All Microbes, All The Time

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University of California, Davis

@phylogenomics

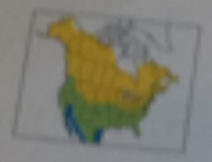
February 23, 2017

The Story of a Bird

National Geographic Society

Field Guide to the

Birds of North America



American Robin *Turdus migratorius* L 10" (25 cm)
Gray-brown above, with darker head and tail; bill yellow; underparts brick red; lower belly white. Most western birds are paler and duller overall than eastern and southwestern forms. In most eastern birds (shown here), tail has conspicuous white corners. Juvenile's underparts are tinged with cinnamon, heavily spotted with brown. Compare with spotted thrushes (page 326). Common and widespread, the Robin brightens both forest and suburb with its loud, liquid song, a variable cheerily *cheer-up cheerio*. Varied calls include a rapid *tut-tut-tut*. Often seen on lawns, head cocked as it searches for earthworms; also eats insects, berries. Nests in shrubs and trees and on sheltered windowsills, eaves. In winter, found in most woodlands, swamps, suburbs, parks. Numbers vary greatly from winter to winter in the southwest and in California.

Rufous-backed Robin *Turdus rufopalliatus* L 9½" (24 cm)
Mexican species, casual visitor in winter to southern Arizona, rare from southern and southwest Texas to southern California. Distinguished from American Robin by bright reddish-brown back and wing coverts, gray head, and more extensively streaked throat. Somewhat secretive; found in treetops and dense shrubbery.

Clay-colored Robin *Turdus grayi* L 9" (23 cm)
Mexican species, casual visitor and very rare breeder in southernmost Texas. Brownish-olive above; tawny-buff below; pale buffy throat is lightly streaked with olive. Lacks white around eye conspicuous in American Robin. Very shy; forages in dense thickets, streamside brush, woodlands. Calls include a nasal *meeoo*; song resembles American Robin's but is slower, clearer, much less varied.

Aztec Thrush *Ridgwayia pinicola* L 9½" (24 cm)
Mexican species, rare visitor to southeastern Arizona, southern Texas. Male is sooty-brown above, with white patches on wings and uppertail coverts; tail broadly tipped with white; breast is dark; belly and undertail coverts white. Female is paler. Juvenile is heavily streaked above with creamy-white; underparts whitish, heavily streaked with brown.


North Sea
Dundee
Glasgow
Edinburgh
Newcastle
Upon Tyne
Sunderland
Middlesbrough
Darlington
Belfast
Isle of Man
Irish Sea
Blackpool
Leeds
Preston
Liverpool
Manchester
Dublin
Stoke-on-Trent
Nottingham
Wolverhampton
Leicester
Norwich
Birmingham
Ipswich
Northampton
Gloucester
Oxford
Luton
Chelmsford
Swansea
Cardiff
Swindon
London
Bexley
Bristol
Woking
Maidstone
Southampton
Eastbourne
Exeter
Bournemouth
Portsmouth
Plymouth
Esbjerg
Cuxhaven
Leeuwarden
Groningen
Assen
Oldenburg
(Oldenburg)
Alkmaar
Hoorn
Zwolle
Emmen
Almelo
Nordhorn
Haarlem
Leiden
Nederland
(Netherlands)
Enschede
Rotterdam
Münster
Breda
Nijmegen
Roosendaal
Eindhoven
Essen
Wuppertal
Brugge
Bruxelles
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Weert
Roermond
Calais
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Hasselt
Leverkusen
Kortrijk
Maastricht
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België
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Liège
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Last Updated: Tuesday, 9 March, 2004, 11:21 GMT

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Twitchers watch robin served rare

Birdwatchers from all over Britain who gathered in Grimsby to catch sight of a rare American robin were horrified to see it eaten by a passing sparrowhawk.

Sparrow hawks hunt insects, mammals, birds and reptiles

They were still setting up their cameras when the predator swooped down from a row of drab factories and warehouses on an industrial estate.

The young bird, from the southern US, "didn't really live to enjoy her moment of fame," a twitcher told the Guardian.

The robin's vivid red breast made it an obvious candidate for a lunch date.

"It was a terrible moment," Graham Appleton, of the British Trust for Ornithology

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- Hopes for big flock at bird count
  24 Jan 04 | Wales
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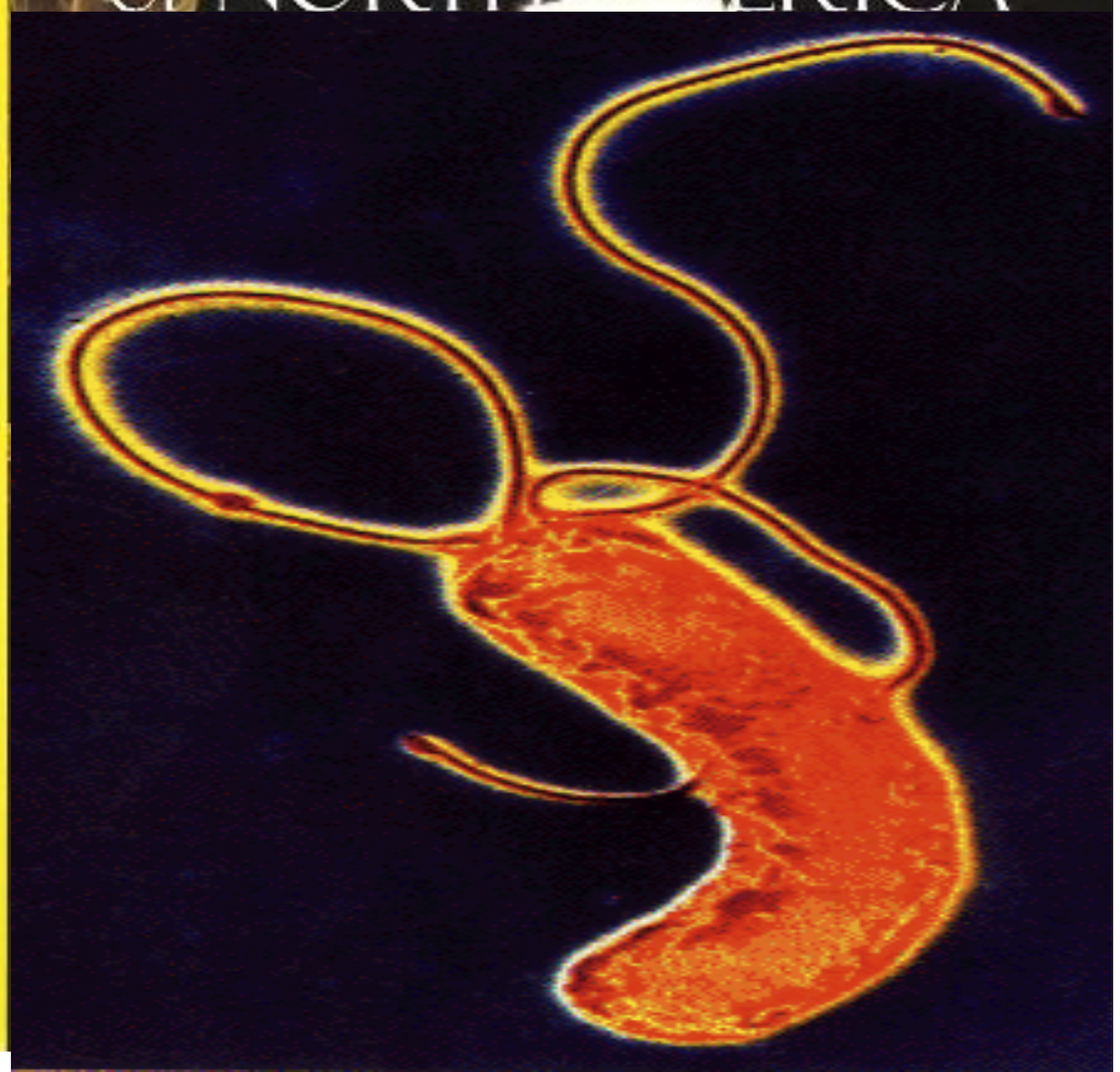
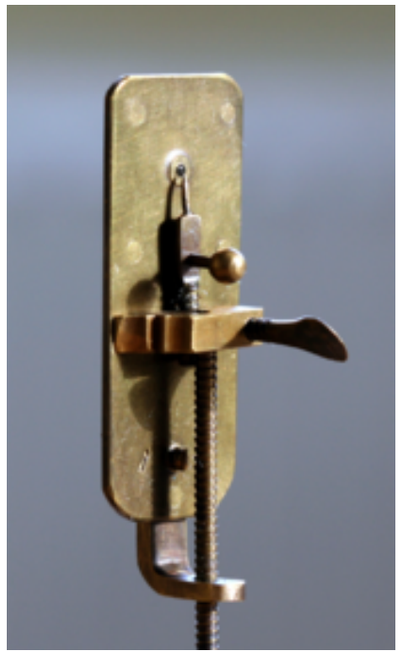
NATIONAL GEOGRAPHIC

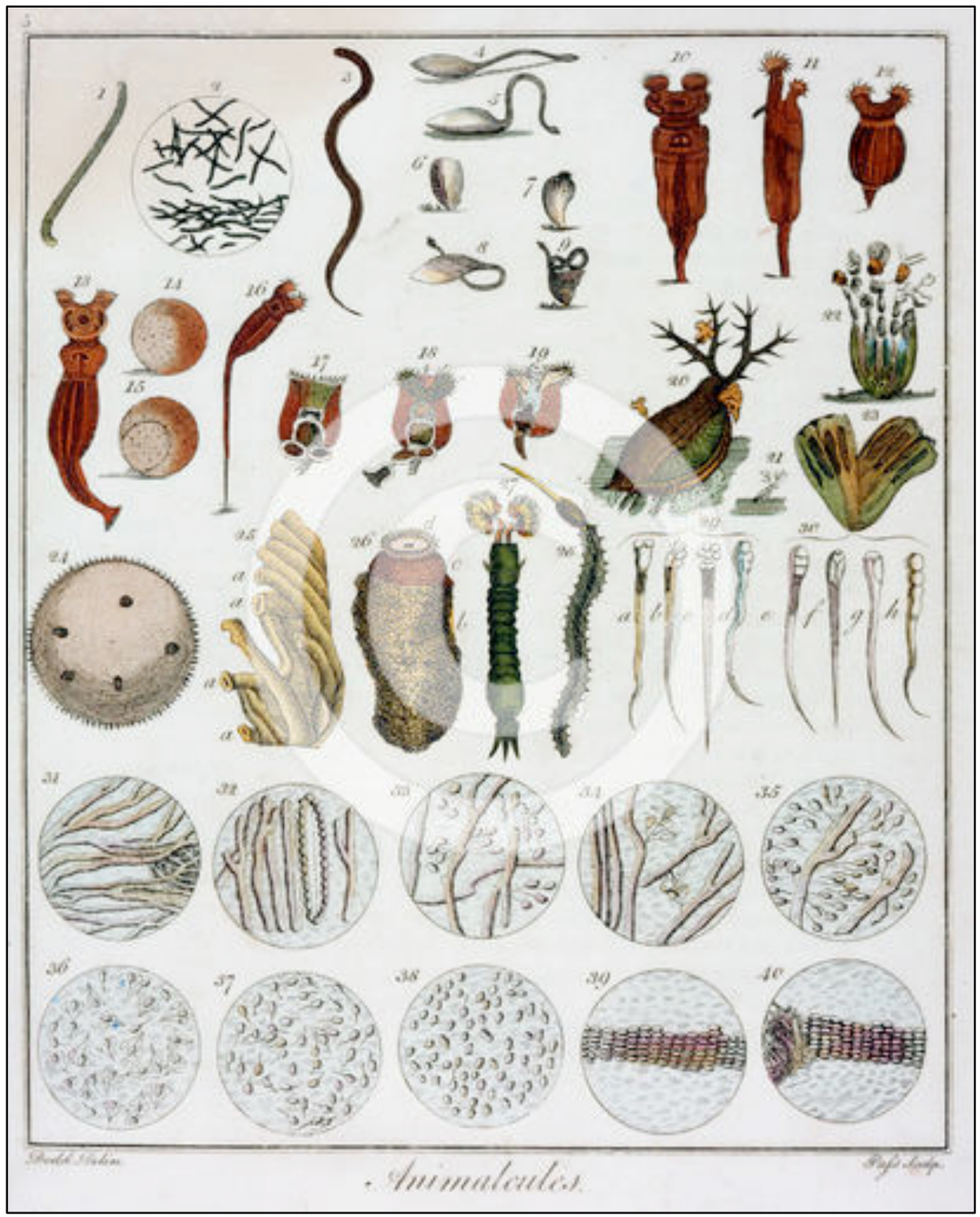
FIELD GUIDE TO THE MICROBES OF NORTH AMERICA



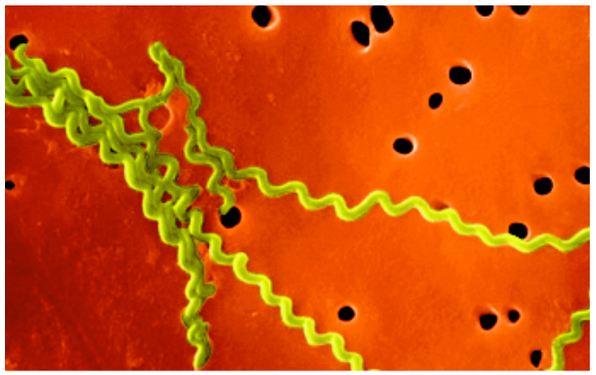
Microbes 101

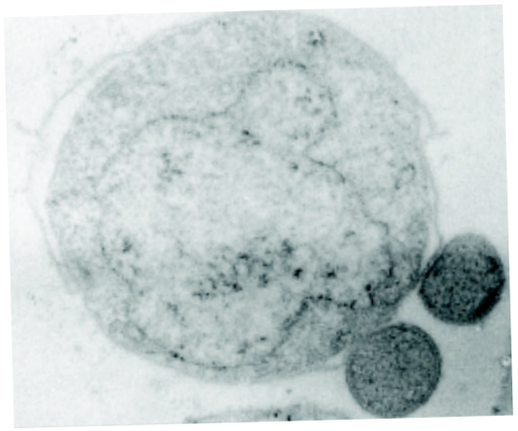


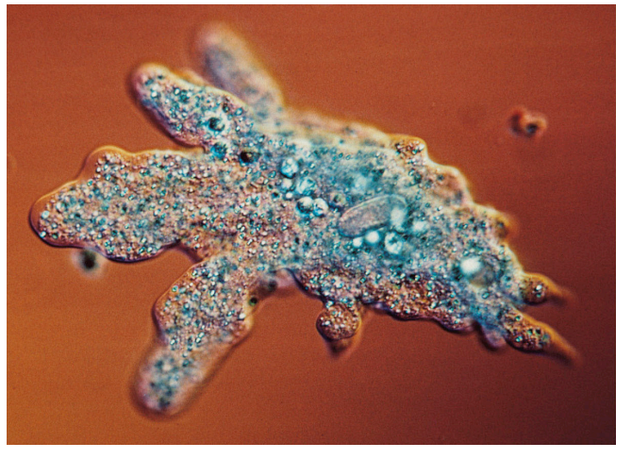
- Microbes are small
- But diversity and numbers are very high
- Most are NOT causes of infectious diseases
- Little known about their diversity in most locations

