JGI JOINT GENOME INSTITUTE
UNITED STATES DEPARTMENT OF ENERGY

Human Microbiome through the Lens of Global Environmental Ecosystems

Rekha Seshadri, PhD

13th Microbiome & Probiotics Forum USA

San Diego, CA

Oct 13, 2025

Joint Genome Institute is a U.S. Dept of Energy User Facility

Mission: Enable large-scale, multi-omic studies of plants, fungi, algae, bacteria, archaea & microbial communities

DoE **Focus** :
energy & environmental challenges

BioSciences

U.S. DEPARTMENT OF ENERGY | Office of Science

BERKELEY LAB

Enabling high quality User Science since 2004

Genome Targets:

- Plant
- Fungal & Algal
- **Metagenome**
- **Microbial**

Infrastructure/ Capabilities

DNA Sequencing Platforms

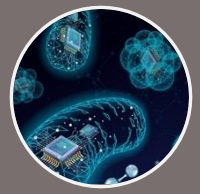
- Illumina NovaSeq X
- PacBio Revio
- Oxford Nanopore PromethION

Advanced Genomic Technologies

- Single-cell Sequencing
- Stable Isotope Labeling
- Methylation/Epigenomics
- Transcriptomics

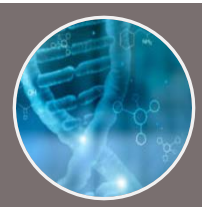
Metabolomics

- Polar-/non-polar LC/MS metabolite profiling
- Targeted and untargeted metabolite analysis



DNA Synthesis

- Design & Pathway Assembly
- Host Engineering

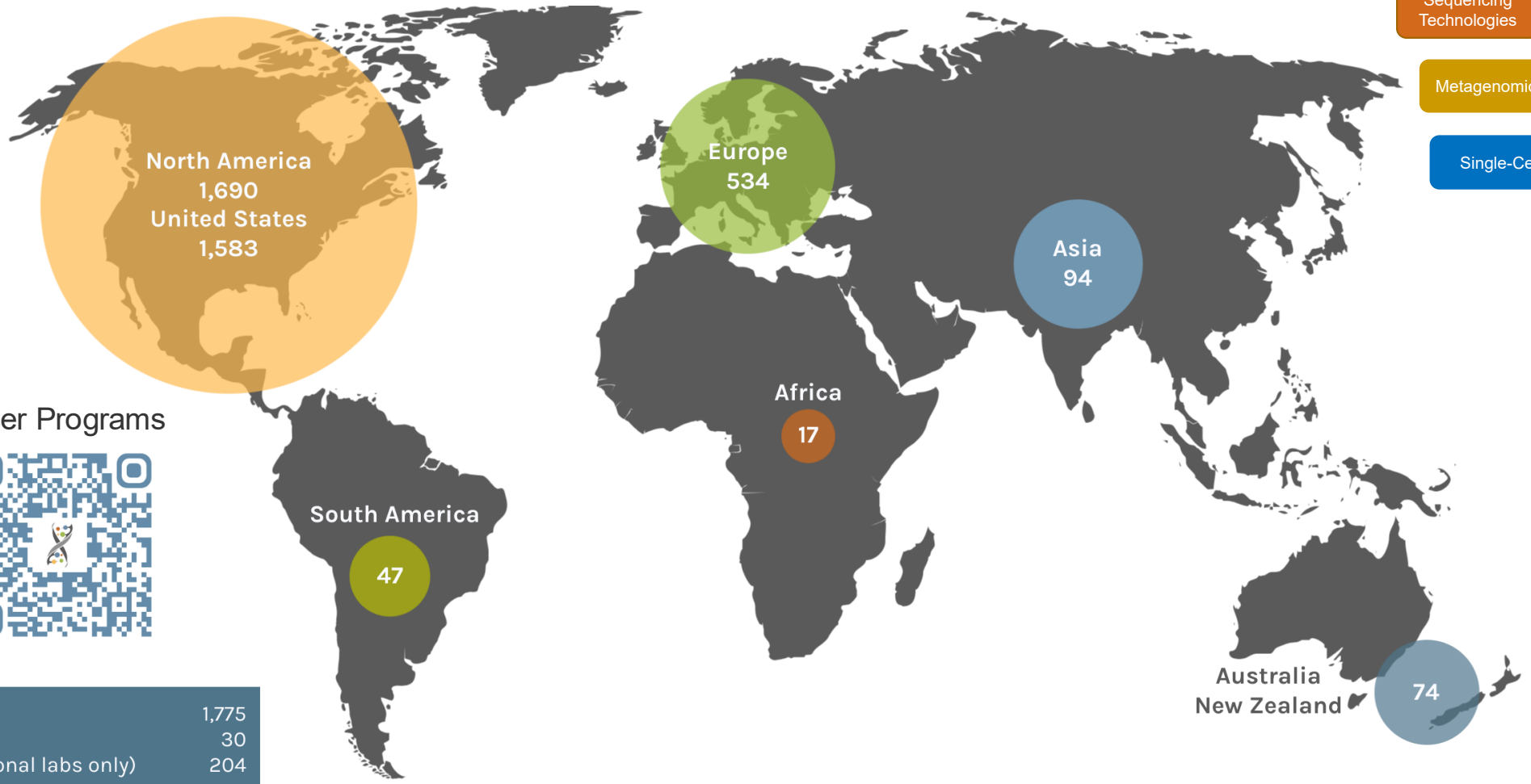


Secondary Metabolites

- Large-scale bioinformatic mining
- Integrated workflows
- BGC exploration

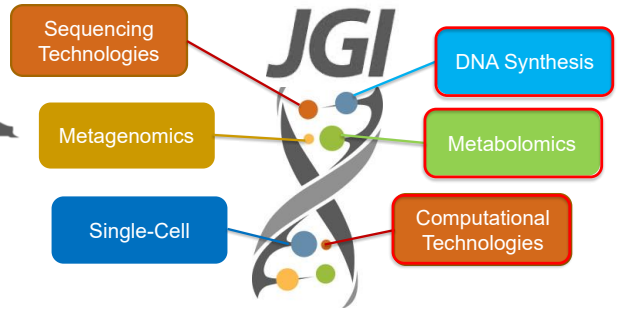
Data Science & Informatics

JGI Worldwide Users



User Programs

Academic	1,775
Industry	30
DOE (national labs only)	204
Government	154
Other	293
Total Users	**2,456**



JGI "services"

Community Science Program (CSP): Genomic Encyclopedia of Bacteria & Archaea

GEBA-pilot (56)

nature — A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea

2007

PNAS — Improving the coverage of the cyanobacterial phylum using diversity-driven genome sequencing

GEBA-I
Diversity

2012

nature biotechnology — 1,003 reference genomes of bacterial and archaeal isolates expand coverage of the tree of life

GEBA-II
Genus coverage

2013

nature genetics — Genomic features of bacterial adaptation to plants

GEBA-III
Soil& Rhizosphere

2014

GEBA
Actinos

2015

Cell Genomics — Expanding the genomic encyclopedia of *Actinobacteria* with 824 isolate reference genomes

