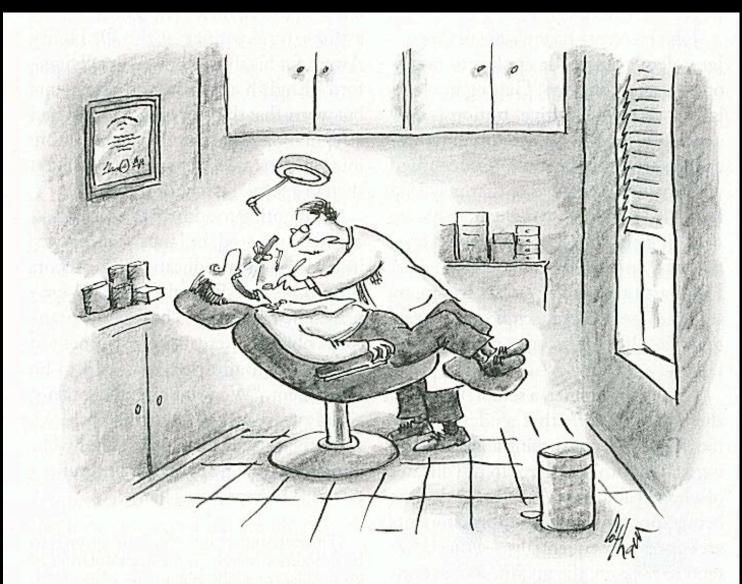
- Perspectives on human-microbe relations: different "lens"
- Sources variation in patterns of diversity
- Stability, resilience and restoration
- Challenges in study of human microbiome



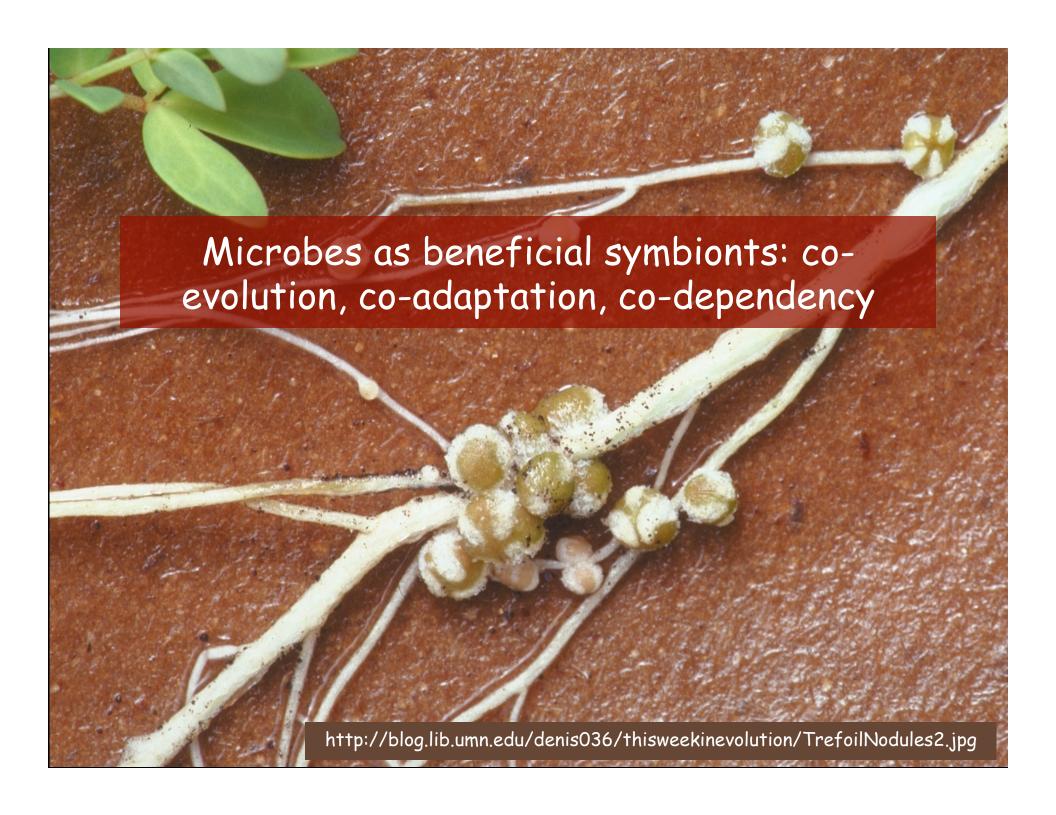
http://www.artchive.com/artchive/b/bruegel/death.jpg



http://www.usatoday.com

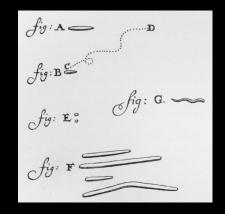


"I see it, but it scampers away from the light."