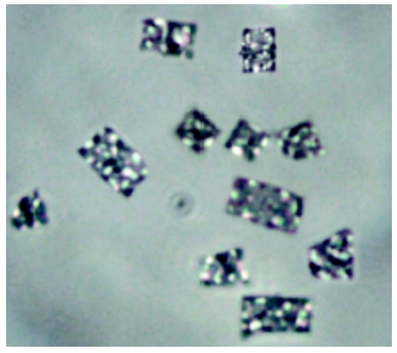


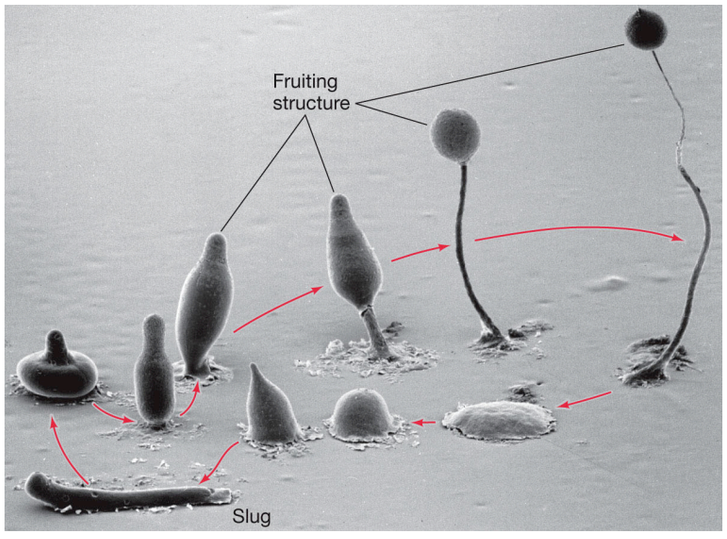
Diversity of Form

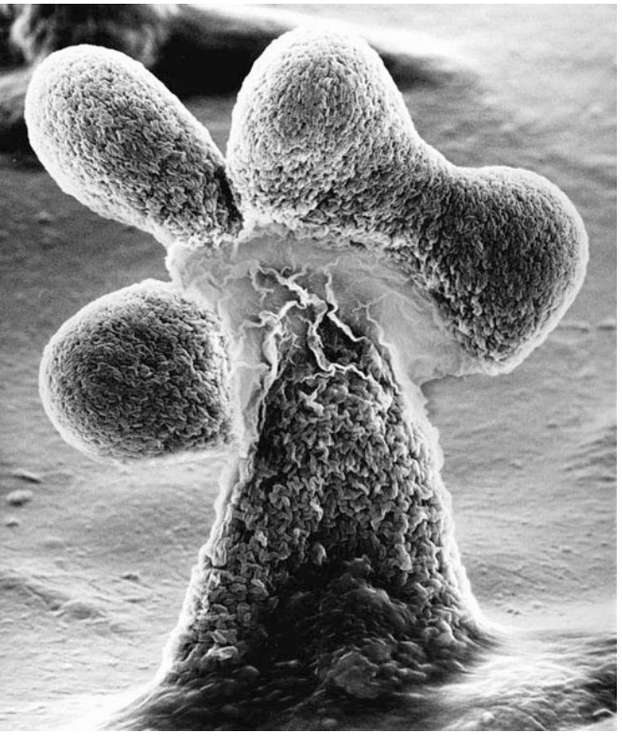


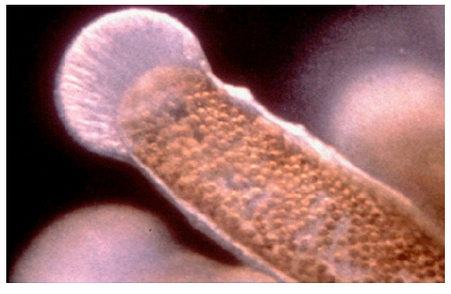


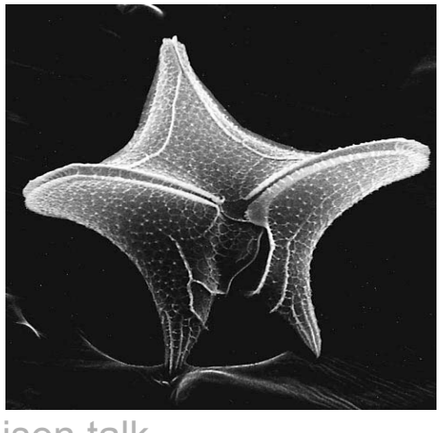












Diversity of Function

The Bad

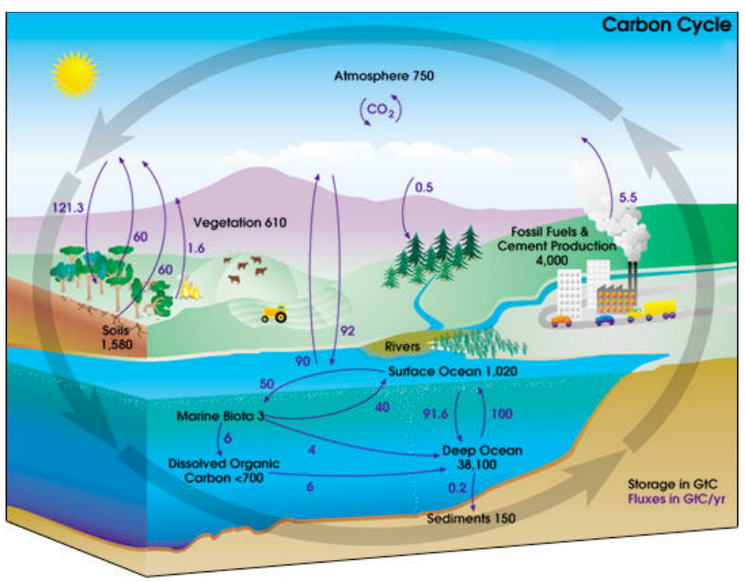
The Good

The Unusual

The Consumable

The Burnable

The Planet

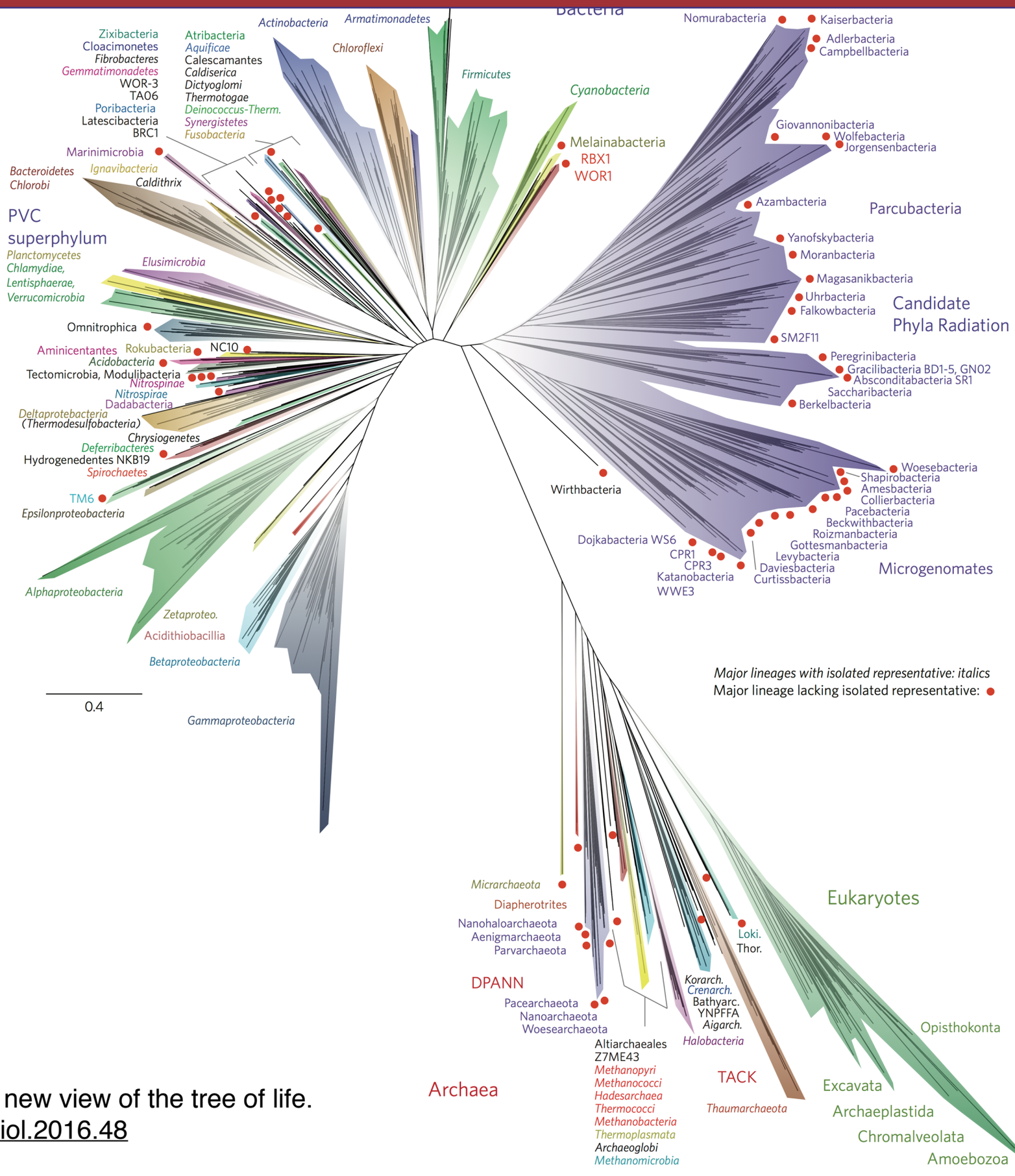


Genetic and Evolutionary Diversity

Laura Hug
U. Waterloo

Jill Banfield
UC Berkeley

92 Bacterial Phyla
25 Archaeal Phyla
5 Eukaryotic Supergroups



Hug et al. Nature Microbiology. A new view of the tree of life.
http://dx.doi.org/10.1038/nmicrobiol.2016.48

Genetic and Evolutionary Diversity

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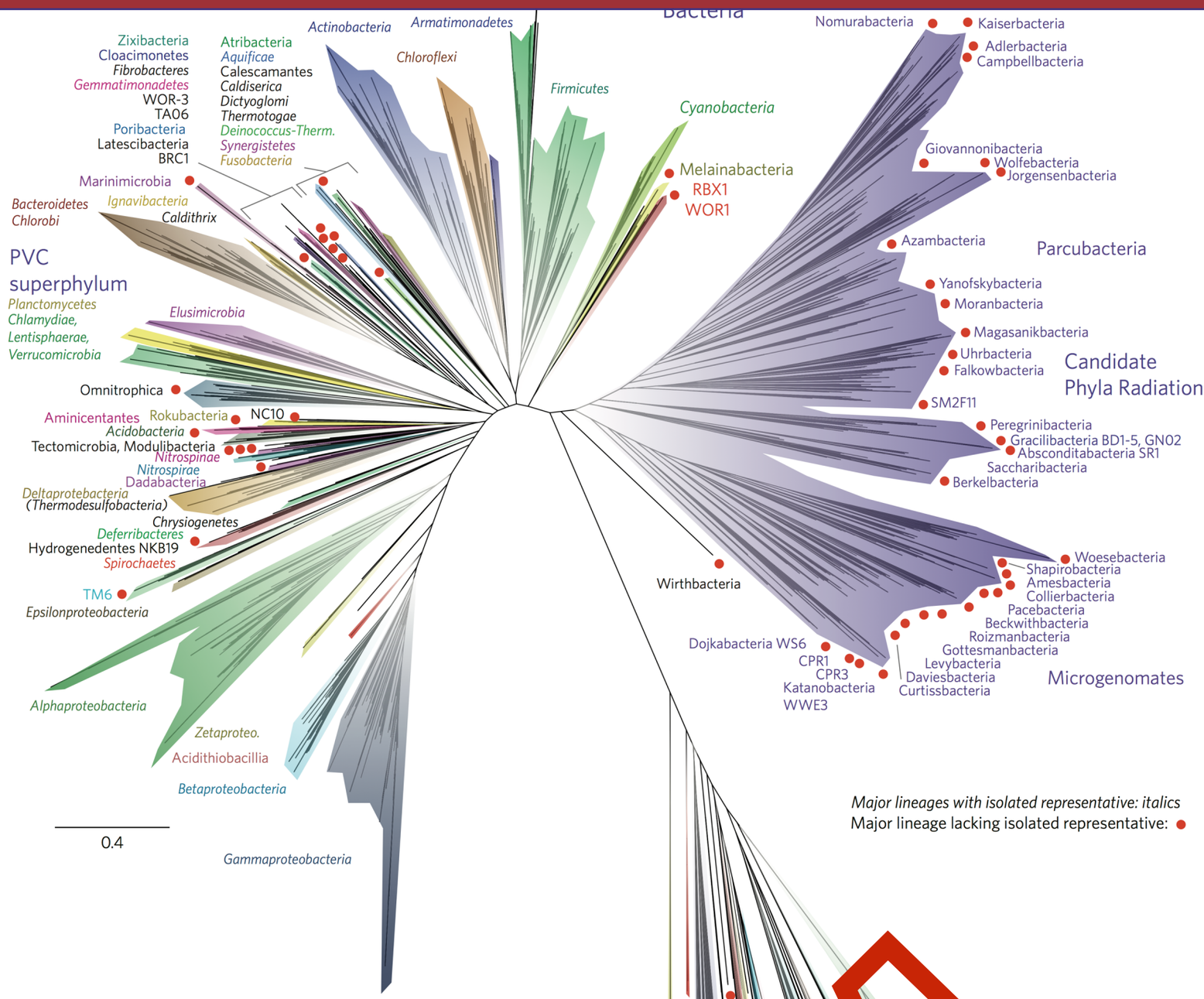

92 Bacterial Phyla
25 Archaeal Phyla
5 Eukaryotic Supergroups

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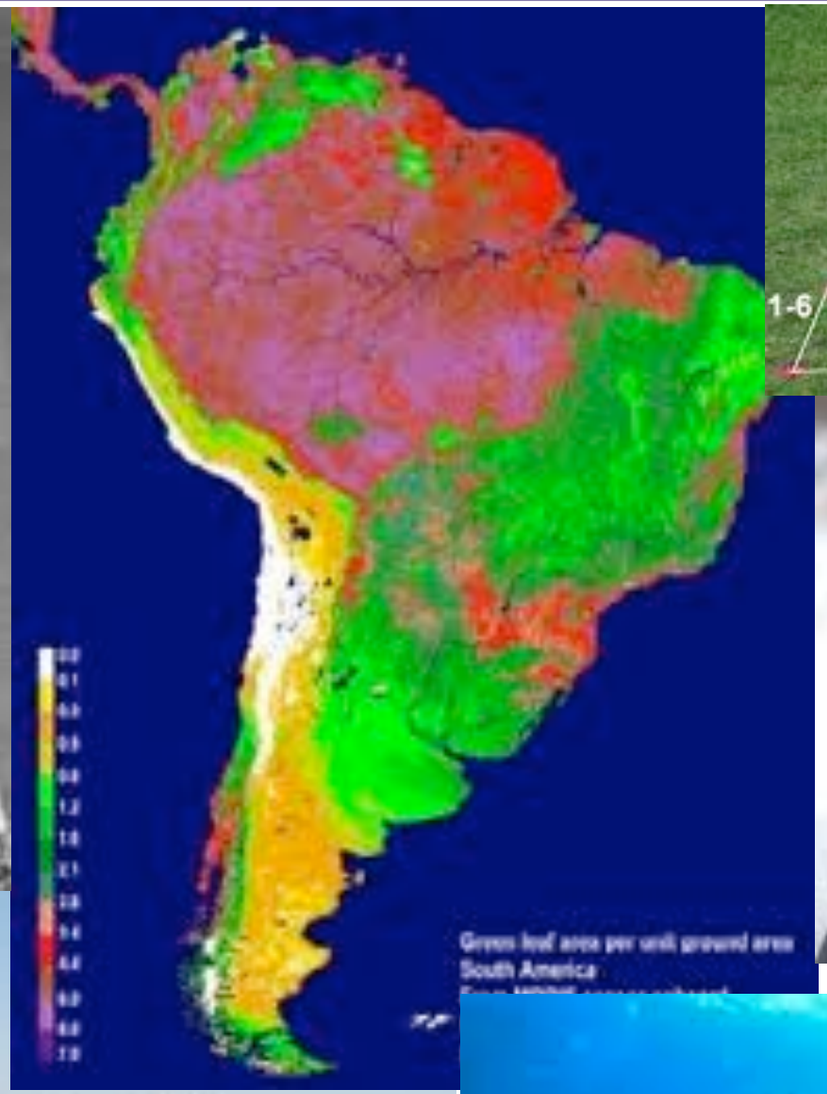
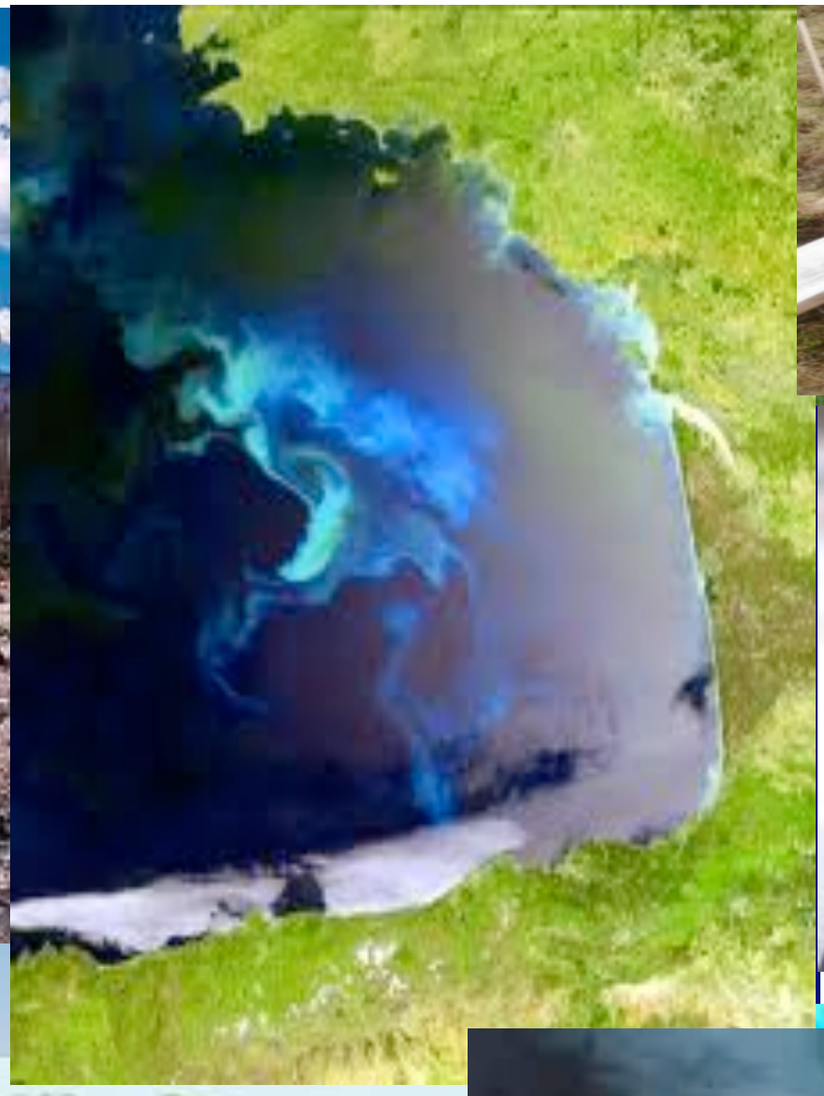
Studying Microbes