GEBA-IV
Ubiquitous OTUs

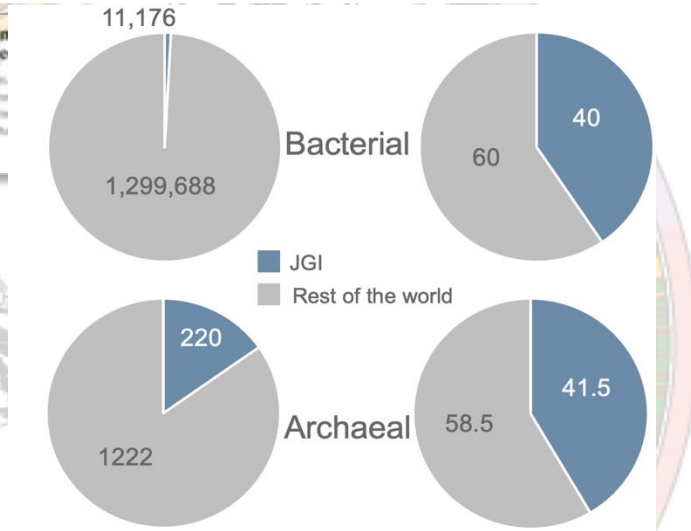
GEBA-V
Pangenomes

2017

nature biotechnology — Cultivation and sequencing of rumen microbial members from the Hungate1000 Collection