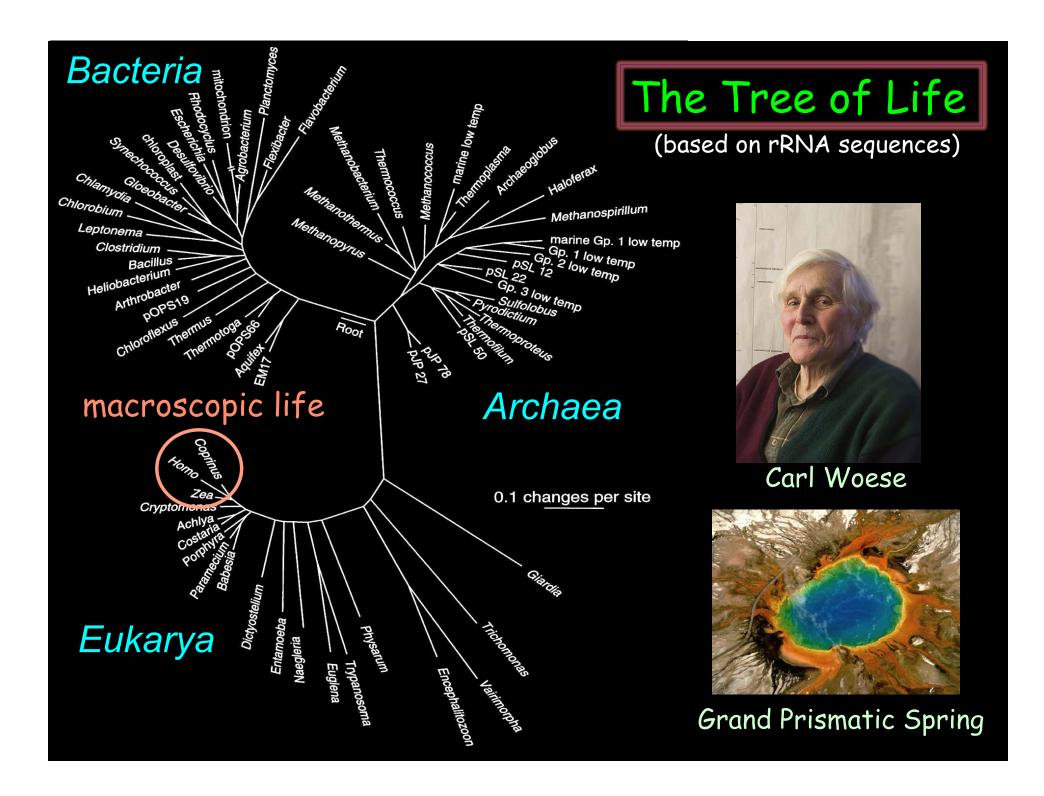


How we have looked at microbial world

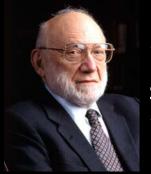
Antony van Leeuwenhoek, 1683 ('animalcules')



- Razumov AS, 1932 ('Great plate anomaly')
- Dubos R et al., 1965 (co-evolution)
- Moore W, 1975, 76; Savage DC, 1977 (cell counts, ecology)



An evolving view of our relationship with the microbial world



"We should think of each host and its parasites as a superorganism with the respective genomes yoked into a chimera of sorts."

Science 288:287, 2000

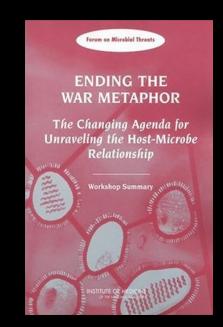
Opinion

TRENDS in Microbiology Vol.9 No.5 May 2001

"A second human genome project"

David A. Relman and Stanley Falkow

The characterization of life is immeasurably enhanced by determination of complete genome sequences. For organisms that engage in intimate interactions with others, the genome sequence from one participant, and associated tools, provide unique insight into its partner. We discuss how the human genome sequence will further our understanding of microbial pathogens and commensals, and vice versa. We also propose criteria for implicating a host gene in microbial pathogenesis, and urge consideration of a 'second human genome project'.



2006

Perspective

Human Microbiome: Communities of microbes (and viruses) that make human body their home



- Re-defining what it means to be "human"
- Humans...as "islands" or habitat patches, occupied by microbial communities

(Based on cell counts, we are 10 parts bacterial, 1 part human...and based on unique genes, we are 150 parts bacterial, 1 part human...)

- Long-term co-adaptation, cross-talk
- Humans as ecological system under selection to minimize conflict between individual members of microbiota and maximize host fitness...

Our 'extended self': human-microbe mutualism

Our benefits (incomplete list)

- Food digestion
- Nutrition (vitamins, energy)
- Xenobiotic processing
- Metabolic regulation, cometabolism
- Development: terminal differentiation of mucosa
- "Education", regulation of immune system
- Epithelial "homeostasis", barrier integrity
- Colonization resistance to pathogens

Our 'extended self': human-microbe mutualism

Their benefits (incomplete list)

- Nutrition
- Habitat
- Dispersal

Shouldn't we be focusing a bit more on their needs?