Field Observations Are Important Tools



Field Observations Important in Microbial Studies

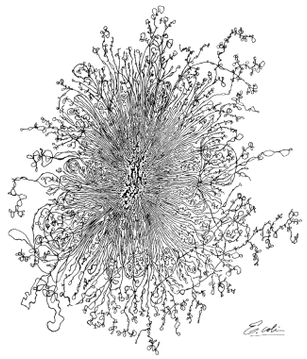


Culturing Microbes

The Great Plate Count Anomaly

Culturing

Count



DNA

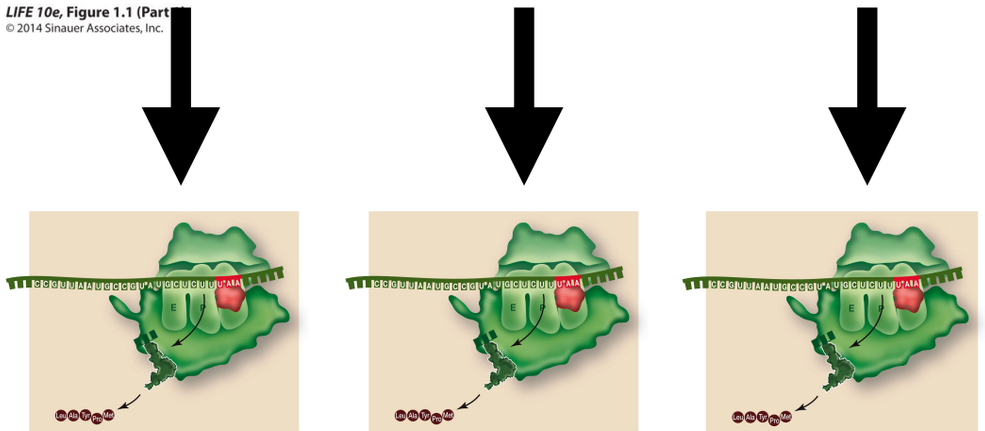
<<<<<

Observation

Count

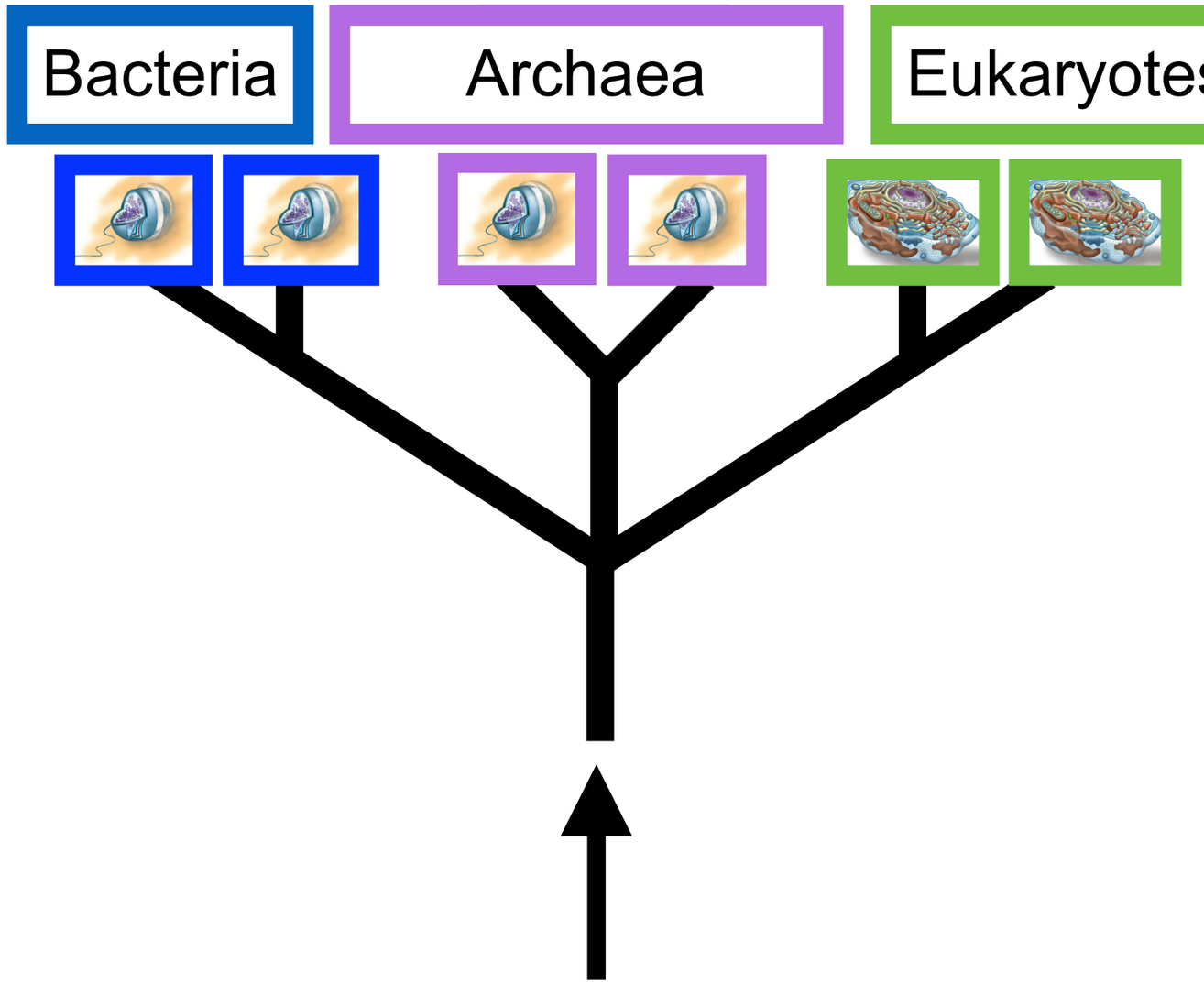
DNA and Microbes 1: Tree of Life

LIFE 10e, Figure 1.1 (Part)



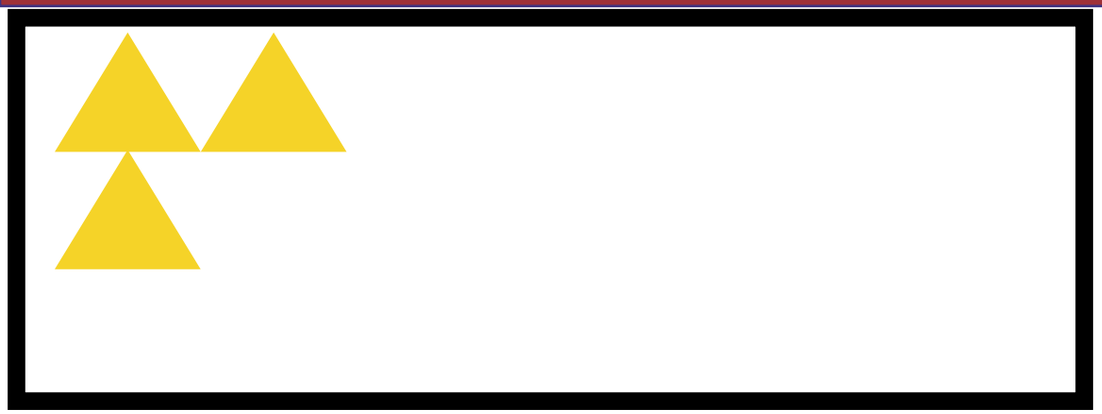
rRNA rRNA rRNA

ACUGC ACUCC ACCCC
ACCUAU AGCUAU AGCUCU
CGUUCG CGAUCG CGCUCG

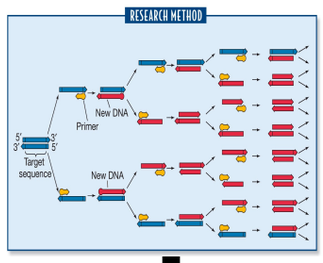


Taxa	Characters	
S		G
R		G
E		G
F		G
C		G
W		G

DNA and Microbes 2: Uncultured



DNA

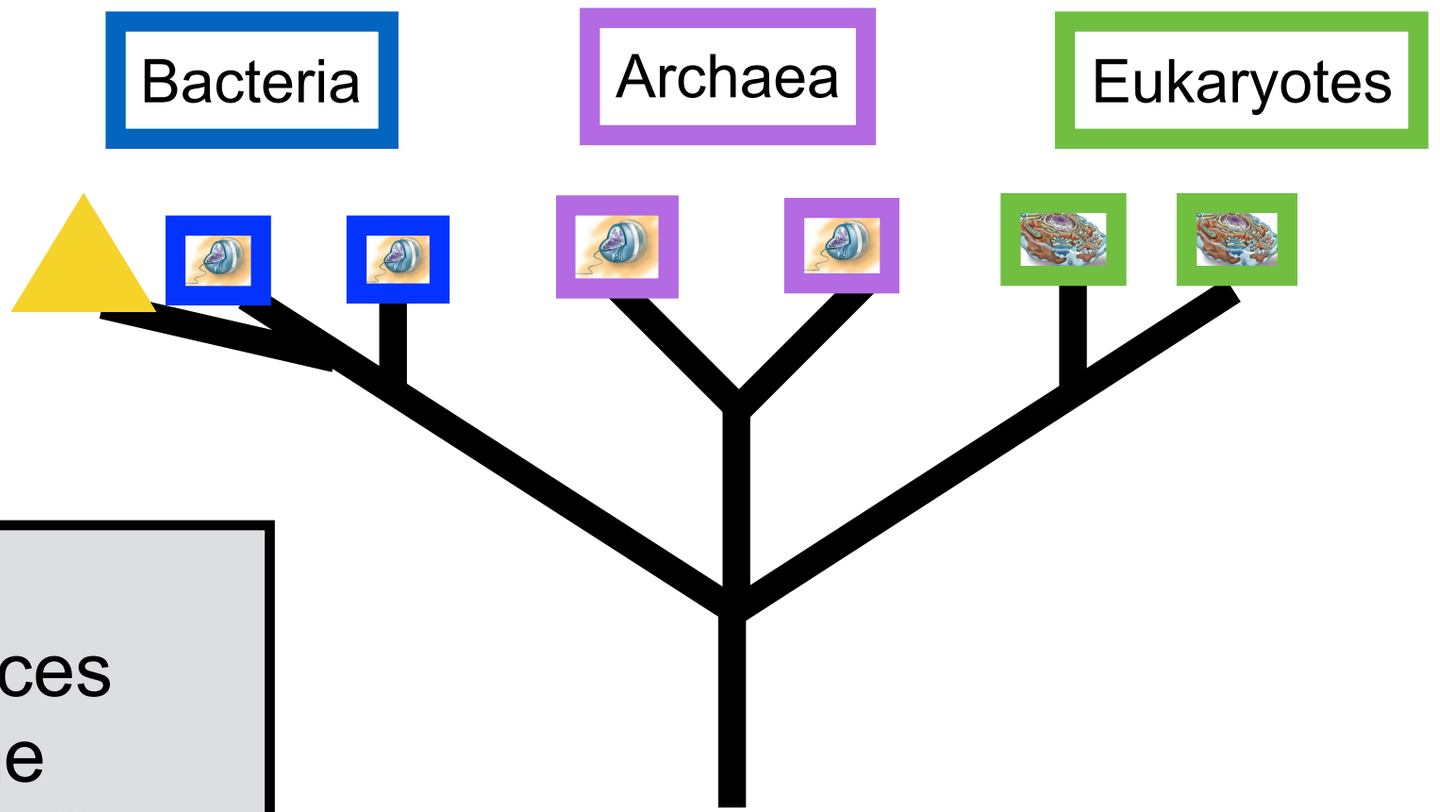


ACTGC
ACCTAT
CGTTCG

ACTGC
ACCTAT
CGTTCG

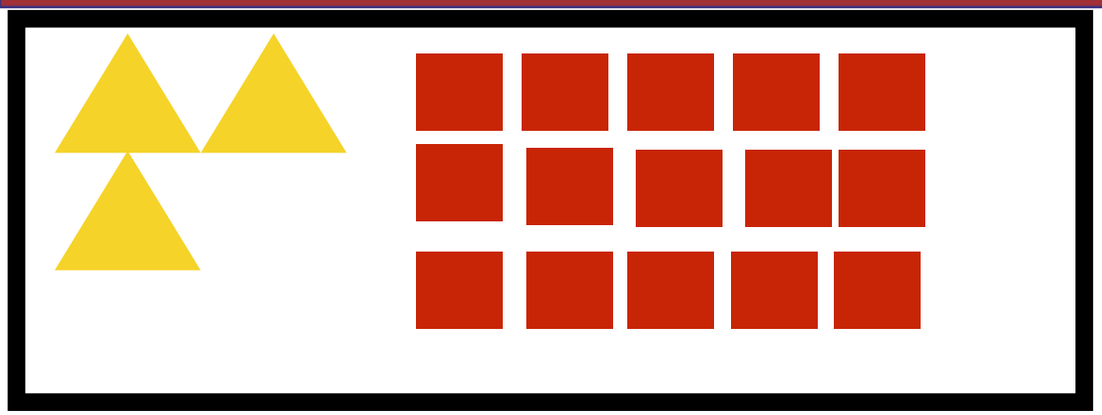
ACTGC
ACCTAT
CGTTCG

Many sequences from one sample all point to the same branch on the tree

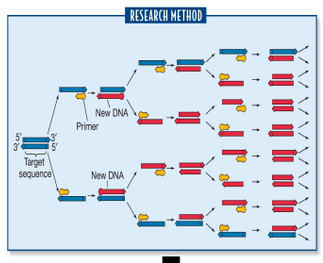


Taxa	Characters
B1	ACTGCACCTATCGTTCG
B2	ACTCCACCTATCGTTCG
E1	ACTCCAGCTATCGATCG
E2	ACTCCAGGTATCGATCG
A1	ACCCCAGCTCTCGCTCG
A2	ACCCCAGCTCTGGCTCG
New1	ACTGCACCTATCGTTCG

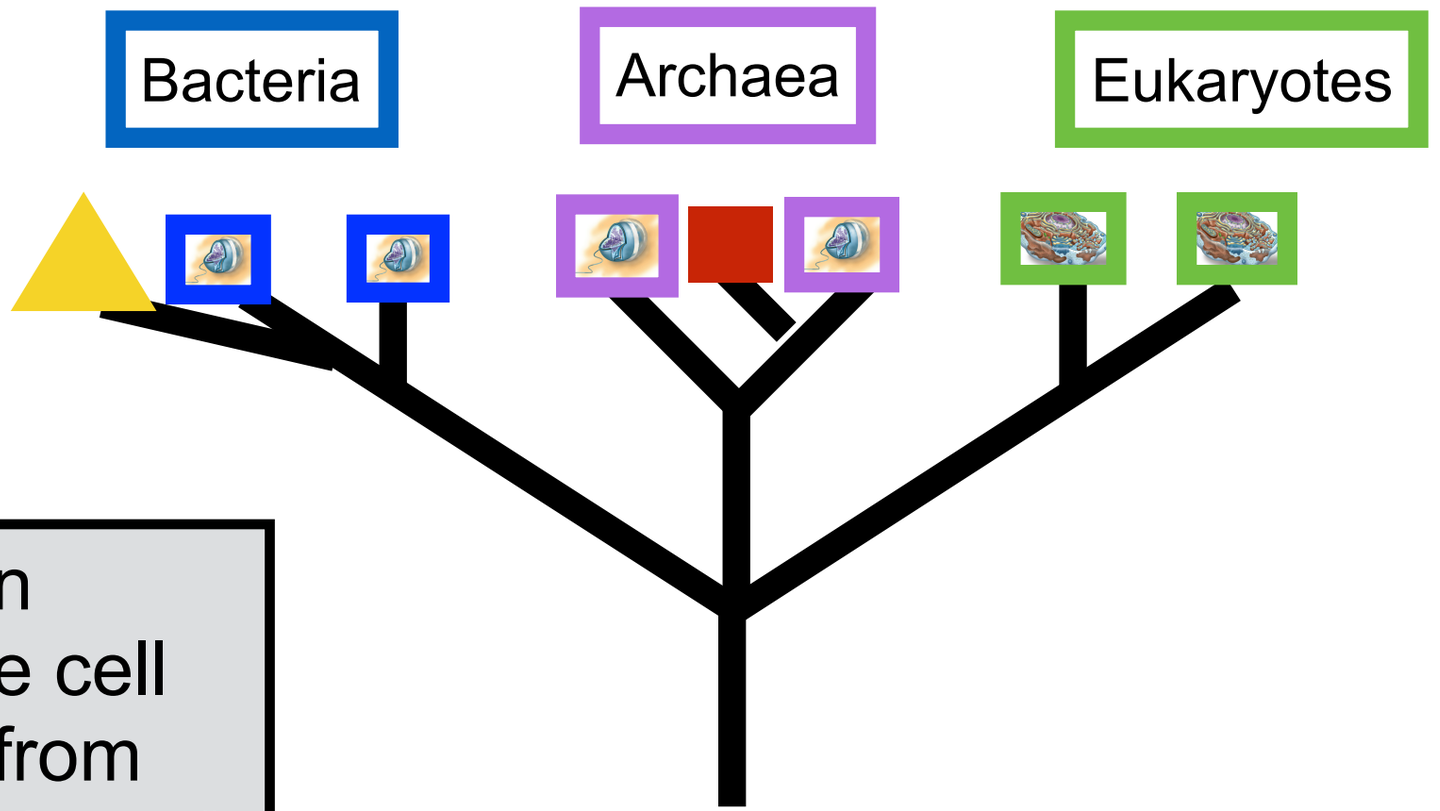
DNA and Microbes 2: Uncultured



DNA



One can estimate cell counts from the number of times each sequence is seen.