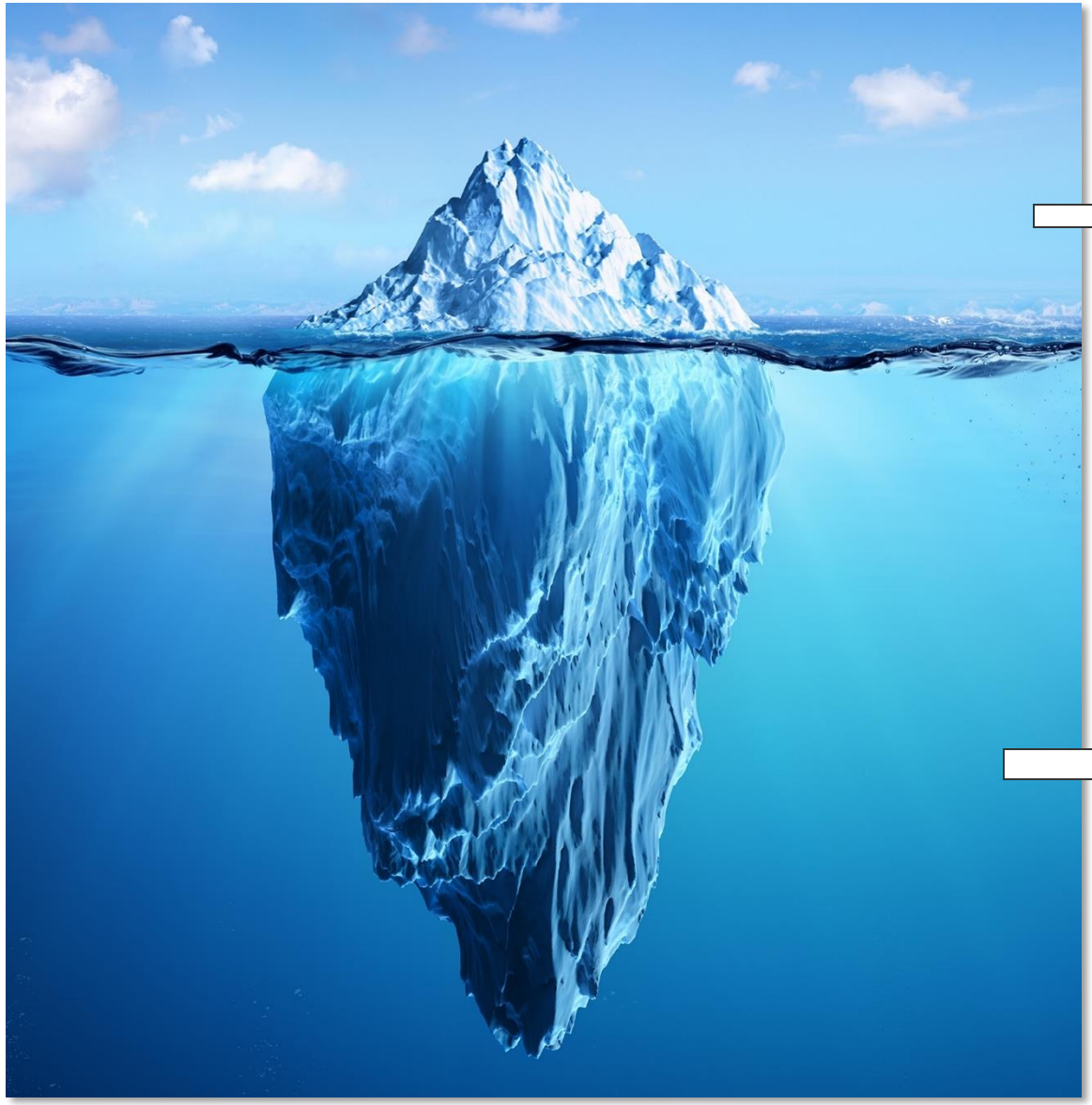
2019

GEBA-10K



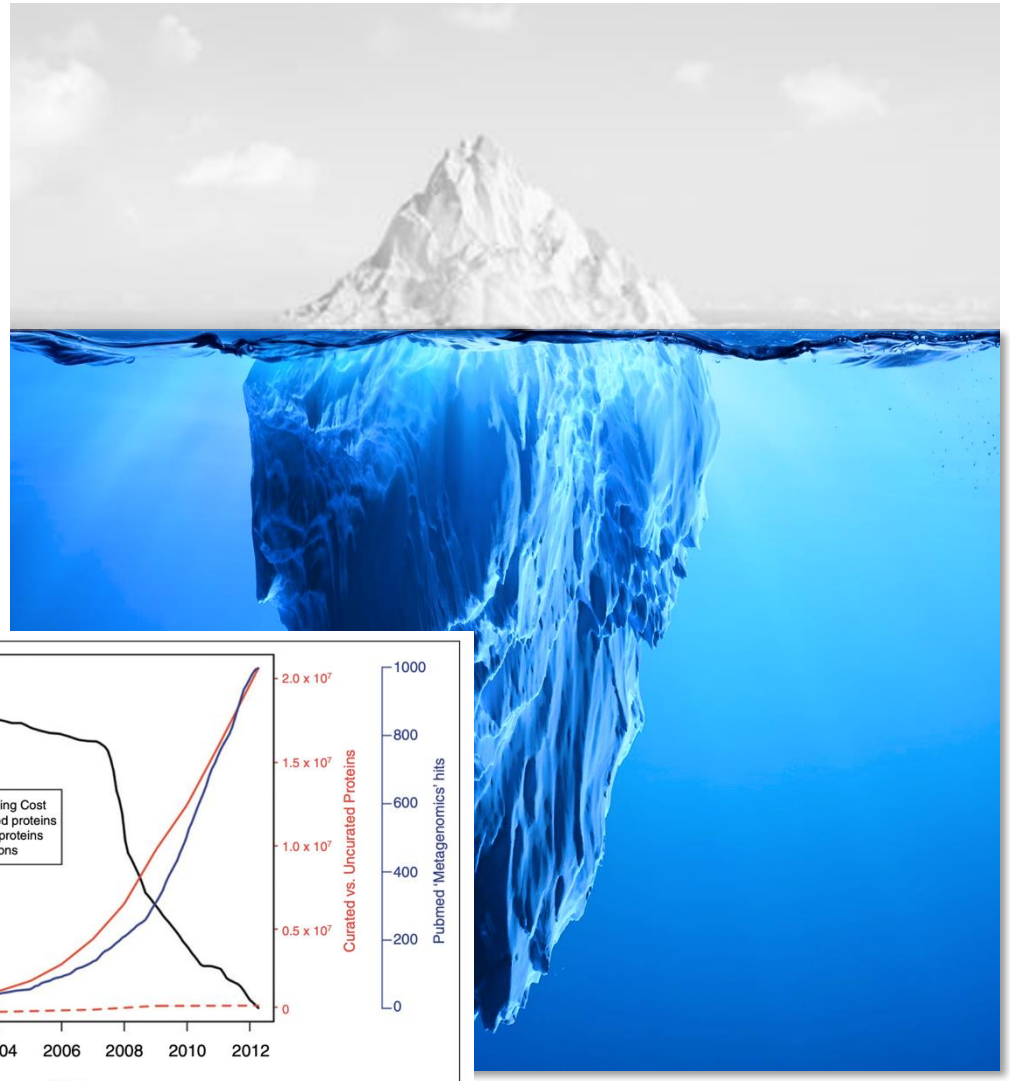
Just 11,000 JGI genomes account for >40% of total diversity from >2 million genomes in GenBank

Microbial Dark Matter



Pioneering metagenomic studies at the JGI

- No cultivation, no prior knowledge required

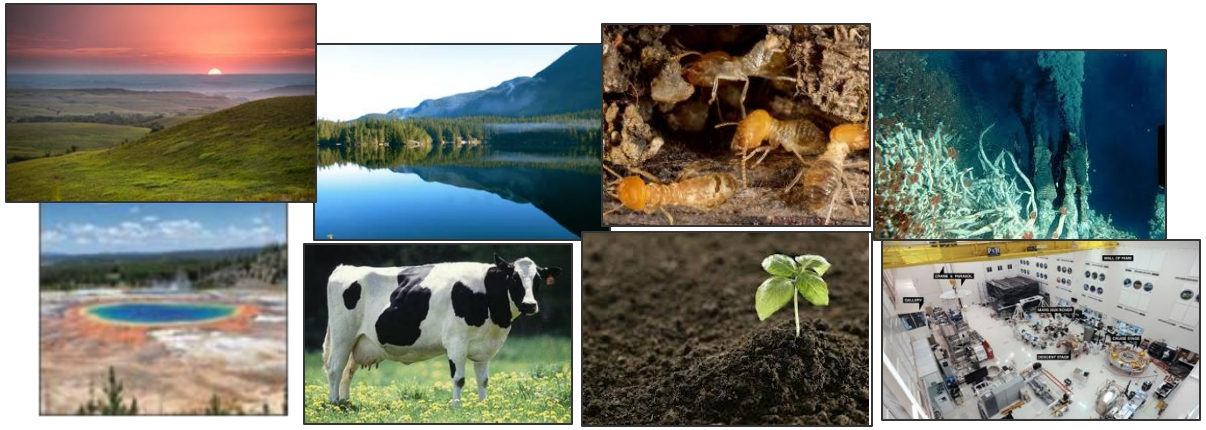


2004

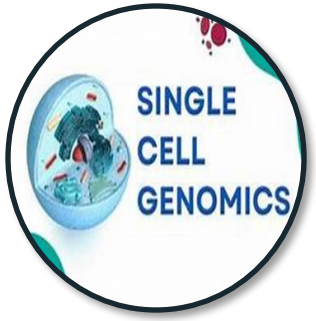
nature

Community structure and metabolism through reconstruction of microbial genomes from the environment

Gene W. Tyson[1], Jarrod Chapman[1,3], Philip Hugenholtz[1], Eric E. Allen[1], Rachna J. Ram[1], Paul M. Richardson[2], Victor V. Solovyev[4], Edward M. Rubin[2], Daniel S. Rokhsar[1,2] & Jillian F. Banfield[1,2]

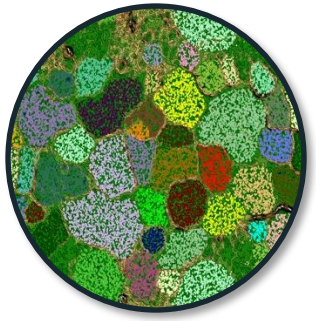


SAGs



Single Amplified Genomes

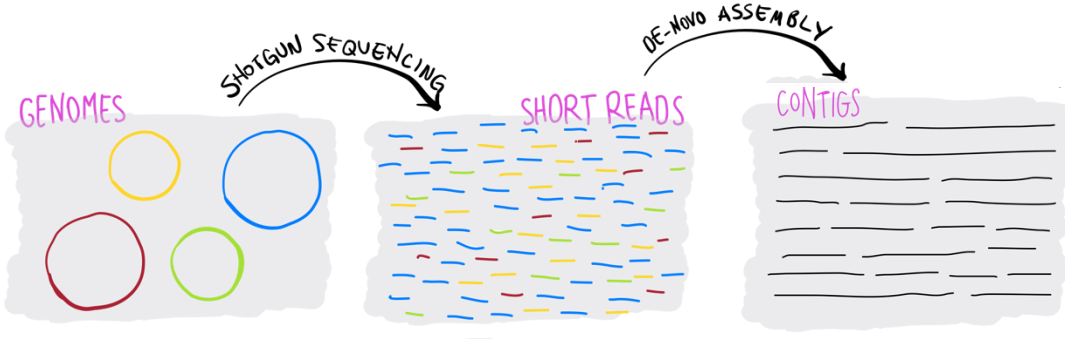
MAGs



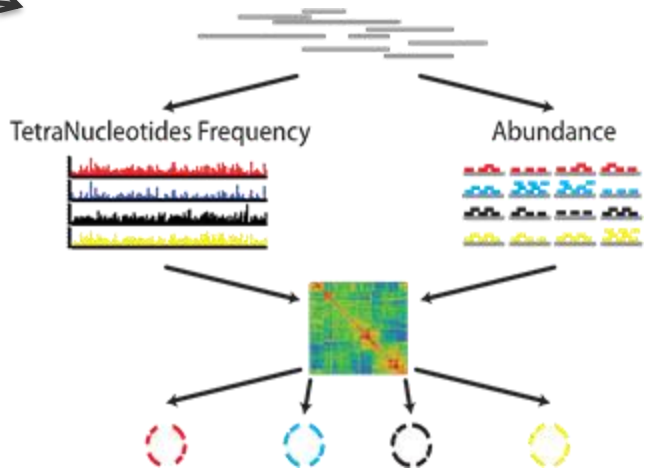
Metagenome Assembled Genomes

Recovering MAGs AT SCALE

"Binning" exploits similarities in **"coverage"** & nucleotide composition to pull together discrete contigs into a MAG