Turnbaugh P et al, Nature 449:804-810, 2007; Dethlefsen L et al, Nature 449:811-818, 2007

Perspective

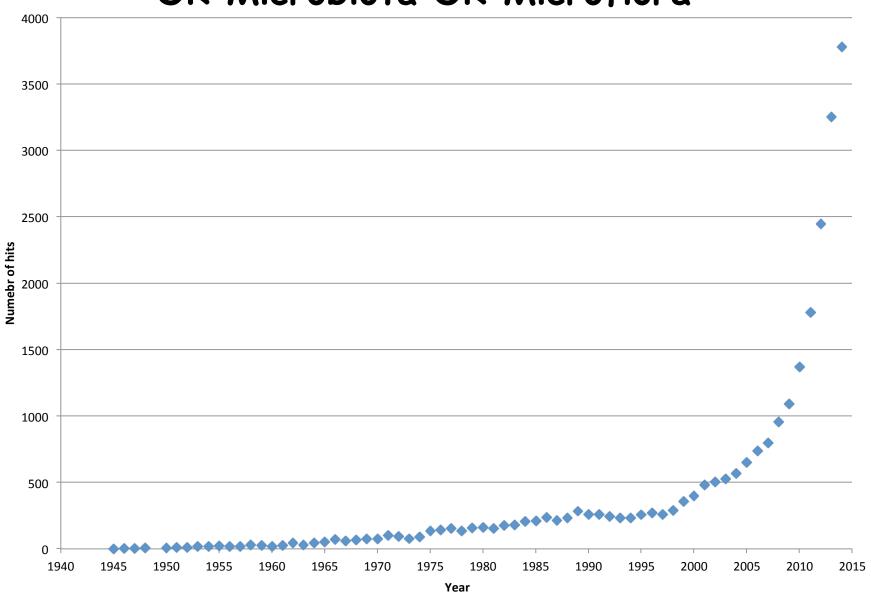
Human Microbiome: Communities of microbes (and viruses) that make human body their home



- Key ecosystem services (benefits)?
- Individuality?
- Stability, resilience?
- Clinical applications?: disease mechanism, risk assessment, new approaches for health maintenance, restoration

(Why now?....technology, convergence of disciplines)

Pubmed Hits for "Microbiome OR Microbiomes OR Microbiota OR Microflora"



Humans and other animals are special places!



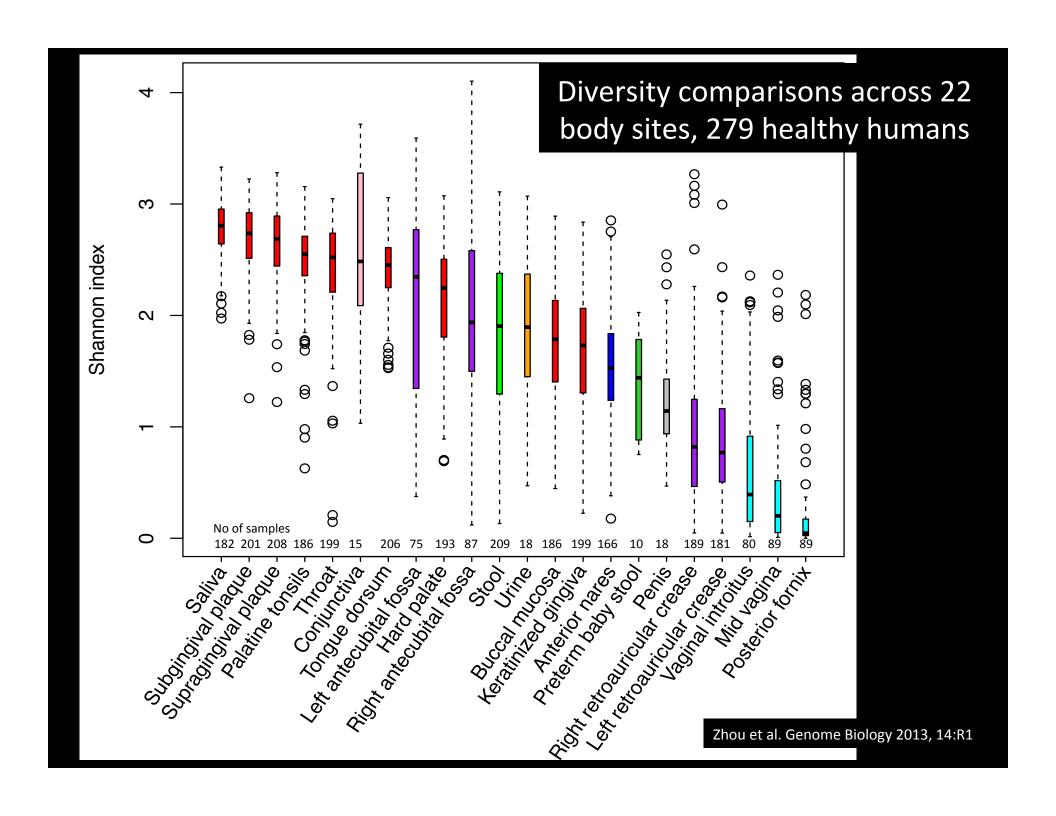
- Who's there?
- What are they doing?