ACTGC
ACCTAT
CGTTCG

ACTGC
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ACCCC
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Taxa	Characters
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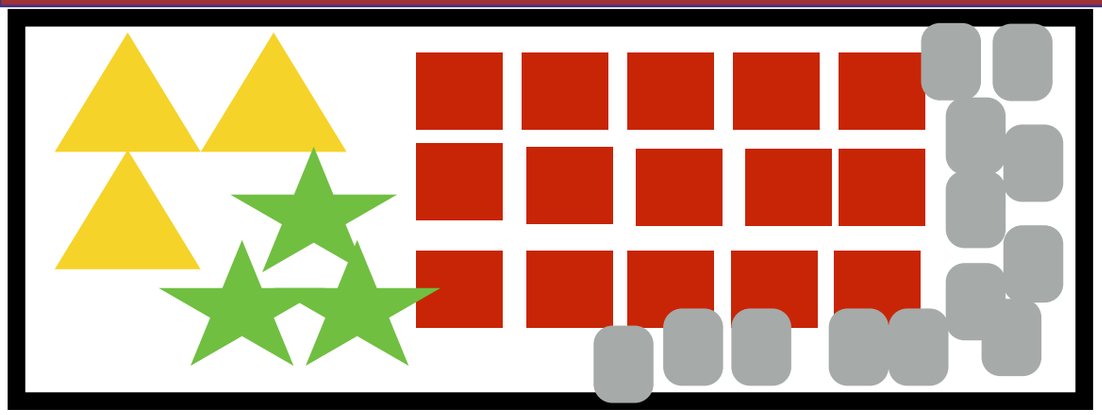
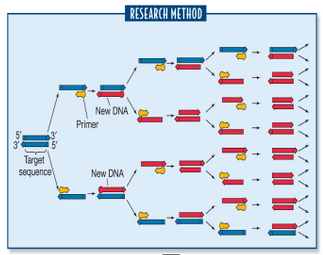
A2	ACCCCAGCTCTGGCTCG
New1	ACCCCAGCTCTGCCTCG
New2	ACTGCACCTATCGTTCG

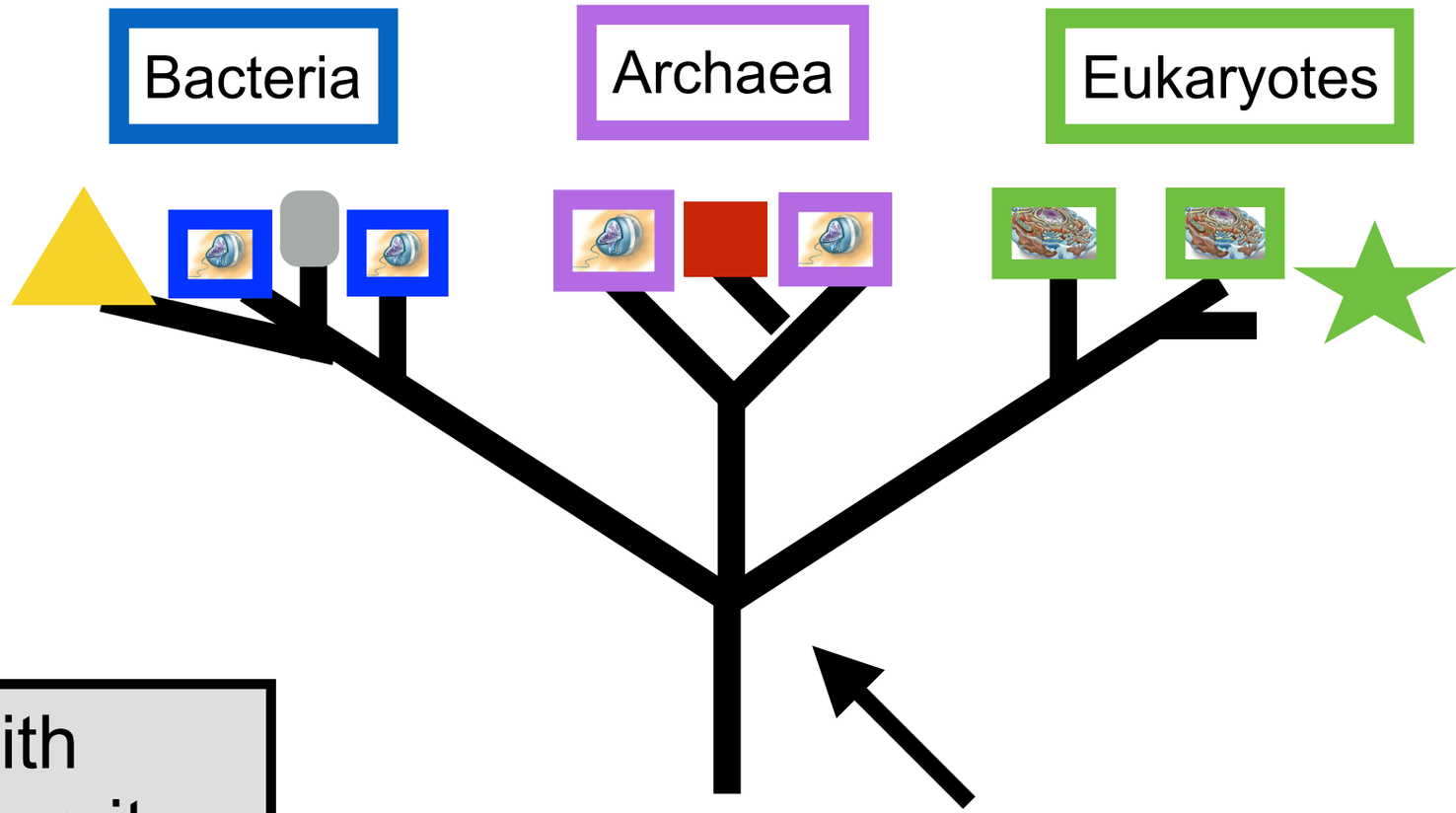
DNA and Microbes 2: Uncultured



DNA



Even with more taxa it still works



ACTGC
ACCTAT
CGTTCG

AGGGG
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CGCTCG

ACTGC
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CGTTCG

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AGCTAT
CGATCG

ACCCC
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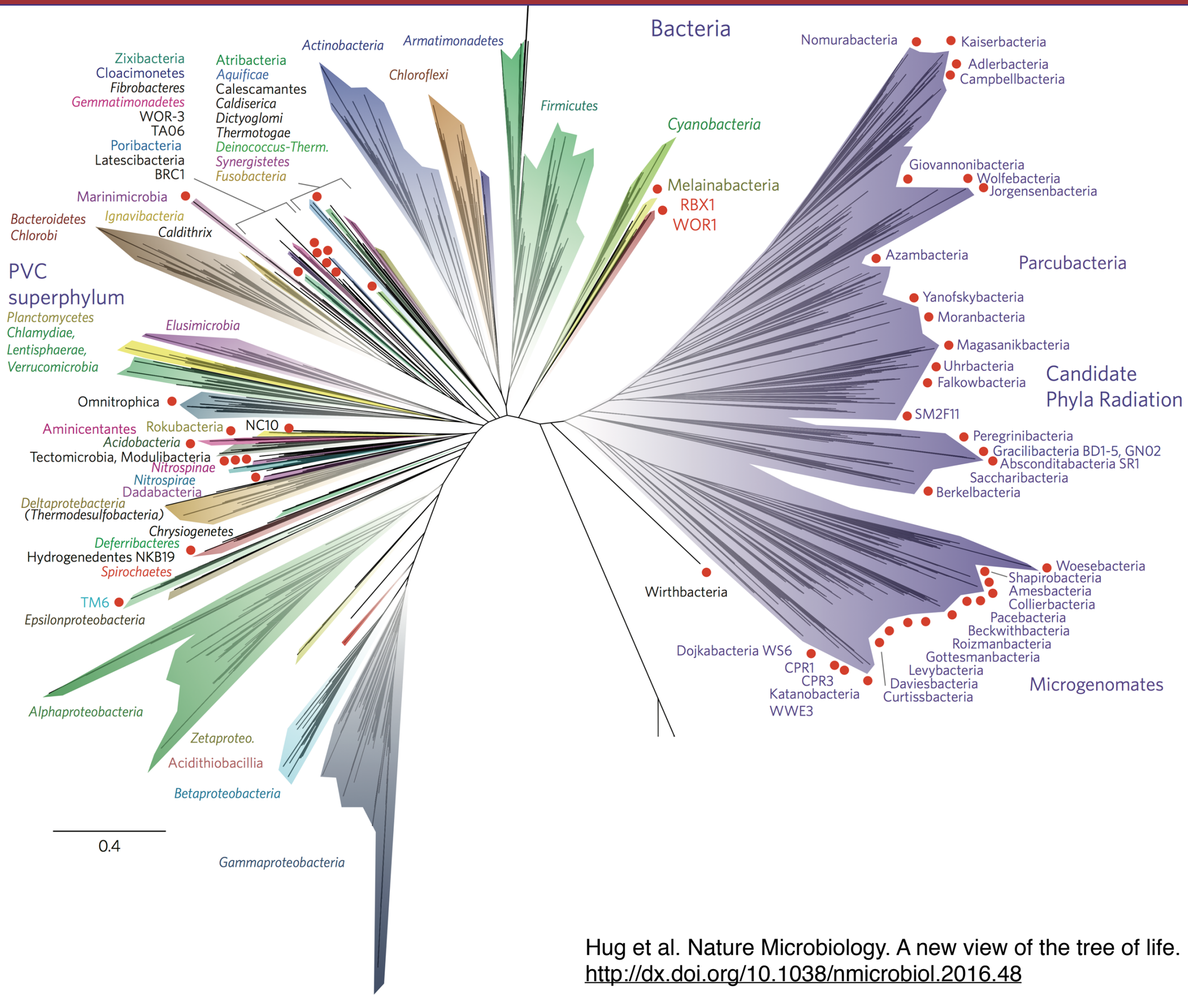
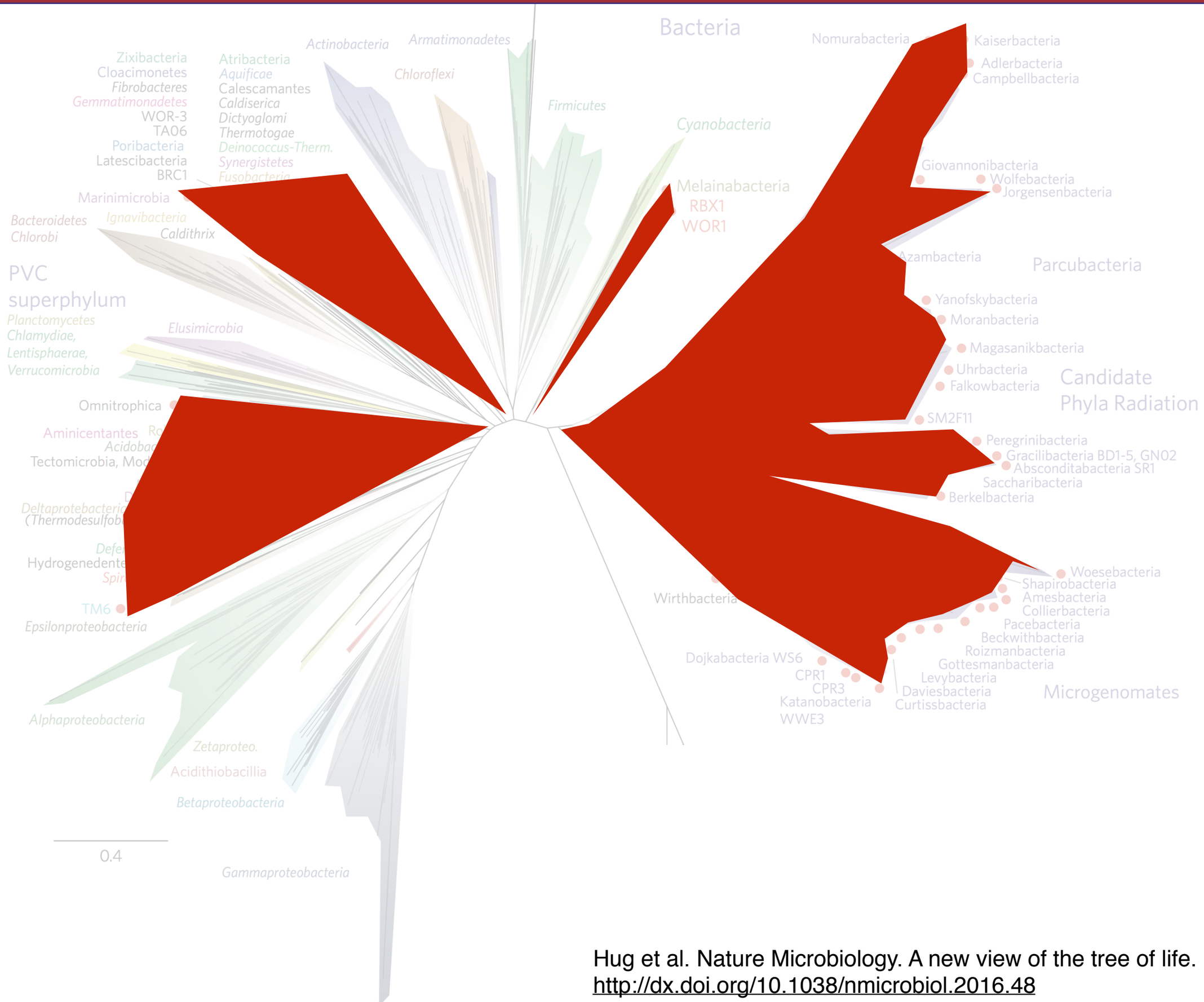
New1	ACCCCAGCTCTGCCTCG
New2	AGGGGAGCTCTGCCTCG
New3	ACTCCAGCTATCGATCG
New4	ACTGCACCTATCGTTCG

Hug et al. 2016 Bacteria



Hug et al. Nature Microbiology. A new view of the tree of life.
http://dx.doi.org/10.1038/nmicrobiol.2016.48