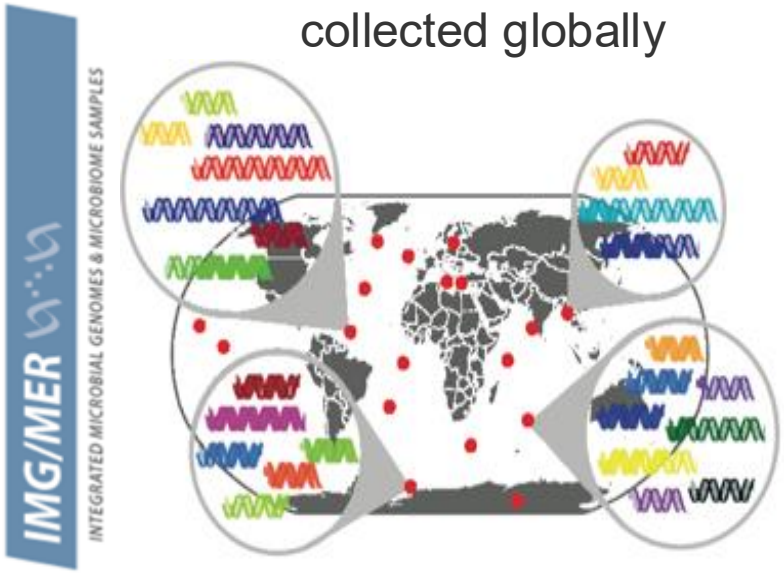


Assembled metagenome



MAGs

Assembled metagenomes collected globally



Global-scale analysis of the human gut microbiome

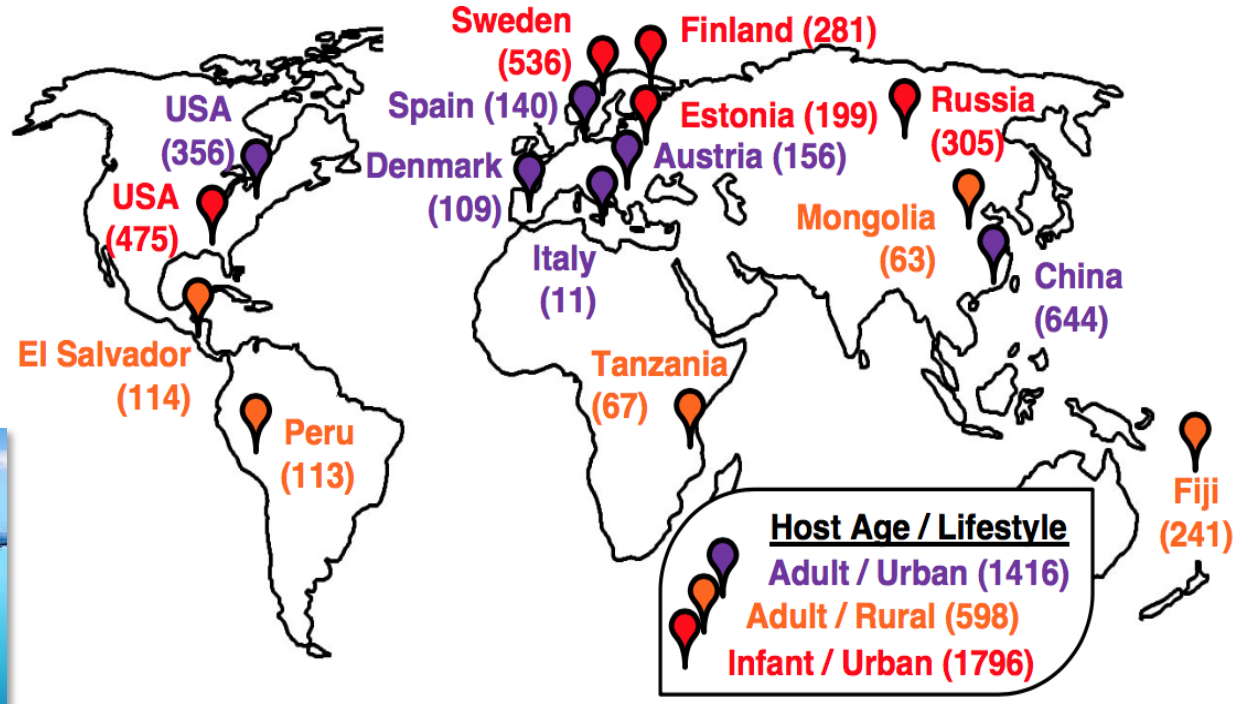
nature

Article | Open access | Published: 13 March 2019

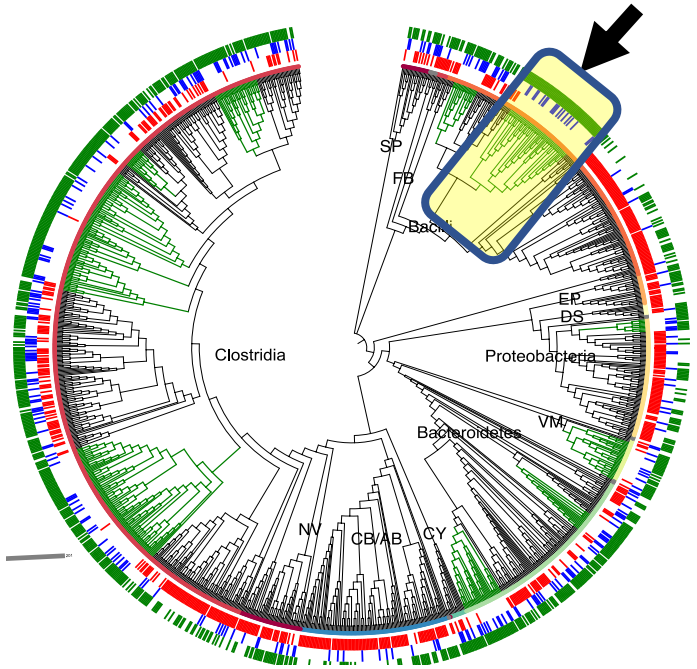
New insights from uncultivated genomes of the global human gut microbiome

Stephen Nayfach, Zhou Jason Shi, Rekha Seshadri, Katherine S. Pollard & Nikos C. Kyrpides