Site-specific distributions of bacterial phyla in **Firmicutes** Mouth (56) Bacteroidetes healthy humans Actinobacteria Proteobacteria Other phyla Skin (48) Oesophagus (43) Size of circles is proportionate Colon (195) Stomach (25) to average number of species-level phylotypes per Vagina (5) individual (in parentheses)

Dethlefsen L et al., Nature 2007; 449:811-818

Sources of variation in patterns of diversity

- Space (habitat, body site)
- Individual
- Health status
- Host genetics
- Environmental exposures
 - Diet
 - Chemical/drug/mechanical disturbance
 - Other aspects of lifestyle? (e.g. geography)
 - Other mammals/hosts
- Time (esp. early in life)



Assessments of the microbiome

- Taxonomic composition (phylogenetically informative genes)
- Metagenomic (gene, genome) composition
- Community-wide transcript profiles
- Community-wide protein profiles
- Community-wide metabolite profiles
 (Community-wide functions?)

 Host (clinical measurements, genetics, gene expression, chemical, etc)

A human gut microbial gene catalogue established by metagenomic sequencing

Qin J et al. Nature 464:59-65, (4 March) 2010

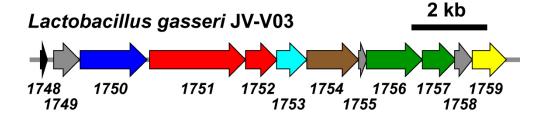
- 576.7 Gb sequence, fecal samples, 124 individuals
- 3.3 million non-redundant genes; 536,000/person
- ~6300 functional groups in minimal gut metagenome
 - biodegradation of complex sugars and glycans (e.g., degradation and uptake pathways for pectin and sorbitol, sugars which are omnipresent in fruits and vegetables, but which are not or poorly absorbed by humans)
 - capacity to ferment (e.g., mannose, fructose, cellulose and sucrose)

Small molecules in the human microbiome

3,118 biosynthetic gene clusters from 755 metagenomic samples (100 healthy humans)

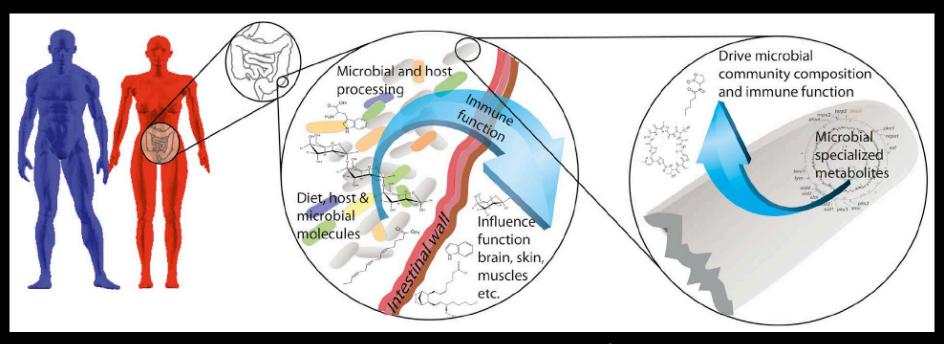
Average gut: 599 gene clusters Average oral cavity: 1,061 gene clusters