Phyla Never Grown in the Lab



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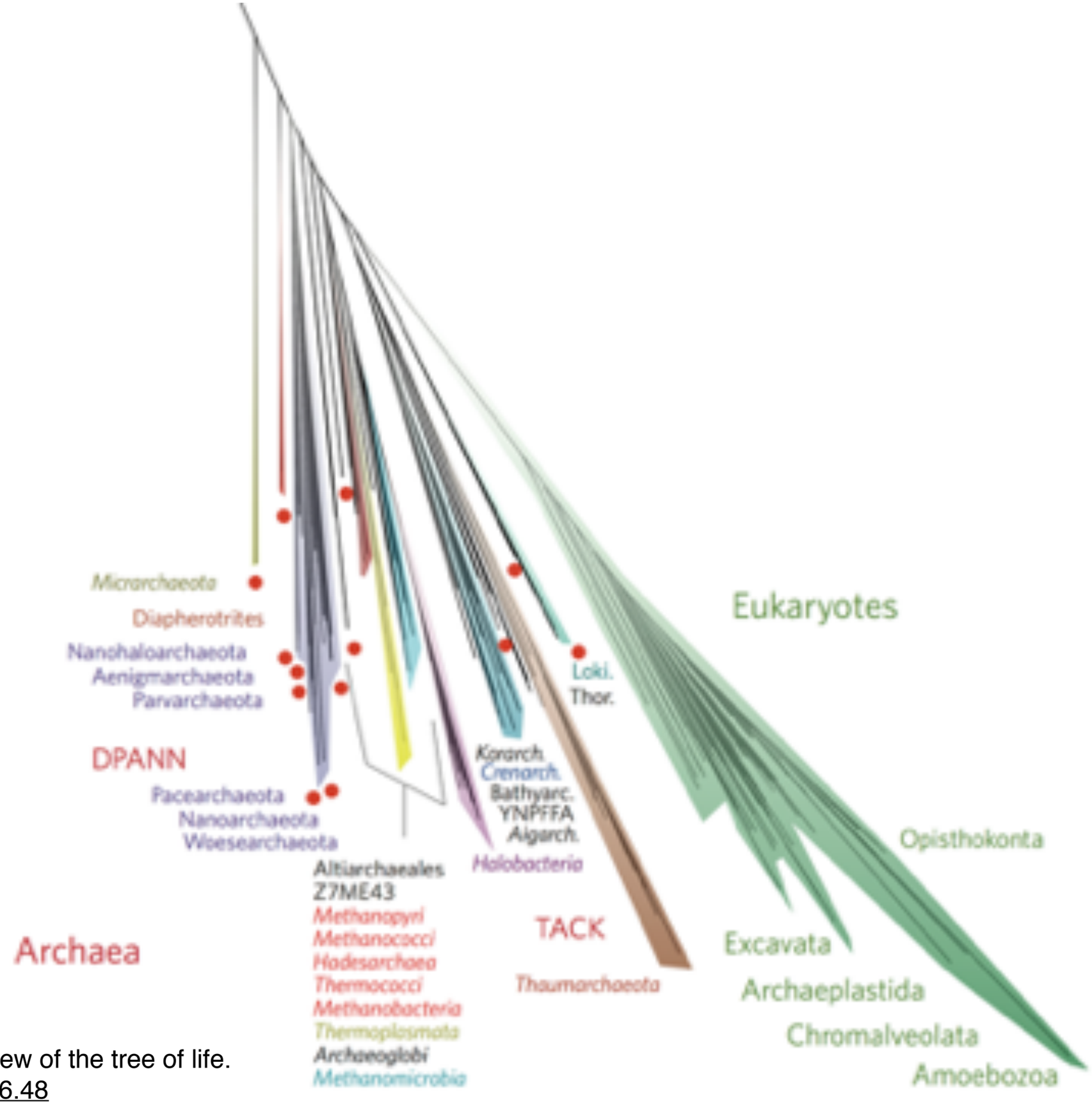

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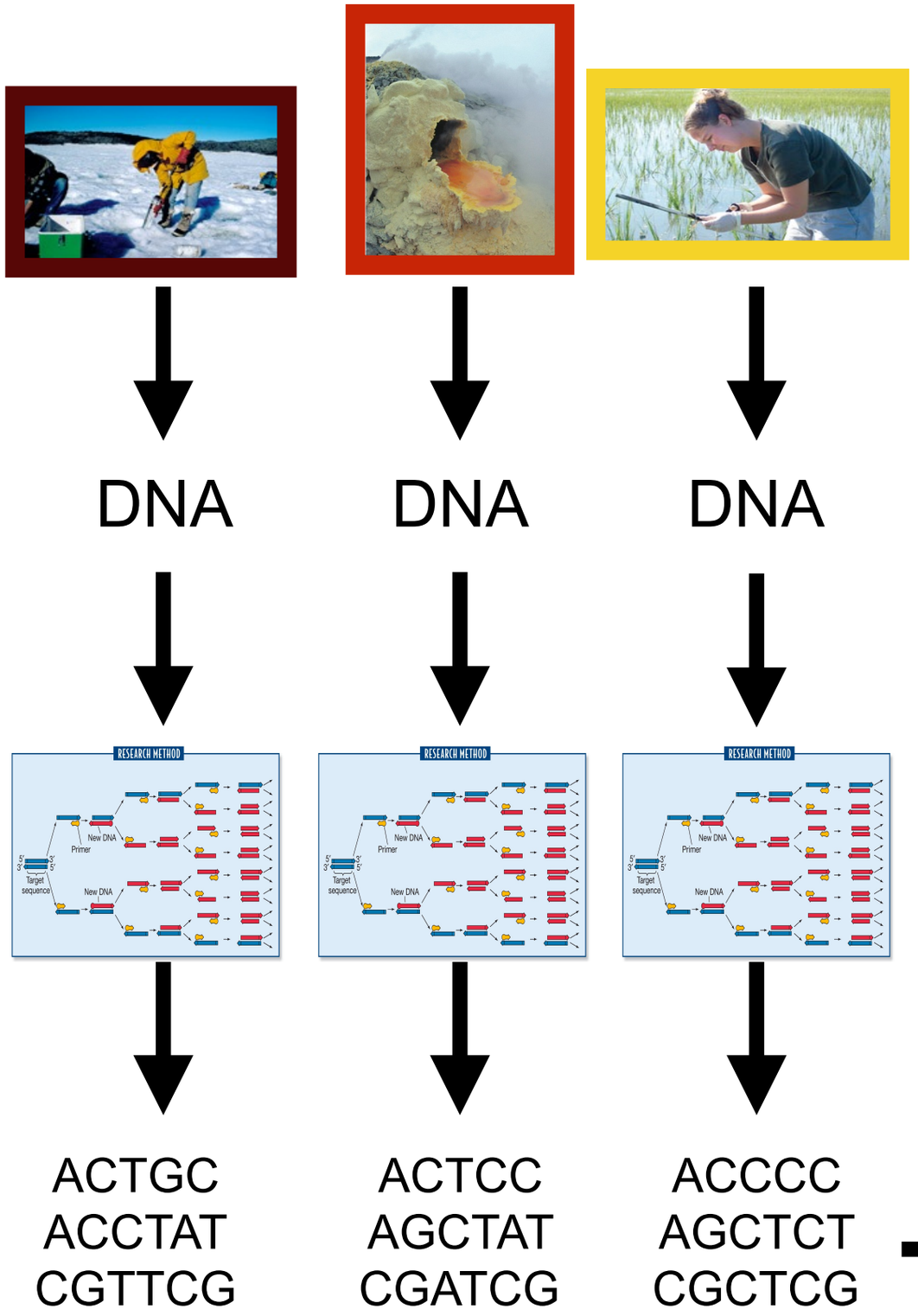
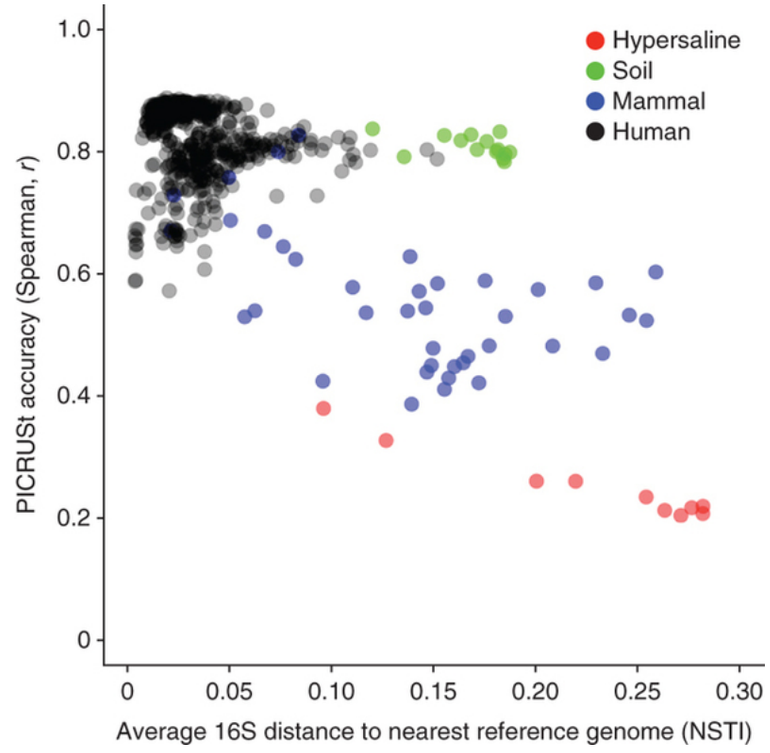
DNA and Microbes 2: Uncultured





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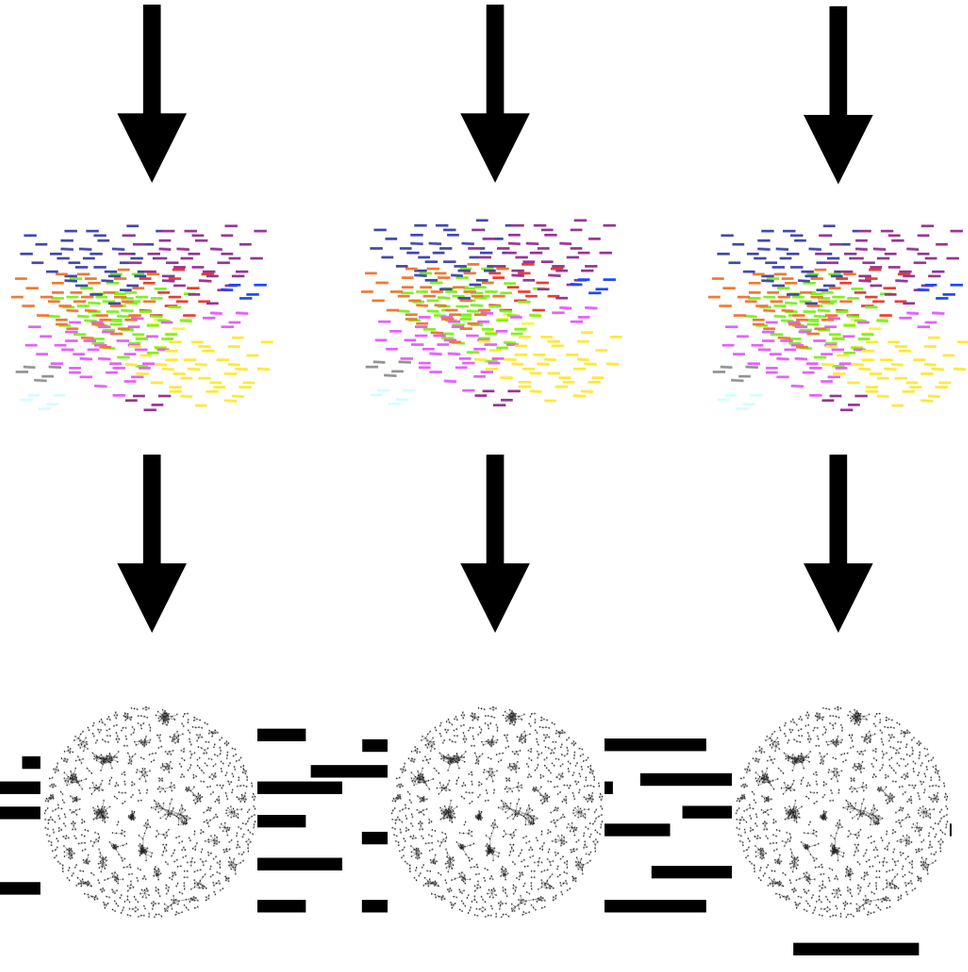
A2	ACCCCAGCTCTGGCTCG
New1	ACCCCAGCTCTGCCTCG
New2	ACGGCAGCTCTGCCTCG

DNA and Microbes 2: Genomes

DNA DNA DNA



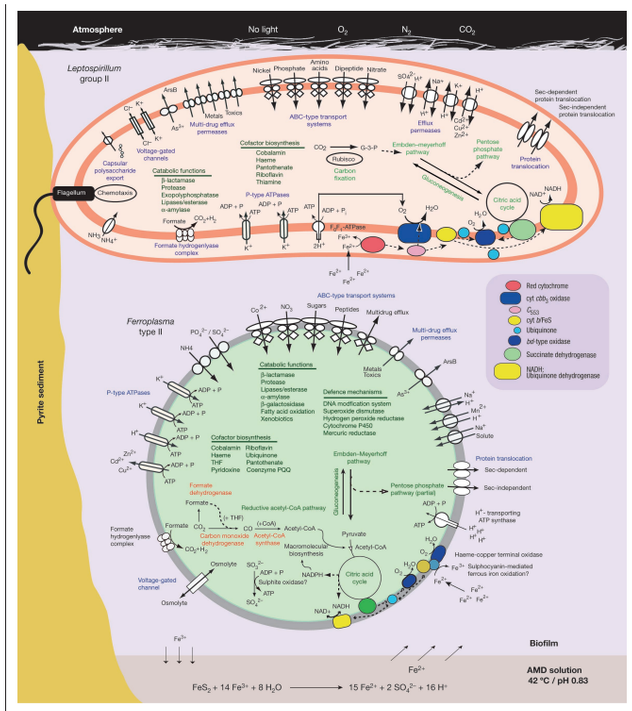


Figure 4 Cell metabolic cartoons constructed from the annotation of 2,180 ORFs identified in the *Leptospirillum* group II genome (63% with putative assigned function) and 1,931 ORFs in the *Ferroplasma* type II genome (58% with assigned function). The cell cartoons are shown within a biofilm that is attached to the surface of an acid mine drainage stream (viewed in cross-section). Tight coupling between ferrous iron oxidation, pyrite dissolution and acid generation is indicated. Rubisco, ribulose 1,5-bisphosphate carboxylase–oxygenase. THF, tetrahydrofolate.

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B2	ACTCCACCTATCGTTCG
E1	ACTCCAGCTATCGATCG
E2	ACTCCAGGTATCGATCG
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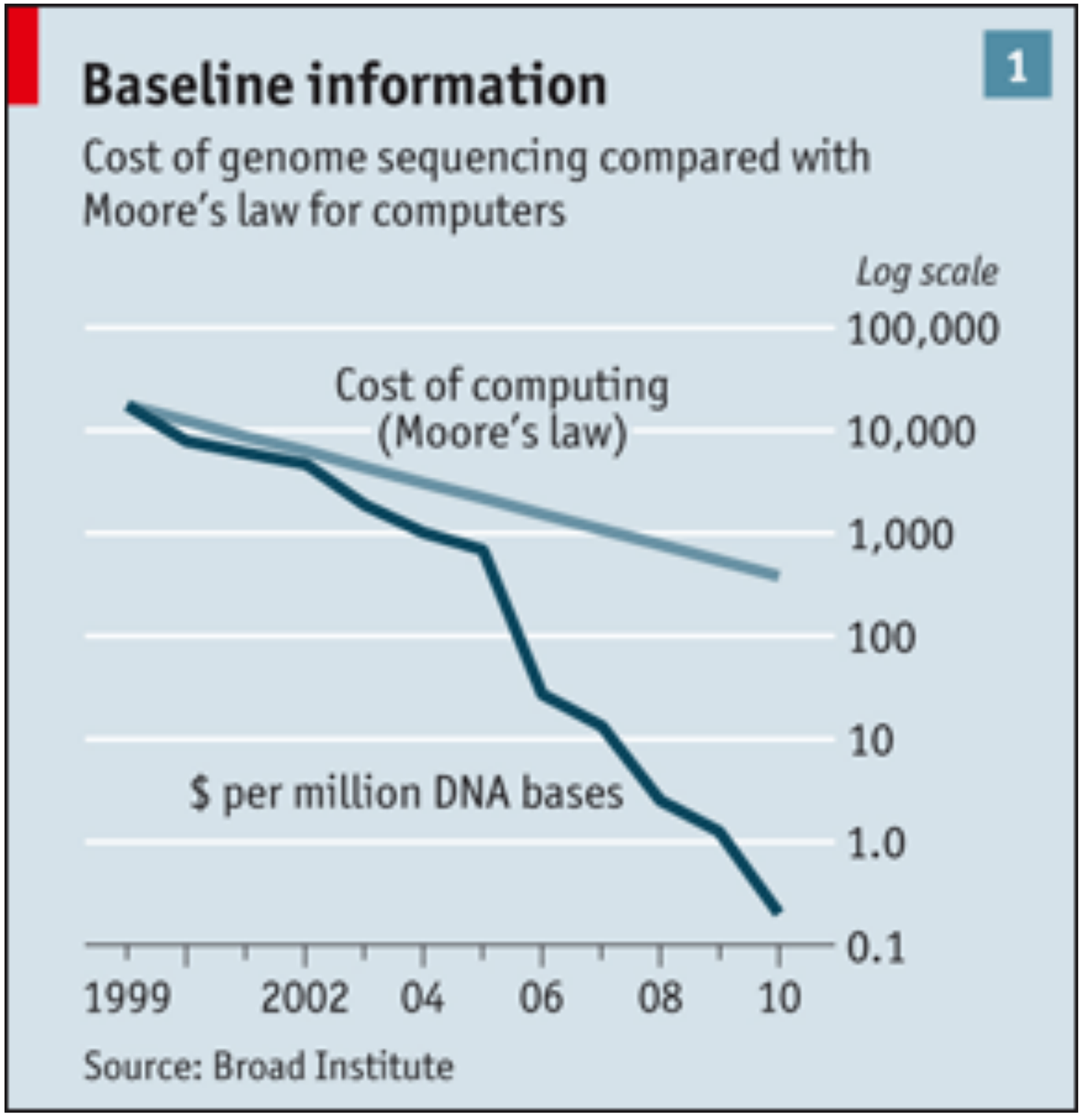
New1	ACCCCAGCTCTGCCTCG
New2	AGGGGAGCTCTGCCTCG
New3	ACTCCAGCTATCGATCG
New4	ACTGCACCTATCGTTCG

Sequencing Has Gone Crazy



The Rise of the Microbiome

- **Organisms are covered in a cloud of microbes**

The Rise of the Microbiome

- **Organisms are covered in a cloud of microbes**

- **This "microbiome" likely is involved in many important phenotypes**

The Rise of the Microbiome

- **Organisms are covered in a cloud of microbes**

- **This "microbiome" <u>LIKELY</u> is involved in many important phenotypes**

The Rise of the Microbiome

- **Organisms are covered in a cloud of microbes**

- **This "microbiome" <u>LIKELY</u> is <u>INVOLVED</u> in many important phenotypes**

The Rise of the Microbiome

- **Organisms are covered in a cloud of microbes**

- **This "microbiome" <u>LIKELY</u> is <u>INVOLVED</u> in many important phenotypes**

- **This microbiome can be incredibly diverse and vary greatly over time and space**

Microbiome and Function

Turnbaugh et al Nature. 2006 444(7122):1027-31.