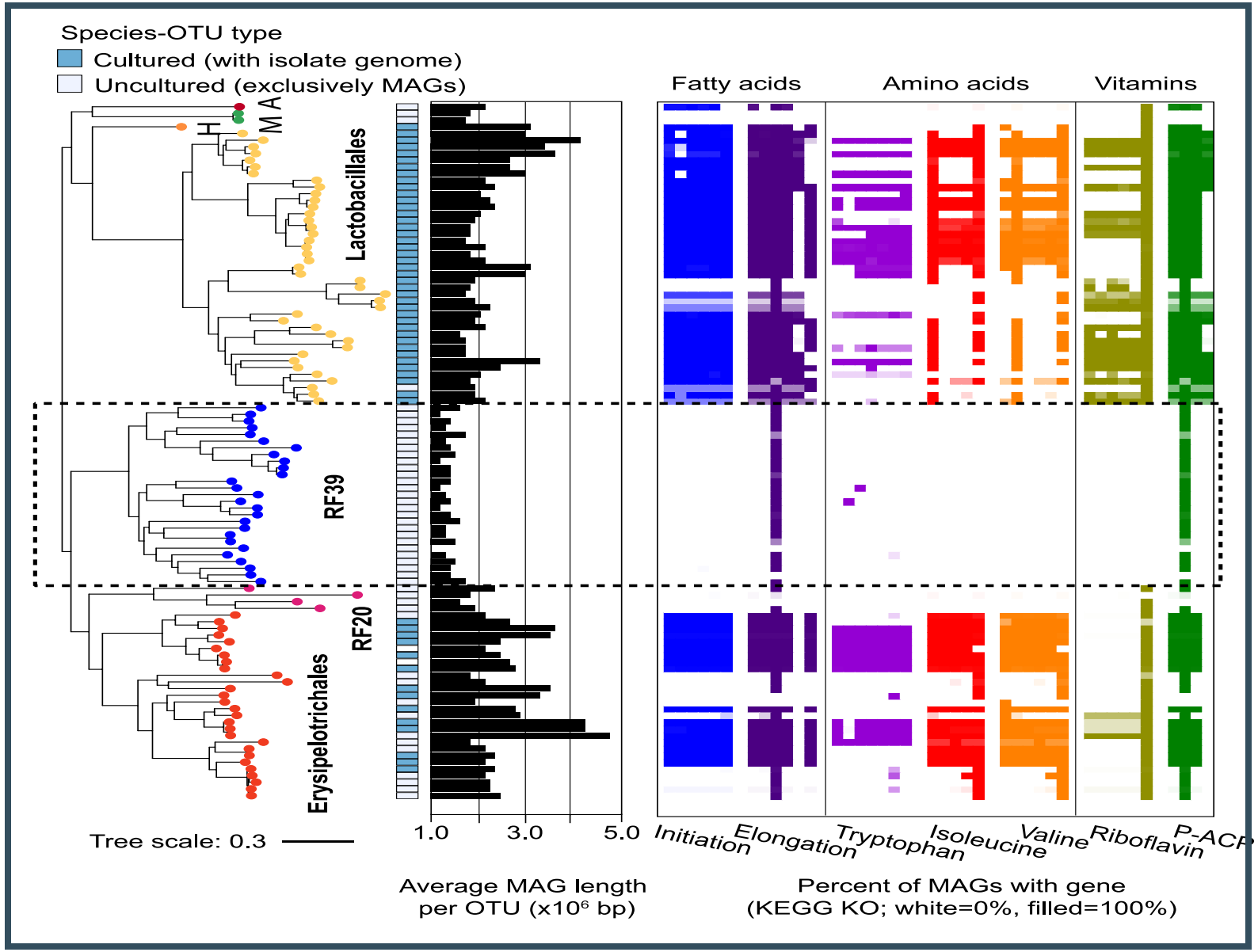
- 3,810 samples from 2,444 individuals
  - multiple geo regions, age groups, lifestyles, and disease states
- 60,664 MAGs reconstructed
  - 4,558 microbial species
  - 80% new



Large Lineages don't have cultured representatives



- RF39 is found in 49% of healthy adults
- Numerous MAGs, (no isolates)
- genome deficits – metabolic dependencies



Unified Human Gastrointestinal Genome Catalog

ARTICLE OPEN https://doi.org/10.1038/s41586-019-1058-x

JGI

New insights from uncultivated genomes of the global human gut microbiome

Stephen Nayfach[1,2*], Zhou Jason Shi[3,4], Rekha Seshadri[1,2], Katherine S. Pollard[3,4,5,6,7,8] & Nikos C. Kyrpides[1,2*]

ARTICLE OPEN https://doi.org/10.1038/s41586-019-0965-1

EBI

A new genomic blueprint of the human gut microbiota

Alexandre Almeida[1,2*], Alex L. Mitchell[1], Miguel Boland[1], Samuel C. Forster[2,3,4], Gregory B. Gloor[5], Aleksandra Tarkowska[1], Trevor D. Lawley[2] & Robert D. Finn[1*]