Dozens of gene clusters with unknown products present in >50% of healthy humans

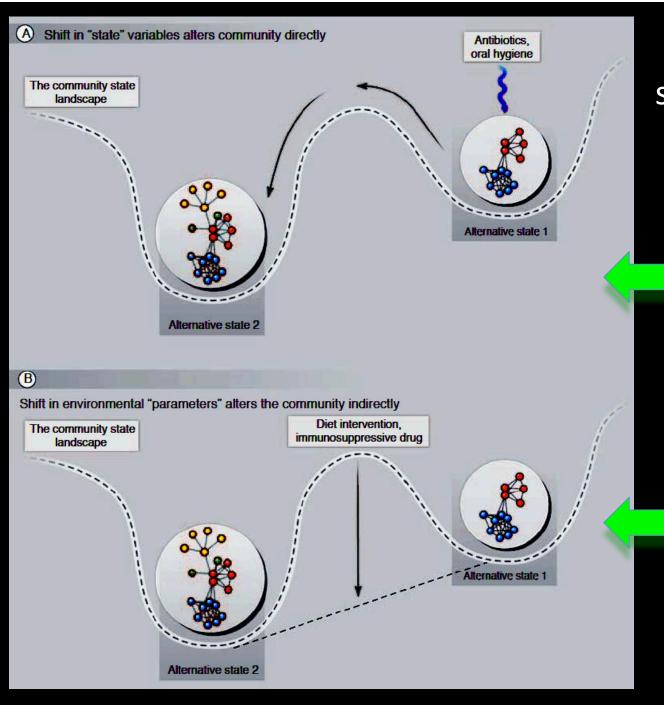


Michael Fischbach, UCSF

They are 'talking' to each other and with us



Immunity 2014; 40:824-832



Community stability landscape

Shift in community state variables

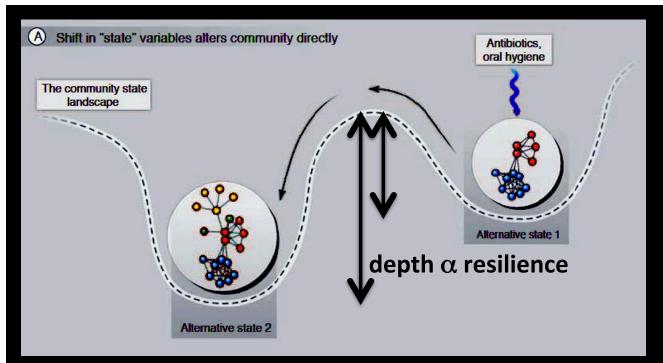
Shift in environmental parameters

Costello EK *et al.,* Science **336**, 1255 (2012)

Disturbance



- Disturbances remove or kill some fraction of the community, creating opportunities for remaining community members or new colonists...effects directed at community and/or host
- Increasingly prominent in "modern" societies?



Resilience:
capacity of
ecosystem to
absorb
disturbance
and retain
same
function(s)...

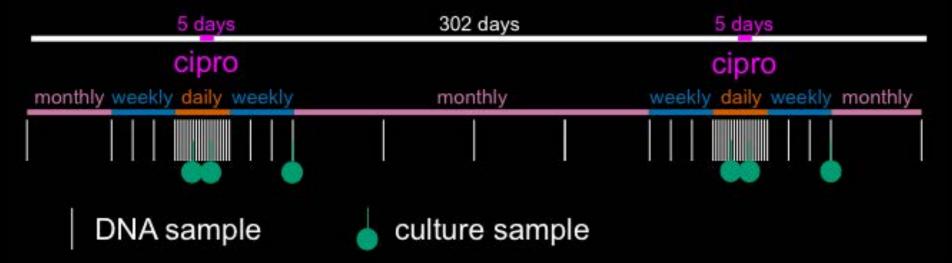


C. S. "Buzz" Hollings (1973)

http://www.flickr.com/photos/sfupamr/5515528060/sizes/l/in/photostream/

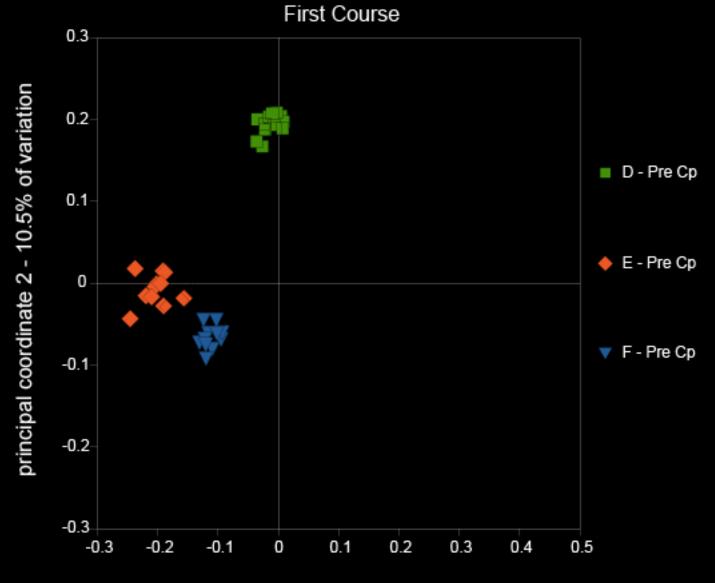
Costello EK *et al.,* Science **336**, 1255 (2012)

Study design



- Healthy subjects ("D", "E", "F"), no abx x 1 yr
- Ciprofloxacin twice, 6 months apart (pulse perturbation)
- Stool samples over 10 months