Microbiomes and Plant Health

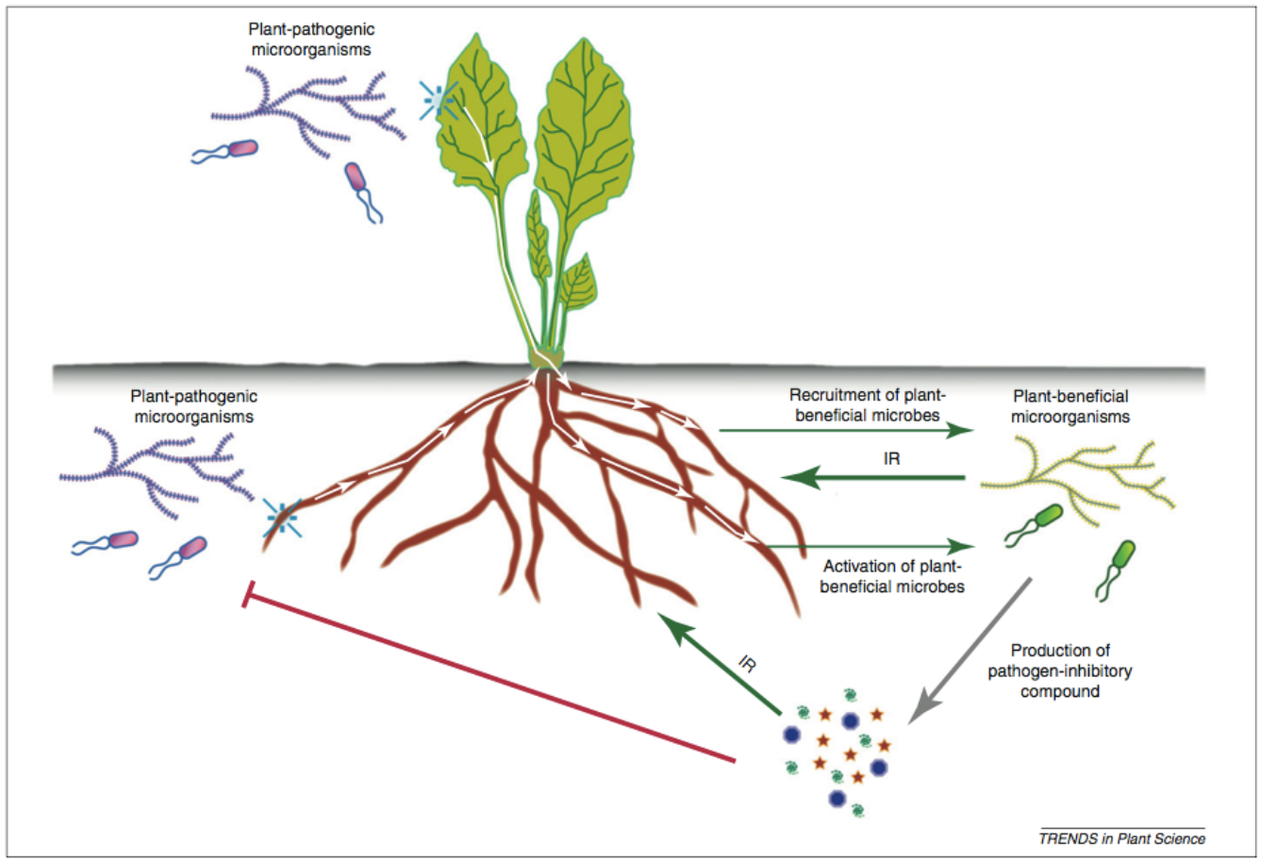
OPEN ACCESS Freely available online

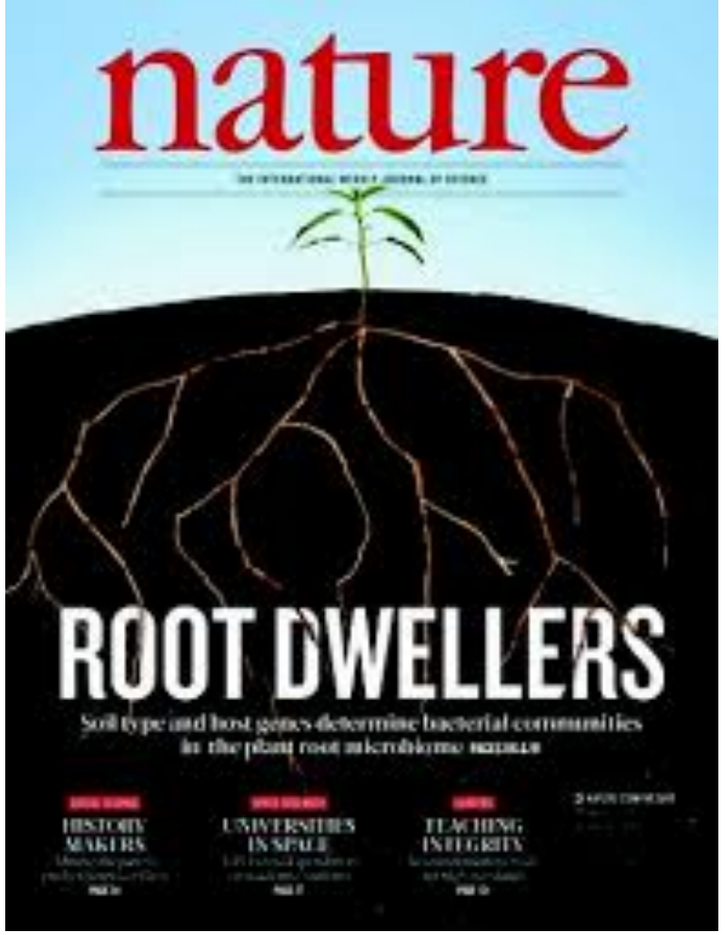
PLOS ONE

A Drought Resistance-Promoting Microbiome Is Selected by Root System under Desert Farming

Ramona Marasco[1], Eleonora Rolli[1], Besma Ettoumi[2], Gianpiero Vigani[3], Francesca Mapelli[1], Sara Borin[1], Ayman F. Abou-Hadid[4], Usama A. El-Behairy[4], Claudia Sorlini[1], Ameur Cherif[2], Graziano Zocchi[3], Daniele Daffonchio[1]*

1 Dipartimento di Scienze per gli Alimenti, la Nutrizione e l'Ambiente, Università degli Studi di Milano, Milan, Italy, **2** Laboratoire Microorganismes et Biomolécules Actives, Université Tunis El Manar, Tunis, Tunisia and Laboratoire Biotechnologie et Valorisation des Bio-Géo Ressources, Institut Supérieur de Biotechnologie, Université de La Manouba, Sidi Thabet, Ariana, Tunisia, **3** Dipartimento di Scienze Agrarie e Alimentari- Produzione, Territorio, Agroenergia; Università degli Studi di Milano, Milan, Italy, **4** Department of Horticulture, Ain Shams University, Cairo, Egypt





Asthma, Dust, Dogs and Microbiomes

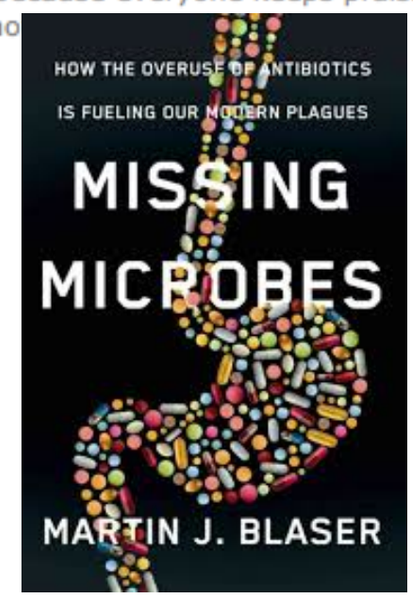
Research Shows How Household Dogs Protect Against Asthma, Infection

Study Led by UCSF, U Michigan Scientists Points to Changes in Gut Microbes

Share this story: Share Tweet g+1

Paws for Thought: Dogs truly do make us healthier

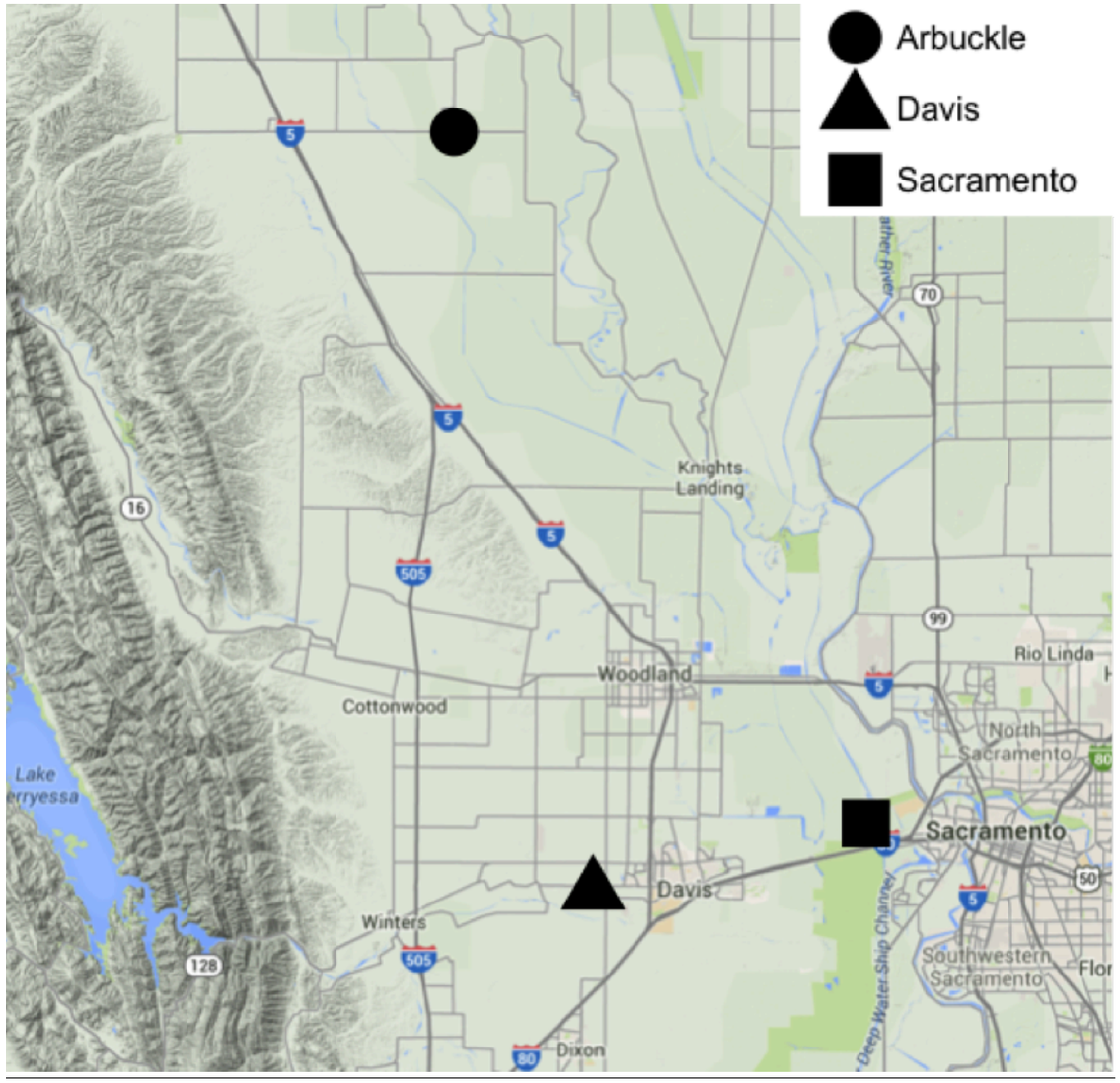
A boy and his dog: How sweet it is and healthy, too! Young Guthrie, who is learning to talk, calls Annie "Good Girl" because everyone keeps praising Annie for being such a "good girl." Courtesy pho

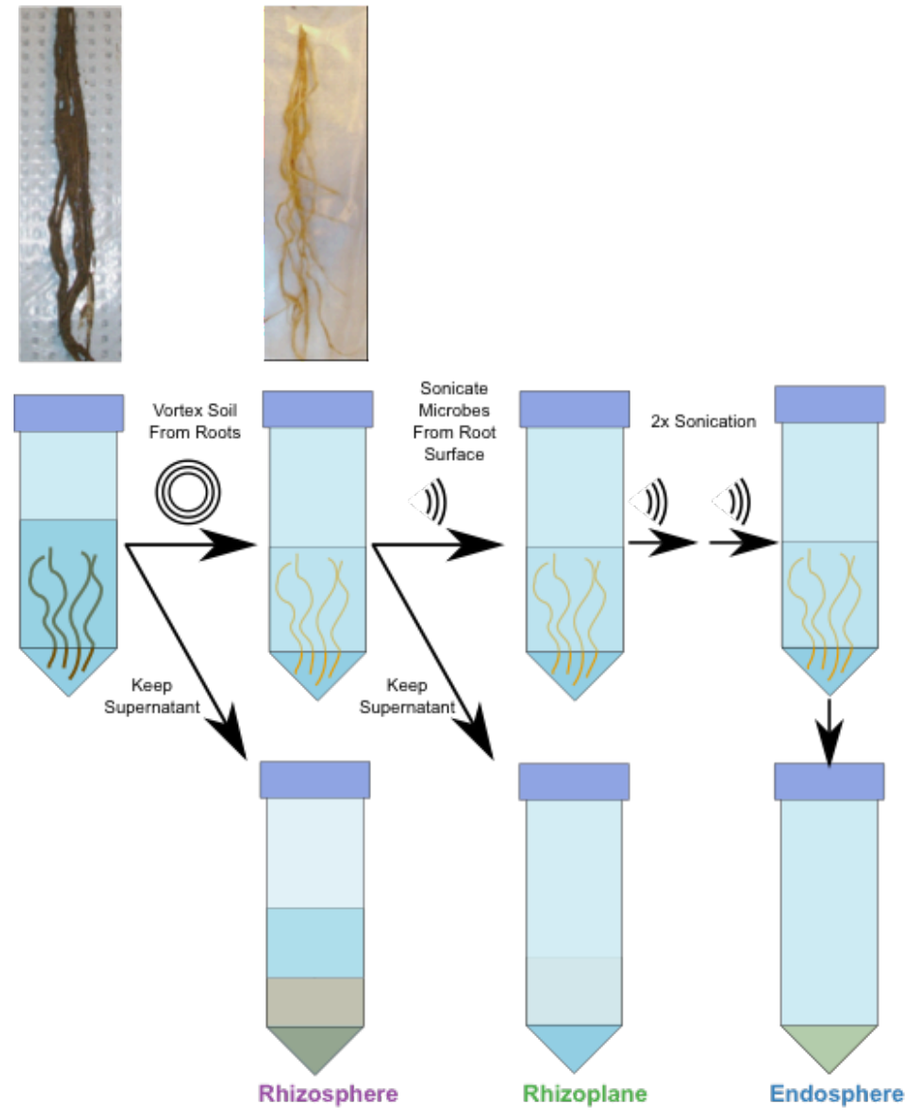


Microbiome Functions

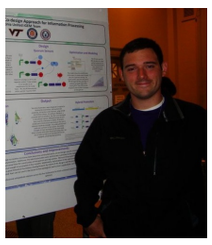
- Pathogen resistance
- Nutrient acquisition
- Stress resistance
  - Drought
  - Temperature
  - Salinity
- General vigor and yield
- Food quality
  - Spoilage
  - Storage
  - Flavors
  - Nutrients