Cell Resource

CIBIO

Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle

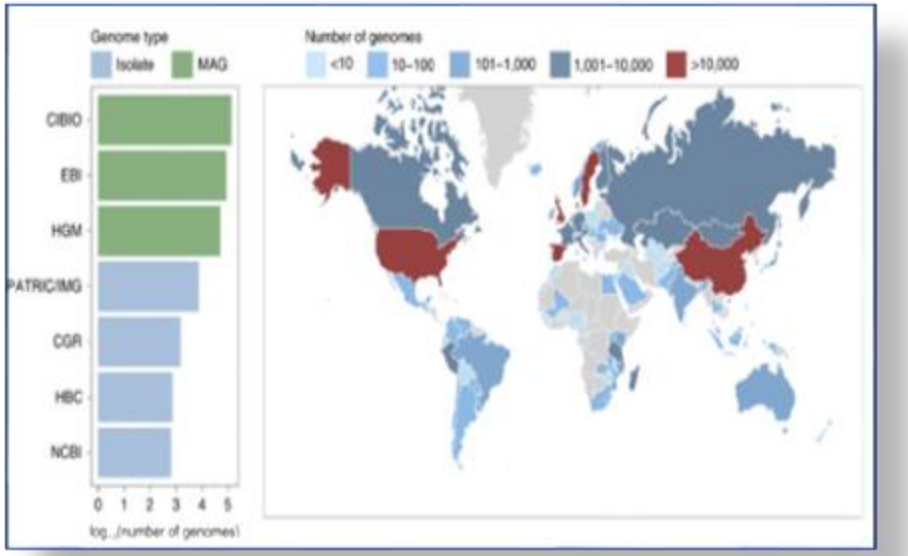
Three Parallel Studies

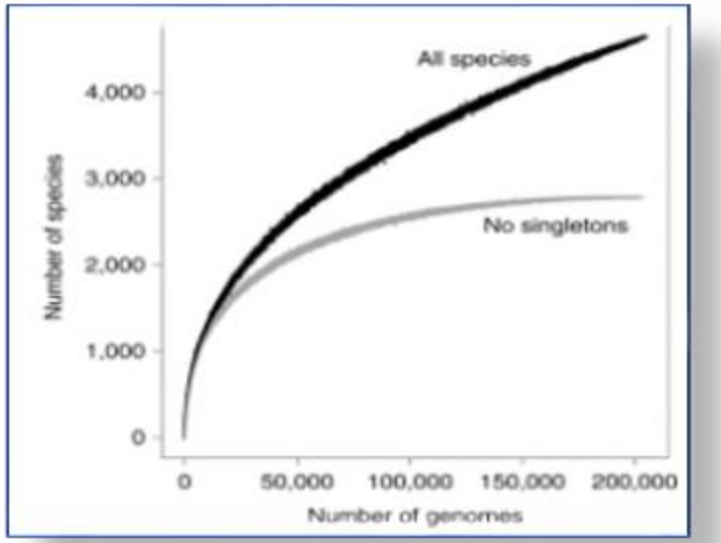
nature biotechnology

A unified catalog of 204,938 reference genomes from the human gut microbiome

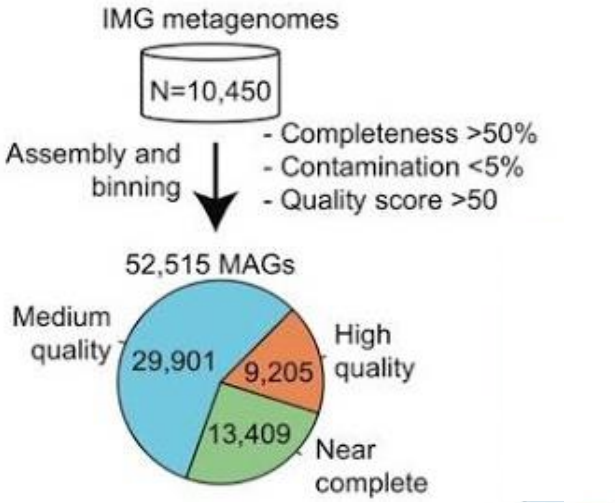
Alexandre Almeida[1,2], Stephen Nayfach[3,4], Miguel Boland[1], Francesco Strozzi[5], Martin Beracochea[1], Zhou Jason Shi[6,7], Katherine S. Pollard[6,7,8,9,10,11], Ekaterina Sakharova[1], Donovan H. Parks[12], Philip Hugenholtz[12], Nicola Segata[13], Nikos C. Kyrpides[3,4] and Robert D. Finn[1]

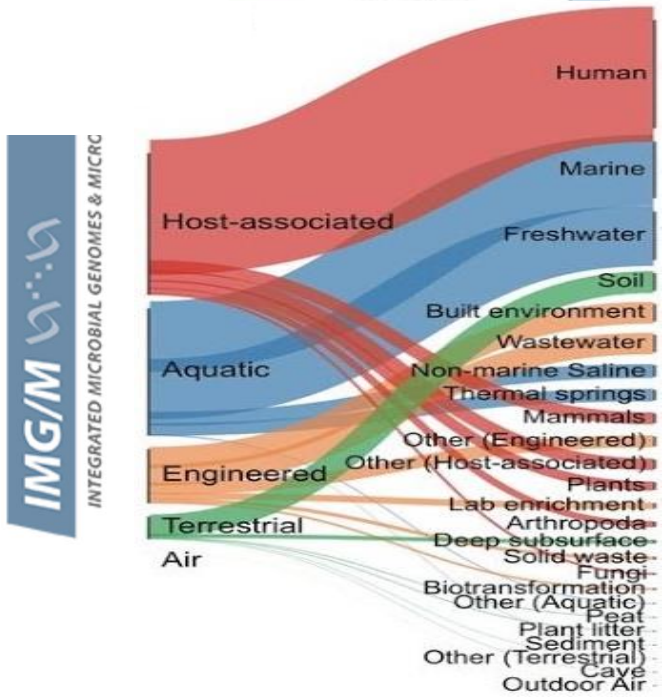
- 11,831 unique samples
- 204,938 NR Genomes
  - 4,644 species
  - 3,750 (81%) Uncultured species
- 625,255,473 proteins
  - 14M clusters



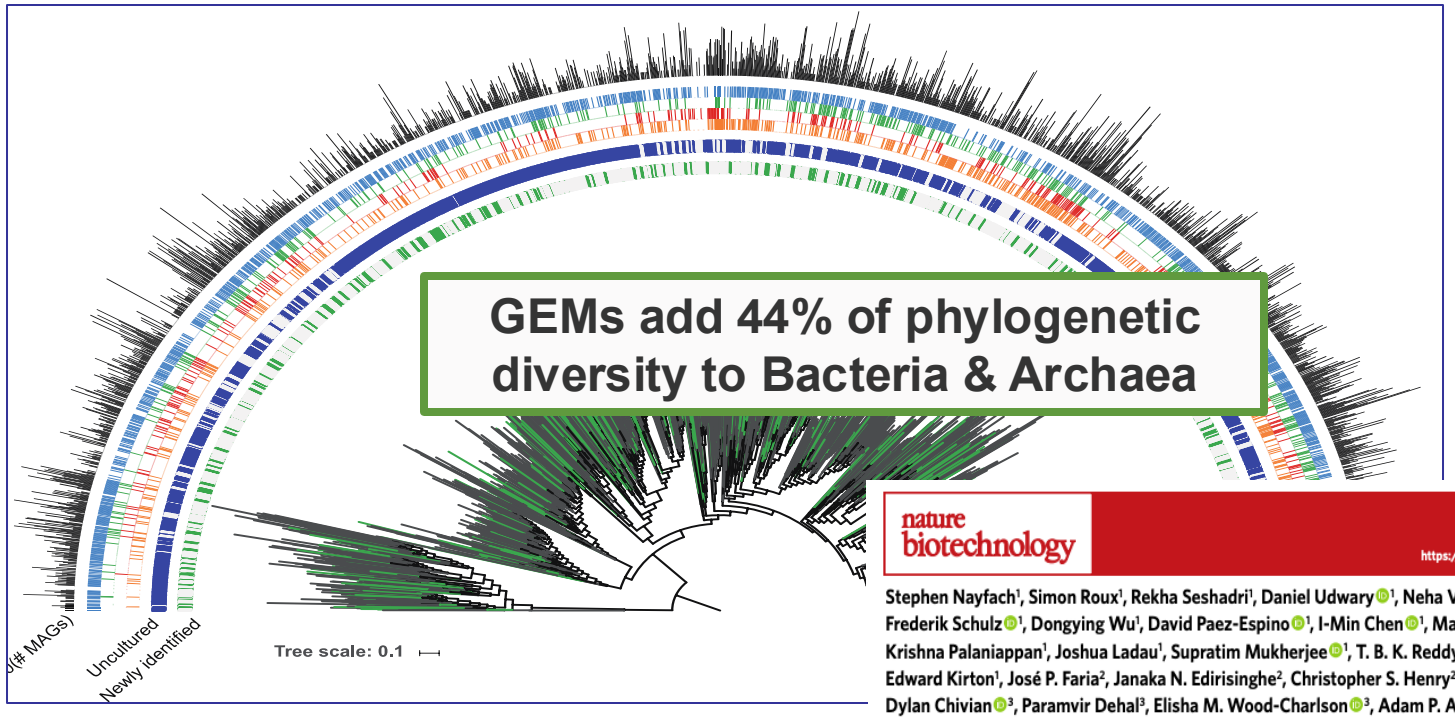


A Genomic Catalog of Earth's microbiomes (GEMs)