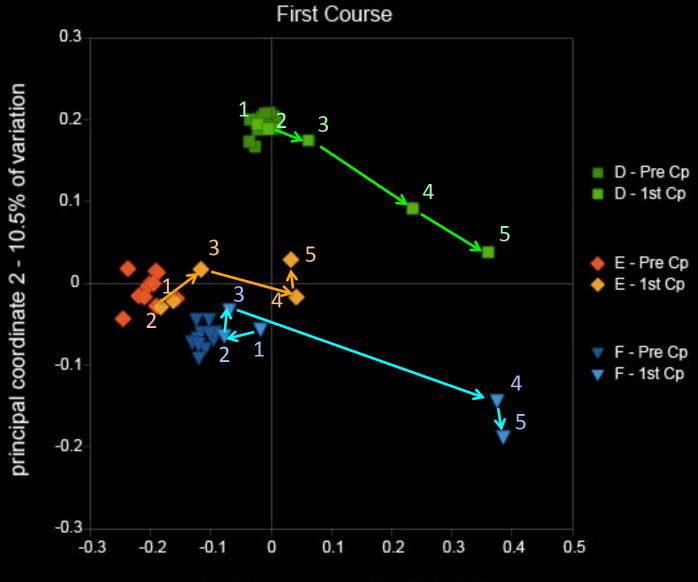
Dethlefsen et al. PLoS Biology 2008; 6:e280 Dethlefsen L, Relman DA. PNAS 2011; 108:4554-61



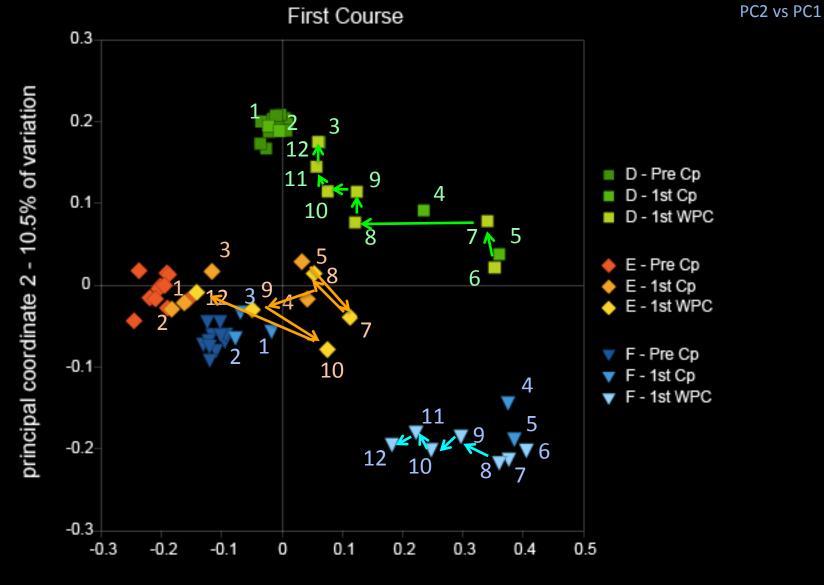
principal coordinate 1 - 13.8% of variation

Individualized patterns of phylogenetic compositional diversity

Relative stability over two months in absence of gross disturbance

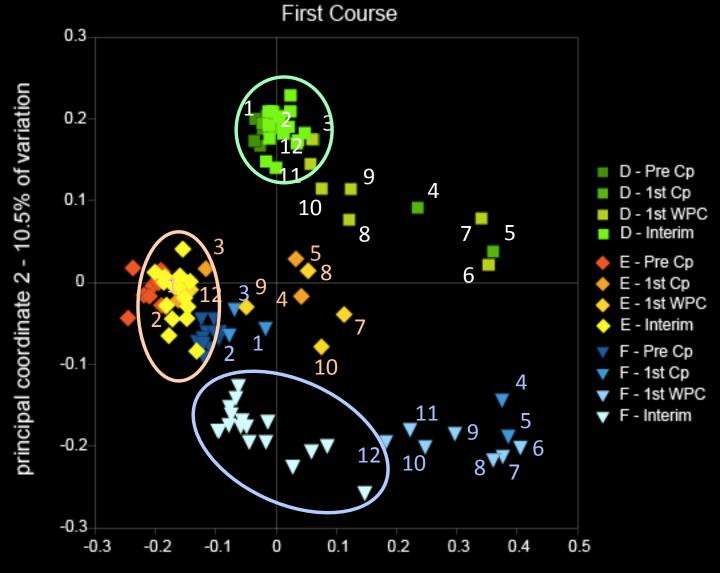


principal coordinate 1 - 13.8% of variation



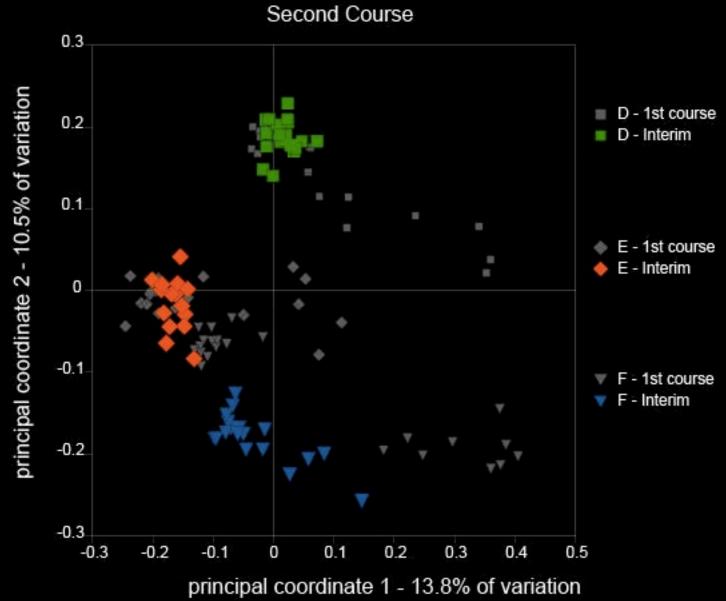
principal coordinate 1 - 13.8% of variation