Example: Rice Microbiome



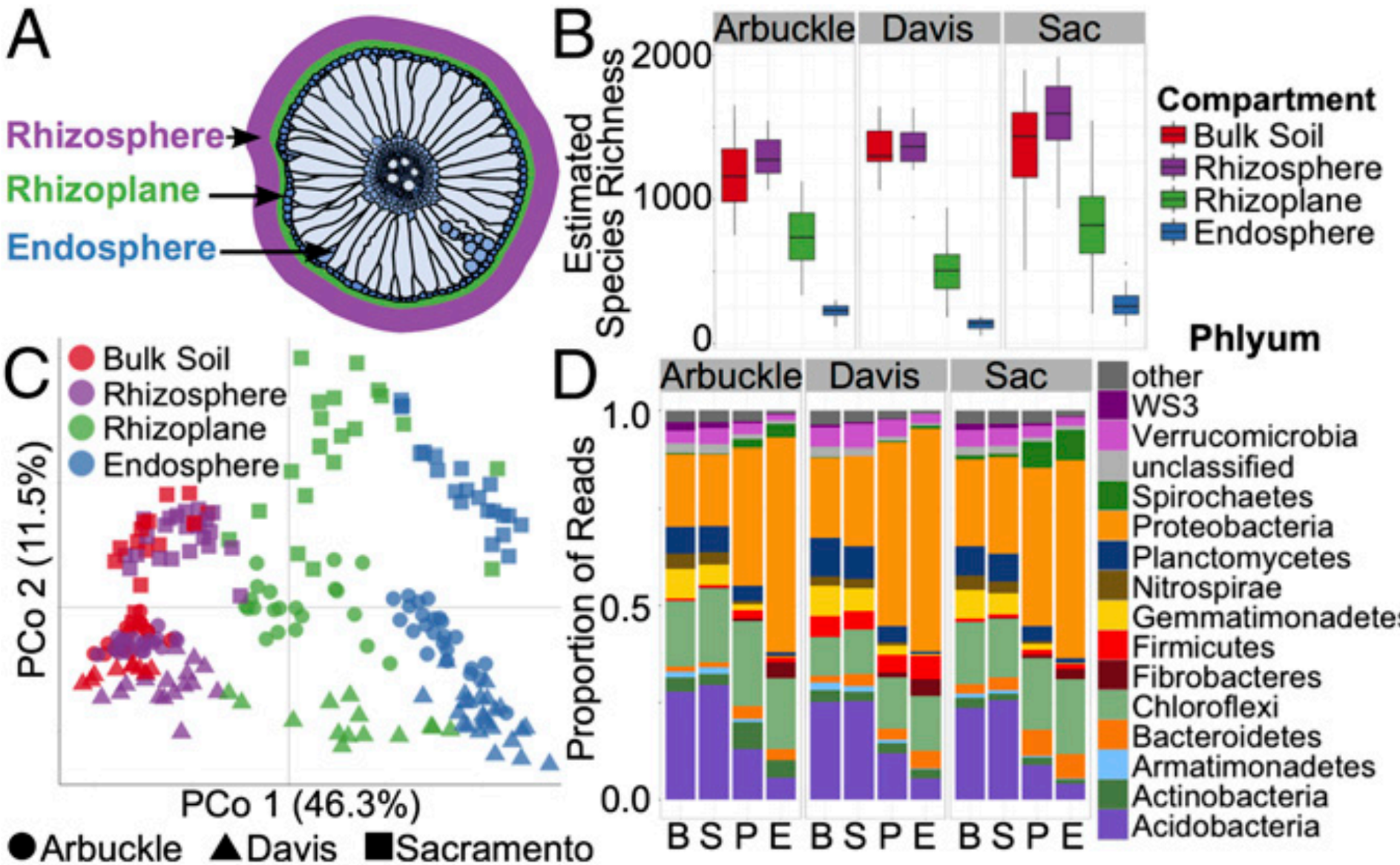


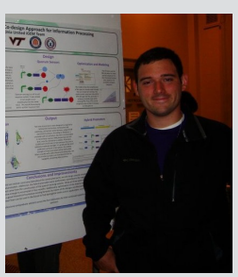
Edwards et al. 2015. Structure, variation, and assembly of the root-associated microbiomes of rice. PNAS



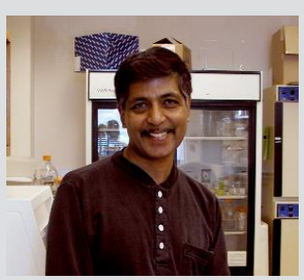

Slides by Jonathan Eisen talk

Rice Microbiome Variation Within Plants





Joseph Edwards @Bulk_Soil



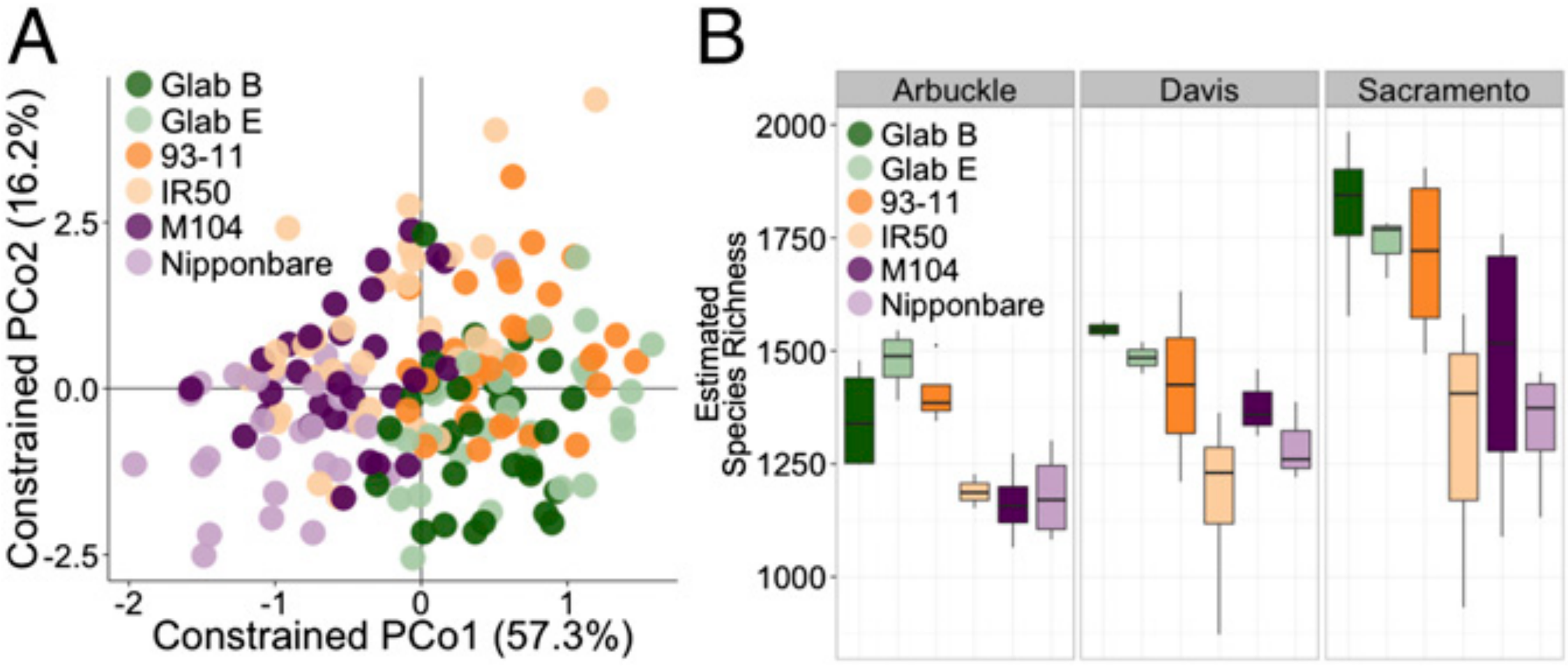
Sundar @sundarlab

Cameron Johnson

Srijak Bhatnagar @srijakbhatnagar

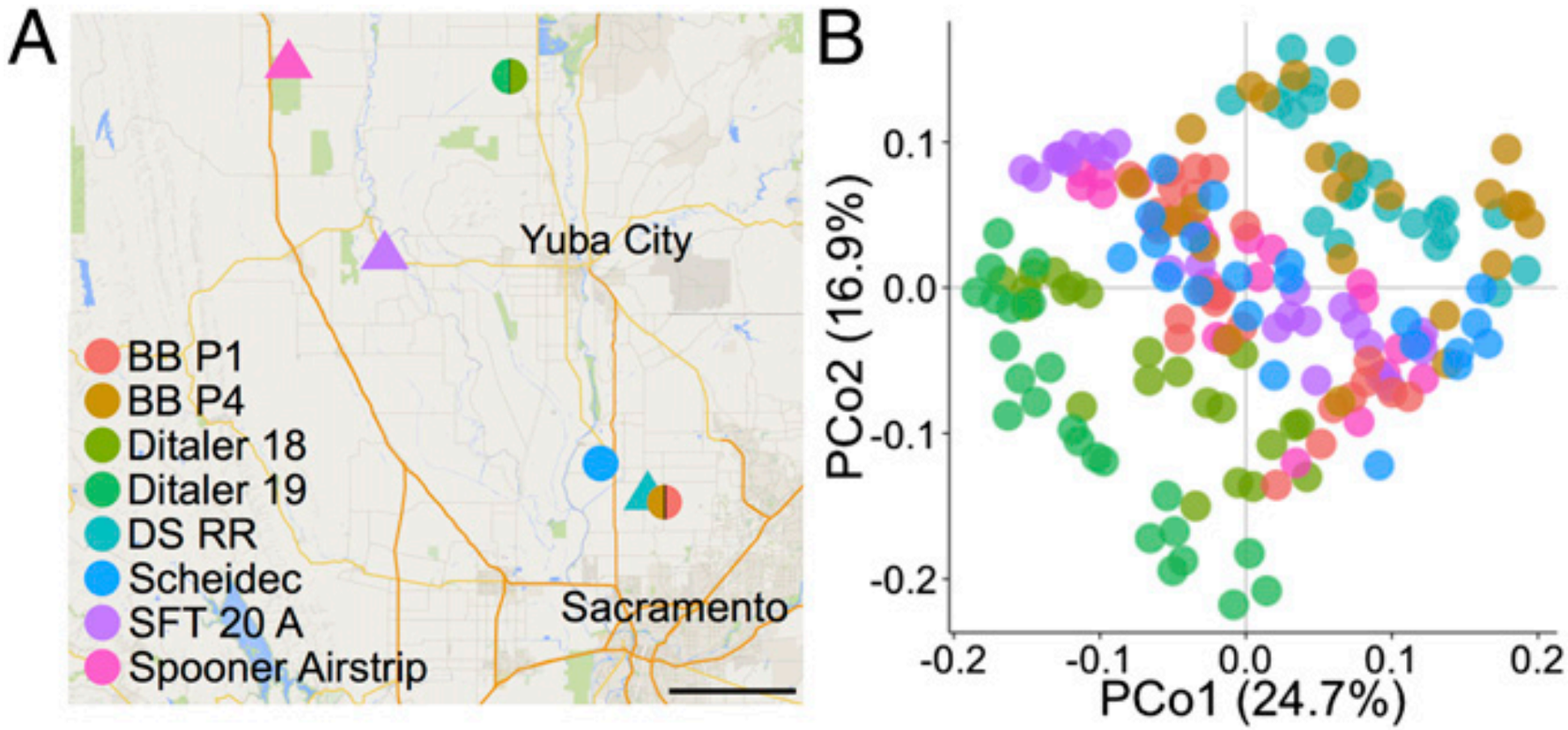
Edwards et al. 2015. Structure, variation, and assembly of the root-associated microbiomes of rice. PNAS 24;112(8):E911-20. doi: 10.1073/pnas.1414592112

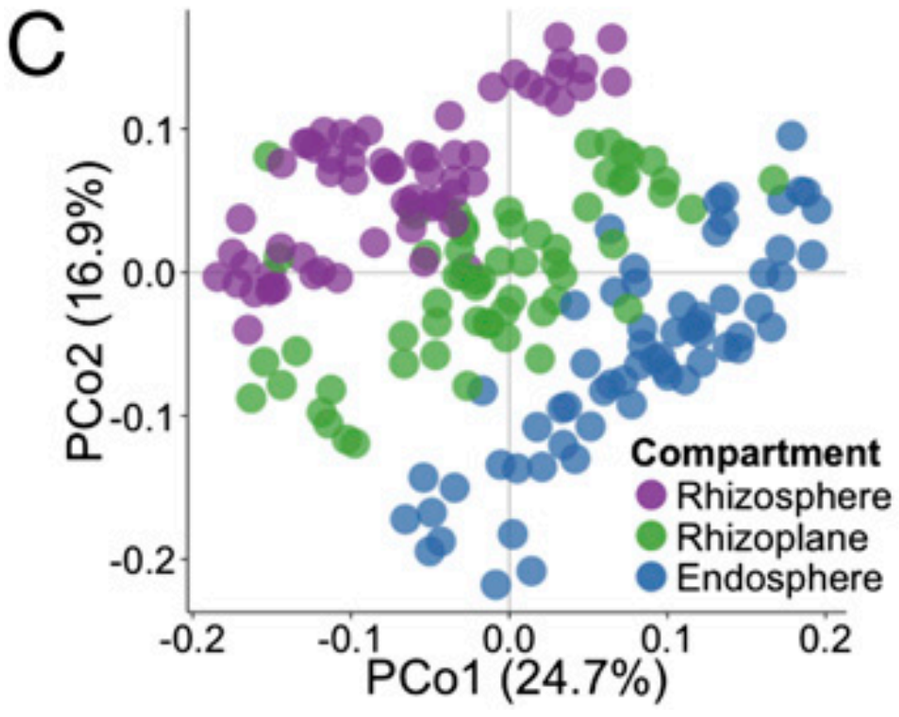
Rice Genotype Affects Microbiome

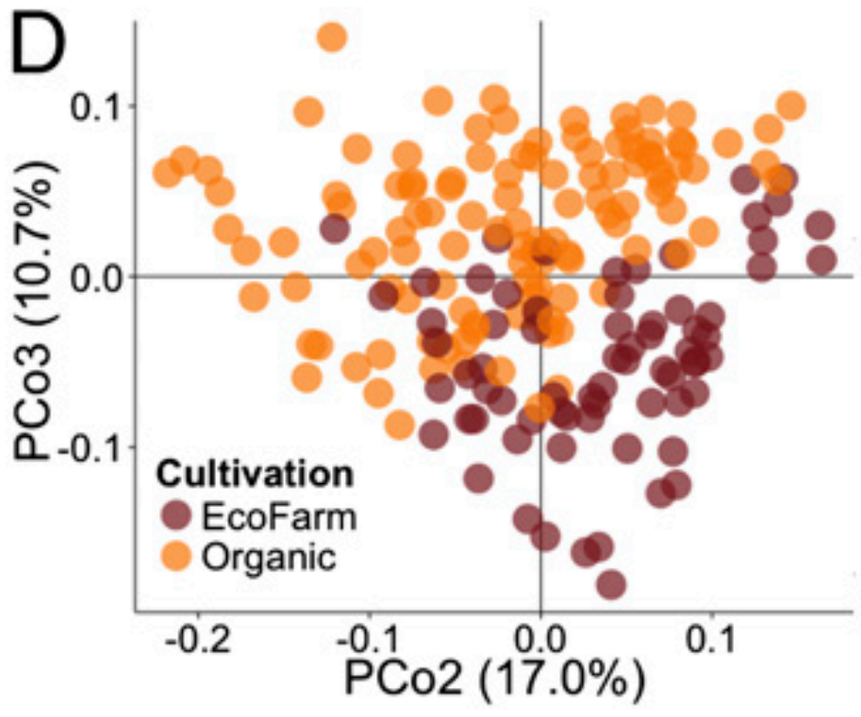


Edwards et al. 2015. Structure, variation, and assembly of the root-associated microbiomes of rice. PNAS 24;112(8):E911-20. doi: 10.1073/pnas.1414592112

Rice: Cultivation Site Effects







Edwards et al. 2015. Structure, variation, and assembly of the root-associated microbiomes of rice. PNAS 24;112(8):E911-20. doi: 10.1073/pnas.1414592112