- 10,450 metagenomes from diverse habitats (IMG/M database)
- 52,515 MAGs reconstructed
  - Grouped into 18,028 species-level OTUs
  - 12,556 were novel species from 135 phyla
- 3x more diversity compared to previous studies



nature biotechnology
RESOURCE
https://doi.org/10.1038/s41587-020-0718-6

Stephen Nayfach[1], Simon Roux[1], Rekha Seshadri[1], Daniel Udwary[1], Neha Varghese[1], Frederik Schulz[1], Dongying Wu[1], David Paez-Espino[1], I-Min Chen[1], Marcel Huntemann[1], Krishna Palaniappan[1], Joshua Ladau[1], Supratim Mukherjee[1], T. B. K. Reddy[1], Torben Nielsen[1], Edward Kirton[1], José P. Faria[2], Janaka N. Edirisinghe[2], Christopher S. Henry[2], Sean P. Jungbluth[1,4], Dylan Chivian[3], Paramvir Dehal[3], Elisha M. Wood-Charlson[3], Adam P. Arkin[3], Susannah G. Tringe[1], Axel Visel[1], IMG/M Data Consortium*, Tanja Woyke[1], Nigel J. Mouncey[1], Natalia N. Ivanova[1], Nikos C. Kyrpides[1] and Emiley A. Eloe-Fadrosh[1]

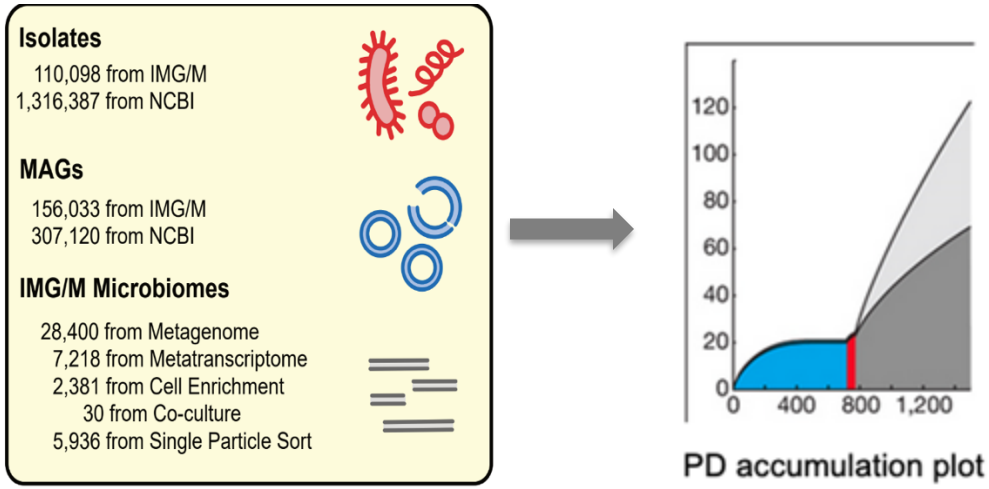
A genome census during the uncultivated data deluge