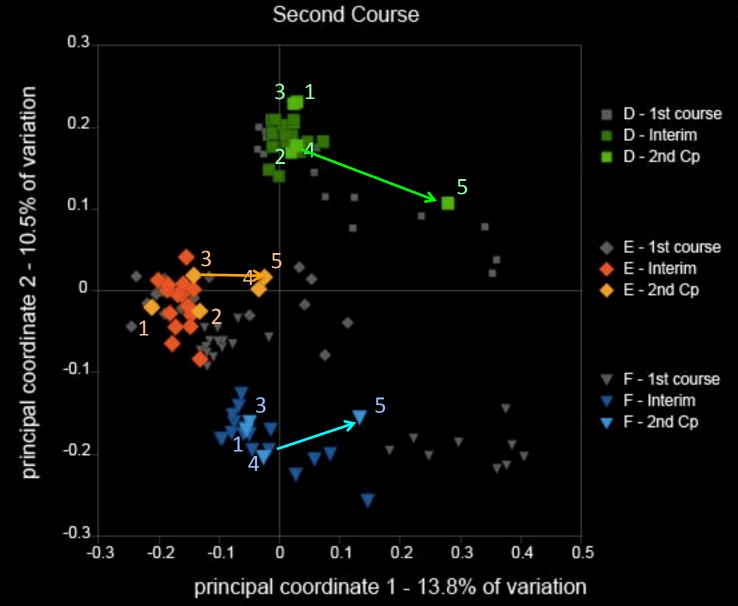


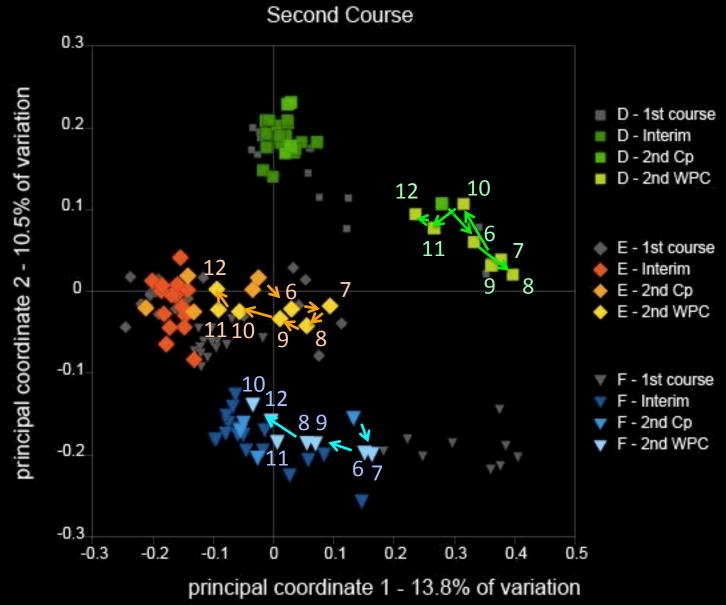


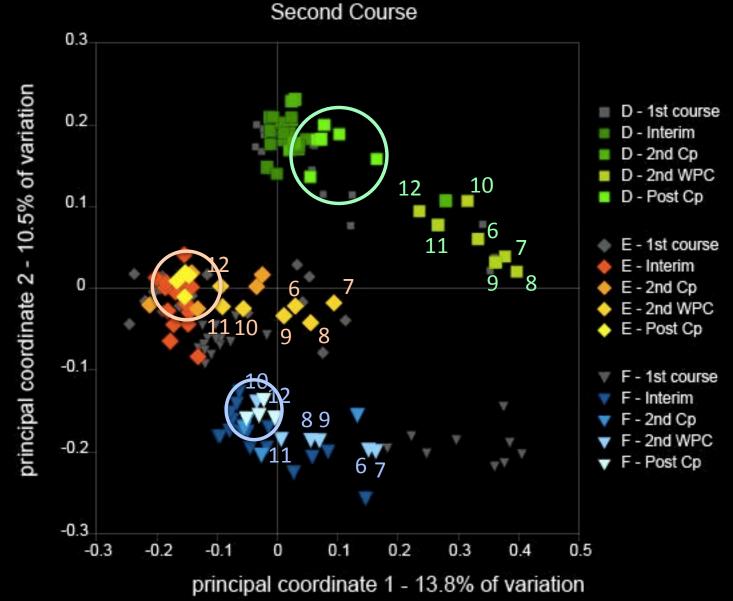
principal coordinate 1 - 13.8% of variation

Shared, as well as individualized responses (complete vs. partial recovery)









Community 'memory'?