Rice: Functional Enrichment x Genotype

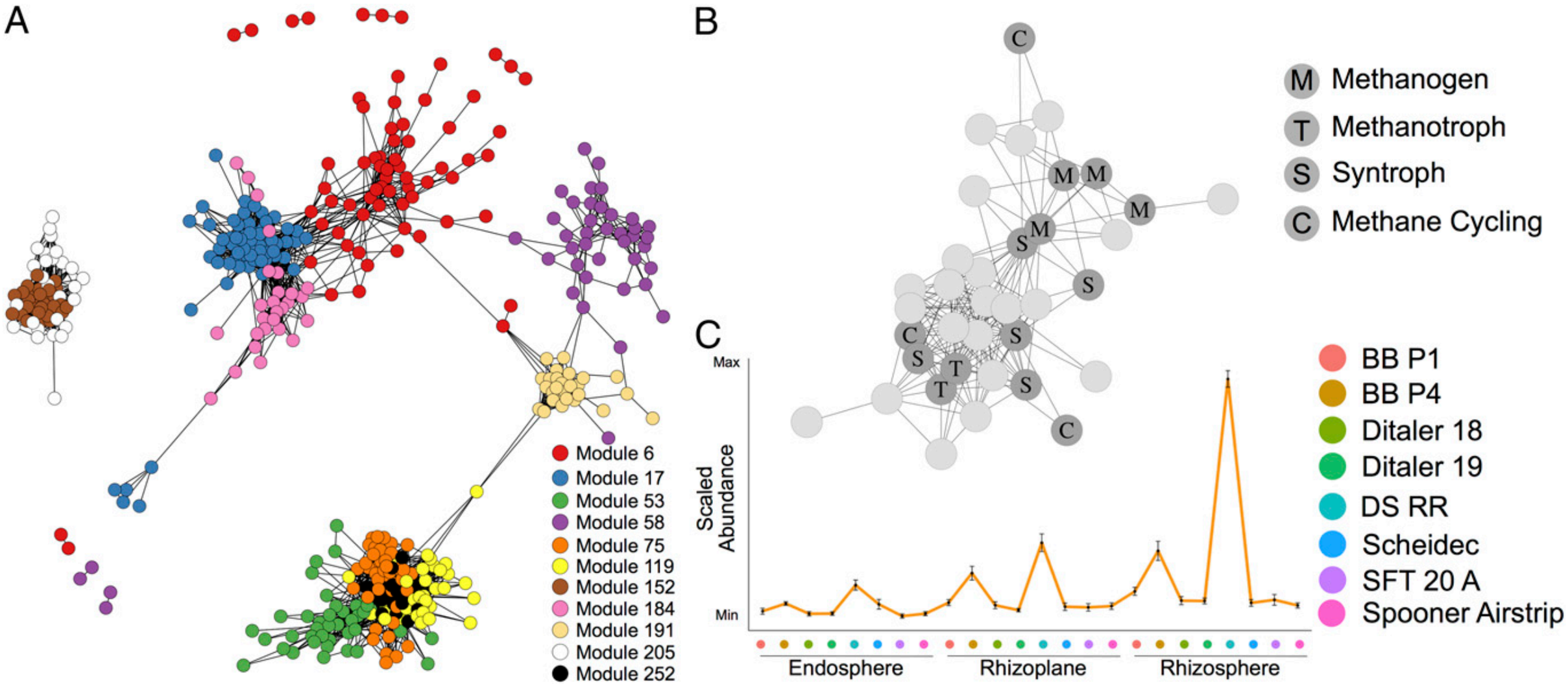
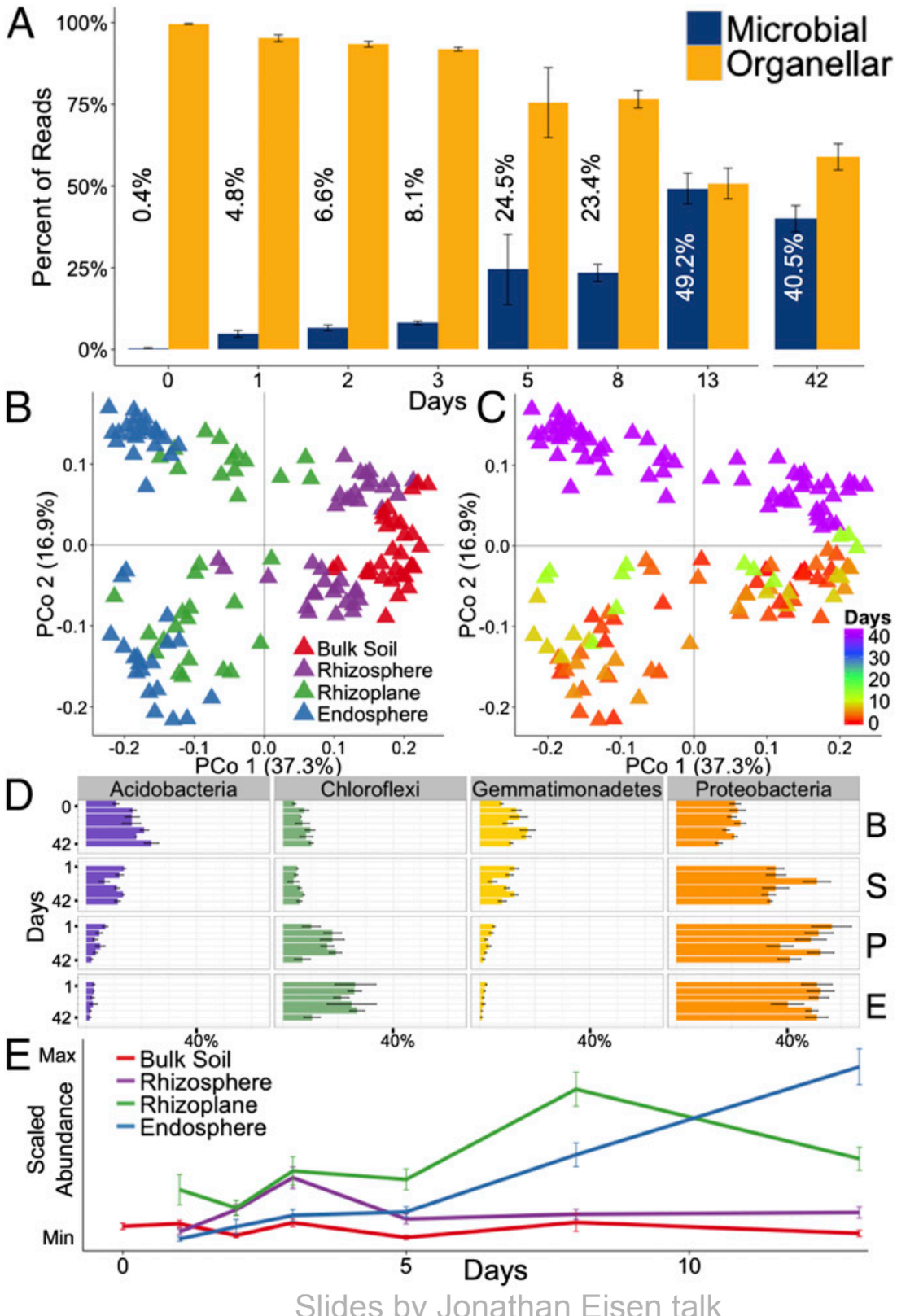


Fig. 5. OTU coabundance network reveals modules of OTUs associated with methane cycling. (*A*) Subset of the entire network corresponding to 11 modules with methane cycling potential. Each node represents one OTU and an edge is drawn between OTUs if they share a Pearson correlation of greater than or equal to 0.6. (*B*) Depiction of module 119 showing the relationship between methanogens, syntrophs, methanotrophs, and other methane cycling taxonomies. Each node represents one OTU and is labeled by the presumed function of that OTU's taxonomy in methane cycling. An edge is drawn between two OTUs if they have a Pearson correlation of greater than or equal to 0.6. (*C*) Mean abundance profile for OTUs in module 119 across all rhizocompartments and field sites. The position along the *x* axis corresponds to a different field site. Error bars represent SE. The *x* and *y* axes represent no particular scale.

Rice Developmental Time Series



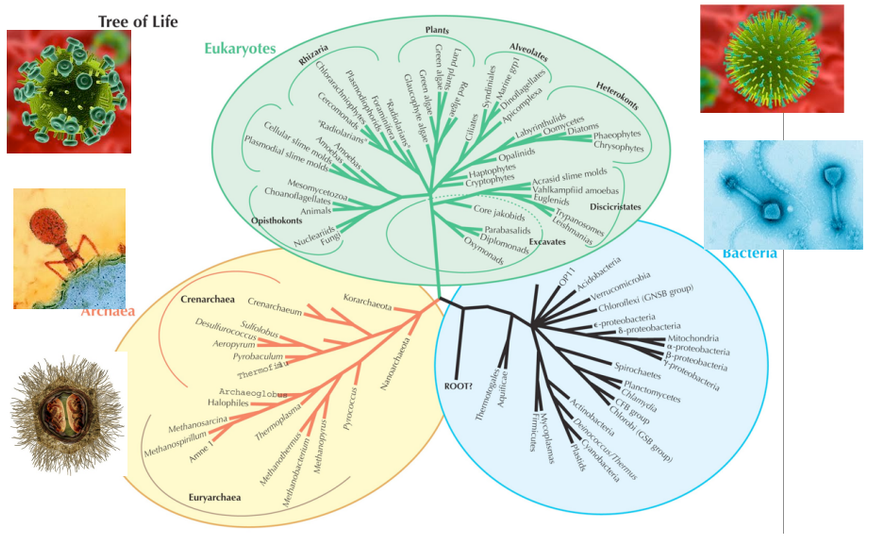
Slides by Jonathan Eisen talk

Fig. 6. Time-series analysis of root-associated microbial communities reveals

Edwards et al. 2015. Structure, variation, and assembly of the root-associated microbiomes of rice. PNAS 24;112(8):E911-20. doi: 10.1073/pnas.1414592112

Major Challenge: Complexity

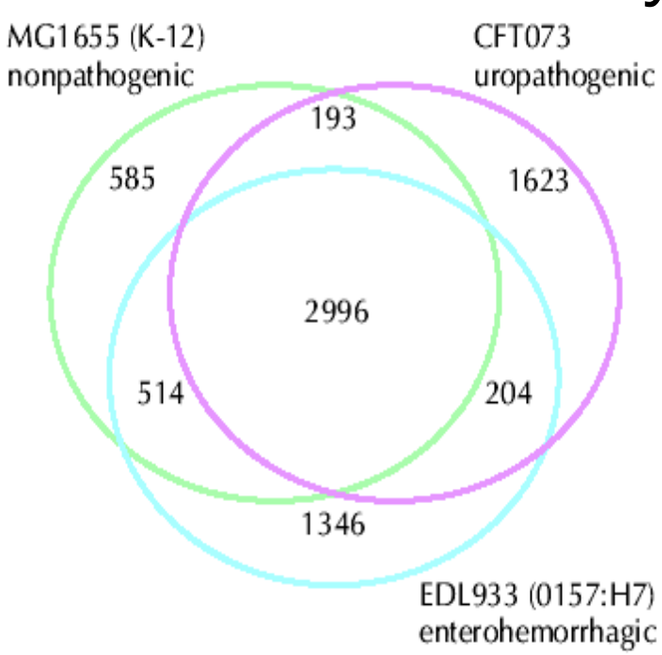
Microbial Diversity



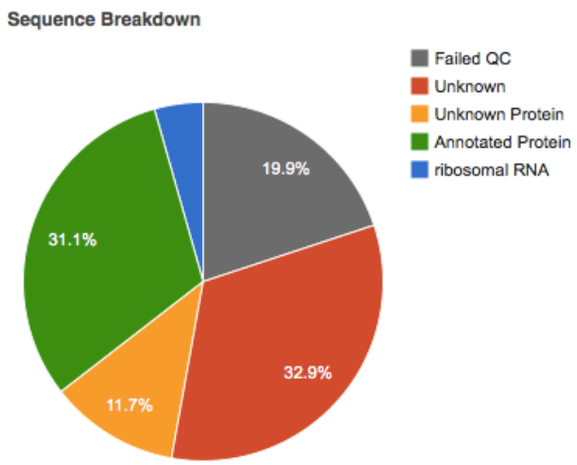
http://bit.ly/HumanMicrobiome

Host Variation

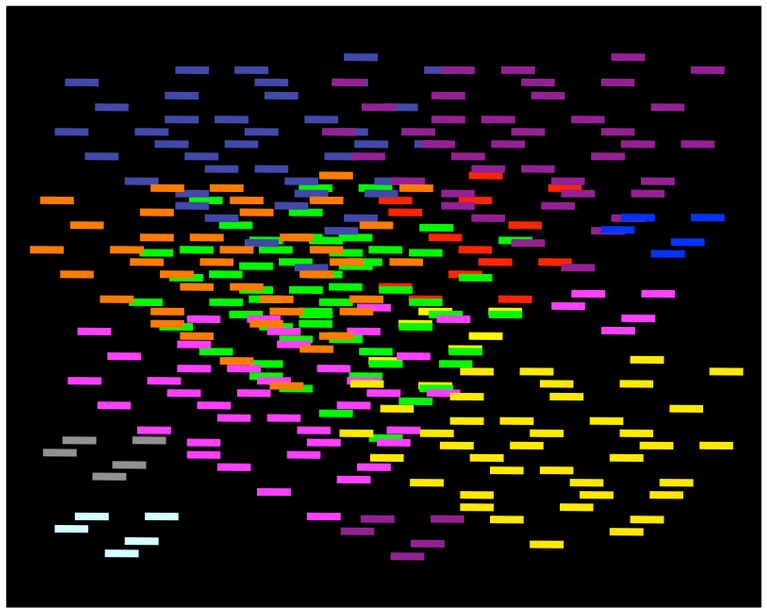
Microbial Diversity2



Functional Diversity



Fragmented Data



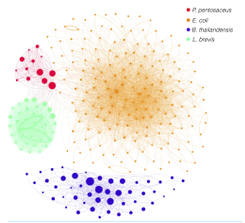
Opportunities

- Probiotics for agriculture
- Manipulate environment to modify microbiome
- Match varieties to environments based on microbiome functions and interactions
- Microbiome as target in breeding

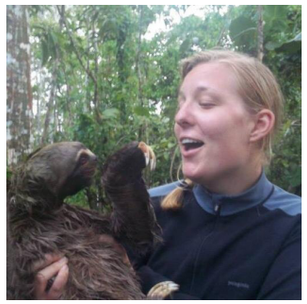
Eisen Lab PhD Students

Russell Neches

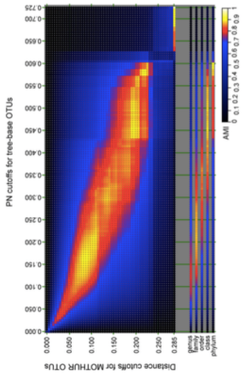
Chris Beitel



Katherine Dahlhausen

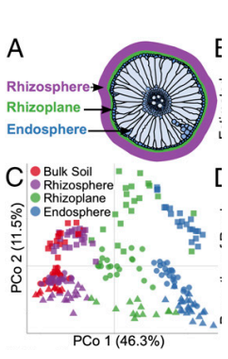


Ladan Daroud



Marisano James

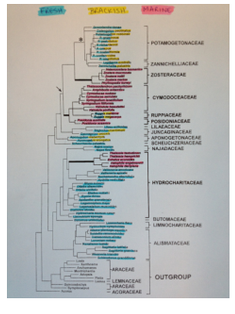
Srijak Bhatnagar



Sonia Ghose

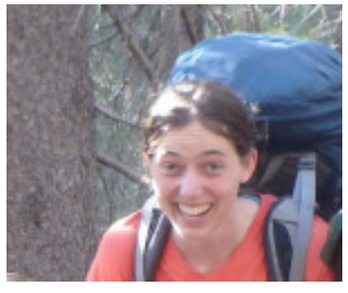
Megan Krusor

Laura Vann

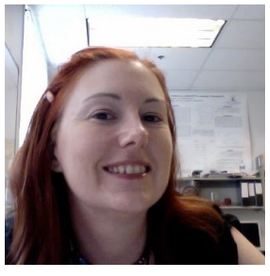


Cassie Ettinger

Erin Calfree

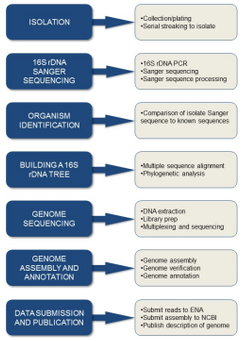


Kate Wall



Eisen Lab Personnel

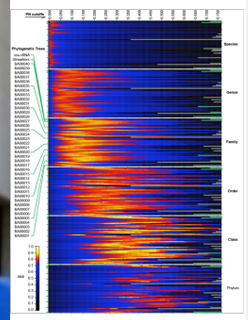
David Coil



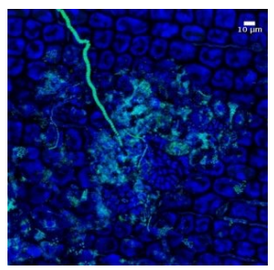
Jenna Lang

Sarah Hird

Dongying Wu

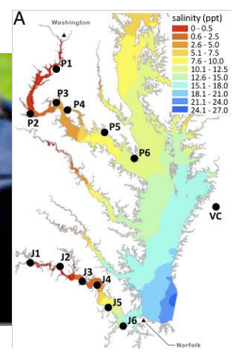


Alana Firl

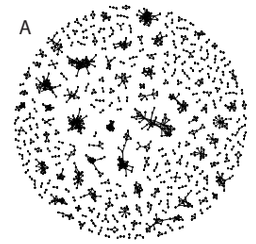


Holly Ganz

Alex Alexiev



Guillaume Jospin

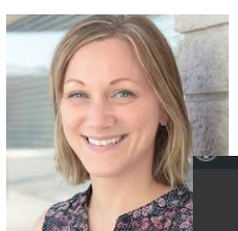


PhyloSift
mining the global metagenome

Karley Lujan
Madeleine Leahy
Jenna Yonenaga
Nicholas Metas-Chapman
Alex Martin
Dana DeVries

Makayla Betts
Briana Pompa-Hogan
Tynisha Koenigsaecker
Greg Kincheloe
Petra Dahms

Mary-Jo Seminoff



microBEnet
microbiology of the Built Environment network

John Zhang