Compounded perturbations: alteration of fitness landscape?

Paine RT, Tegner MJ, Johnson EA. Compounded perturbations yield ecological surprises. Ecosystems 1:535-545, 1998.

Compounded Perturbations Yield Ecological Surprises

Robert T. Paine,1* Mia J. Tegner,2 and Edward A. Johnson3

¹Department of Zoology, University of Washington, Seattle, Washington 98195, USA; ²Scripps Institution of Oceanography, University of California, San Diego, La Jolla, California 92093-0201, USA; and ³Department of Biological Sciences and Kananaskis Field Station, University of Calgary, Calgary, Alberta, Canada T2N 1N4.

Ecosystems (1998) 1: 535-545

ABSTRACT

All species have evolved in the presence of disturbance, and thus are in a sense matched to the recurrence pattern of the perturbations. Consequently, disturbances within the typical range, even at the extreme of that range as defined by large, infrequent disturbances (LIDs), usually result in little long-term change to the system's fundamental character. We argue that more serious ecological consequences result from compounded perturbations within the normative recovery time of the community in question. We consider both physically based disturbance (for example, storm, volcanic eruption, and forest fire) and biologically based disturbance of populations, such as overharvesting, invasion, and disease, and their interactions. Dispersal capability and measures of generation time or age to first reproduction of the species of interest seem to be the important metrics for scaling the size

and frequency of disturbances among different types of ecosystems. We develop six scenarios that describe communities that have been subjected to multiple perturbations, either simultaneously or at a rate faster than the rate of recovery, and appear to have entered new domains or "ecological surprises." In some cases, three or more disturbances seem to have been required to initiate the changed state. We argue that in a world of ever-more-pervasive anthropogenic impacts on natural communities coupled with the increasing certainty of global change, compounded perturbations and ecological surprises will become more common. Understanding these ecological synergisms will be basic to environmental management decisions of the 21st century.

Key words: altered community states; dispersal; multiple disturbances; recovery intervals; scaling disturbances.

Study of the human microbiome: Challenges



- Strain-level characterization
- Getting at function (new ex vivo assays)
- Understanding dynamics (time, space)
- Data integration
- Assessing possible causation

"Community as pathogen" that is, disease due to a community disturbance

"pathogenic states"

Clinical problems associated with the indigenous microbiota

- Chronic periodontitis
- Crohn's disease & other IBD
- Irritable bowel syndrome
- Tropical sprue
- Antibiotic-associated diarrhea
- Obesity, undernutrition
- Bacterial vaginosis
- Premature labor and delivery

Clinical problems associated with the indigenous microbiota

Chronic periodontitis

Cause or effect?
Initiating or propagating?
Mono- or polyfactorial?

- Bacterial vaginosis
- Premature labor and delivery

Clinical Relevance

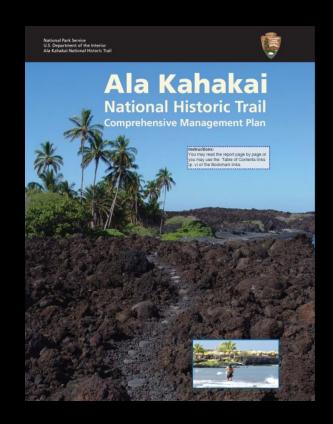


- Ecosystem resilience as critical feature of health; loss leads to increased invasibility (by exotics, e.g., Salmonella), blooms (by natives, e.g., C. difficile)
- Disturbance as a clinical tool: prognostics (pre-disturbance assessment of resilience), therapeutics (establishment of alternative stable state)
- Key ecosystem services?

Park Management Plan (for human microbial ecosystem)



- Habitat restoration
- Promotion of native species
- Targeted removal of invasive species
- Ecosystem service providers? Community and host context?
- Adaptive management: system monitoring to inform decisions



Acknowledgements

Stanford University

Elies Bik
Liz Costello
Les Dethlefsen
Wei-Ting Liu
Katie Shelef
Dan DiGiulio
Diana Proctor
Sunje Pamp
Miling Yan
& rest of Relman Lab



U.C. San Francisco
Gary Armitage
Peter Loomer
Michael Fischbach

U. Colorado Antonio Peña Rob Knight

U.C. Berkeley Jill Banfield

U.C. San Diego Pieter Dorrestein

Susan Holmes (Statistics)

Funding: NIH (NIDCR/OD/NIAID/NIGMS/NIEHS),
US Navy, March of Dimes Foundation,
Keck Foundation, Helmsley Trust, Thomas & Joan Merigan Endowment