SCIENCE ADVANCES | RESEARCH ARTICLE

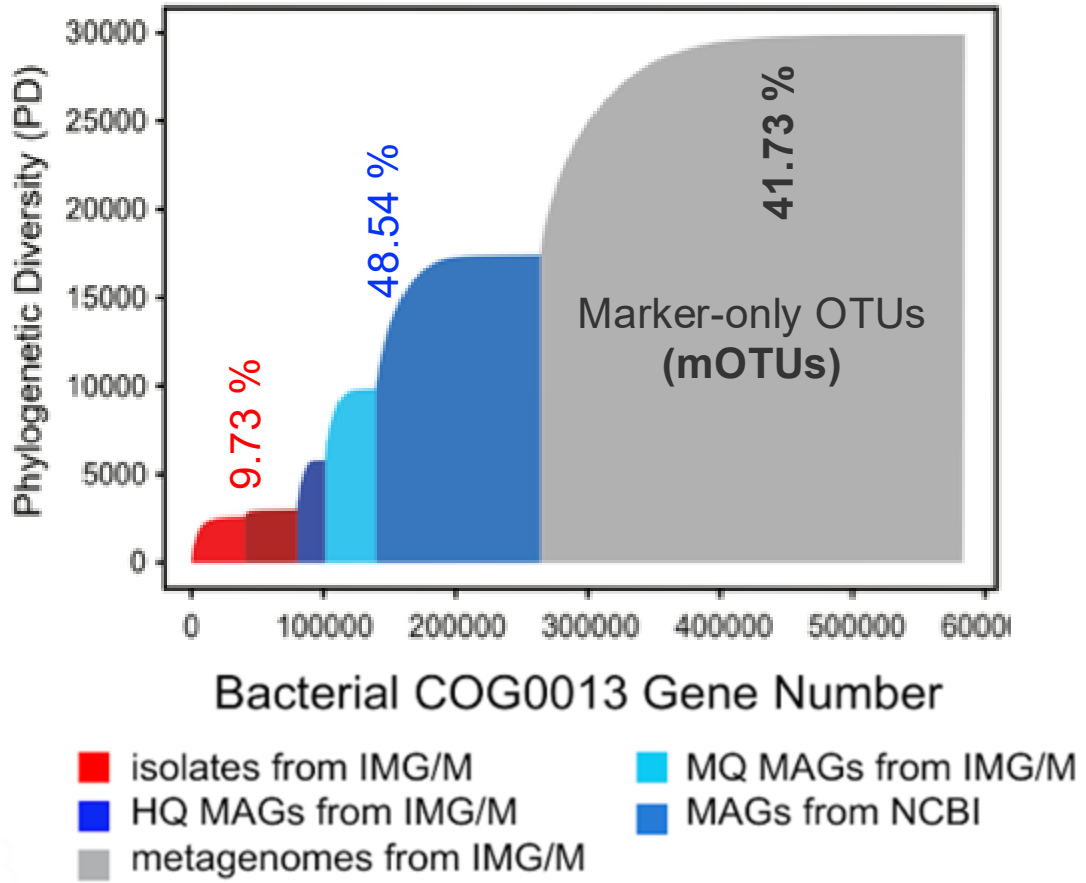
MICROBIOLOGY

A metagenomic perspective on the microbial prokaryotic genome census

Dongying Wu, Rekha Seshadri, Nikos C. Kyrpides, Natalia N. Ivanova*



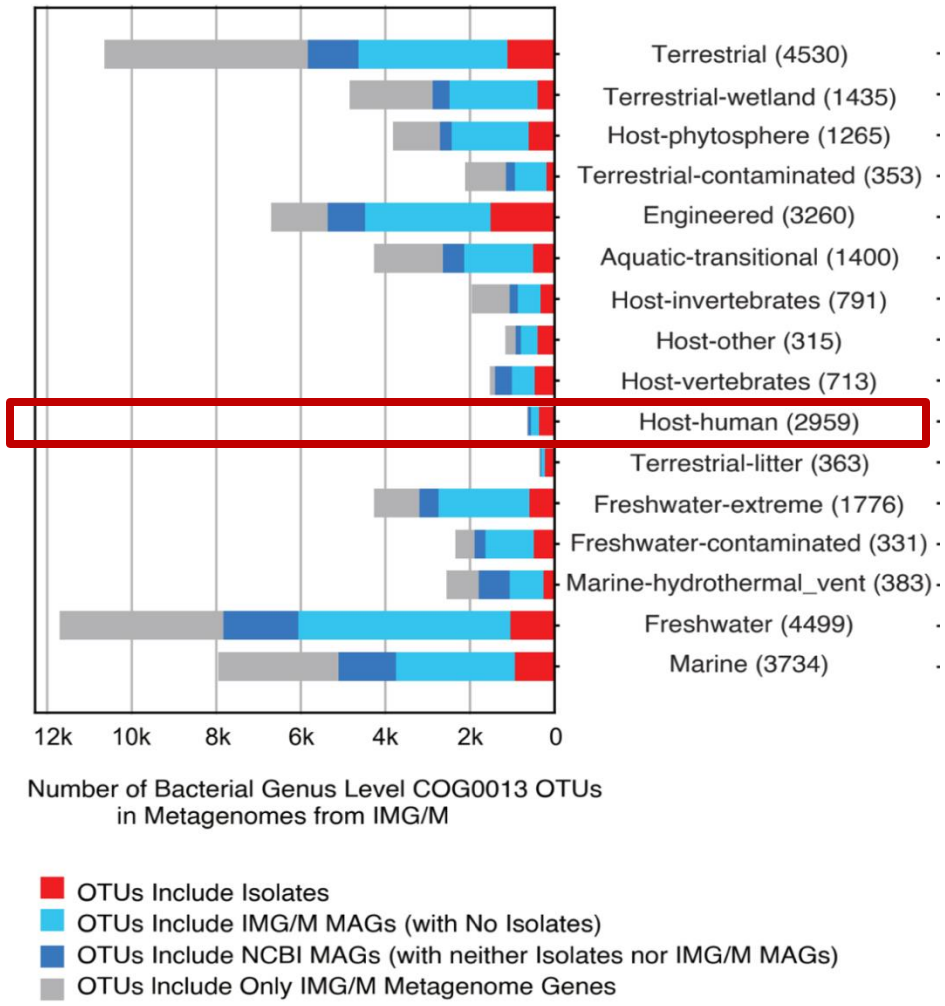
PD accumulation plot

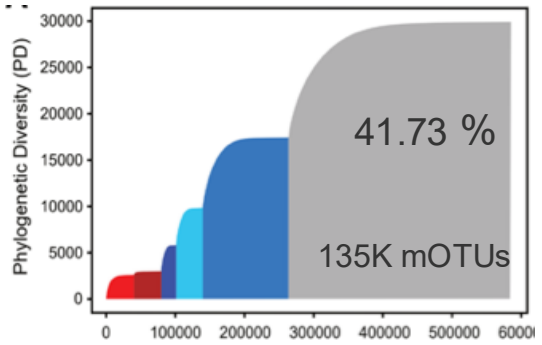


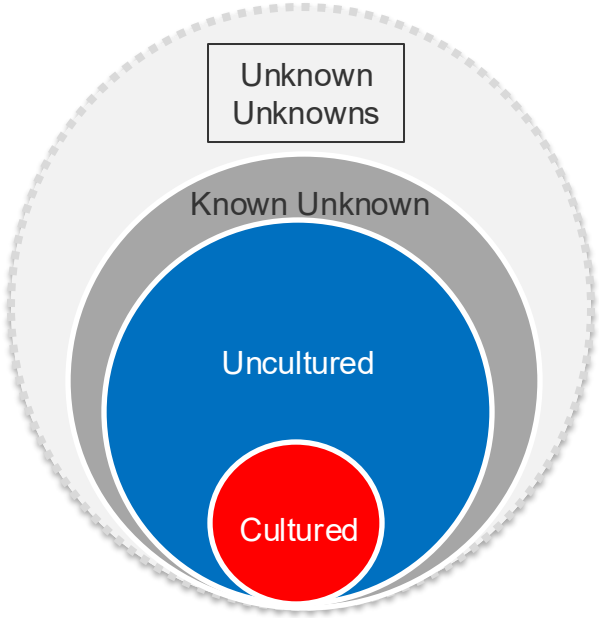
- 41.73% “unrepresented” diversity at lower taxonomic ranks
- mOTUs ~134,966 species in 18,087 metagenomic samples.

Marker-only OTUs by Habitat & Taxonomy

- Diversity hotspots - sediment, soil, freshwater, marine subsurface







#Genus mOTUs

JGI JOINT GENOME INSTITUTE
UNITED STATES DEPARTMENT OF ENERGY

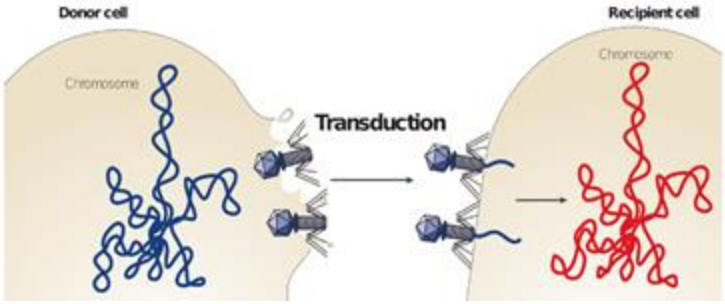
Genome Catalogs of Uncultivated Viruses

But first, why viruses?

Viruses have multi-level impacts

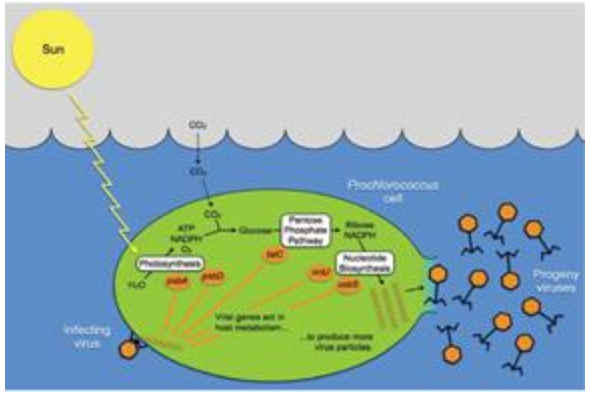
- The most abundant biological entities on earth (estim. >10^{31})
- Parasitize all cellular life forms
- Co-evolution of viruses and host defense systems is key aspect in evolution of both viruses and cells
- Influence microbiome processes

Genetic transfer



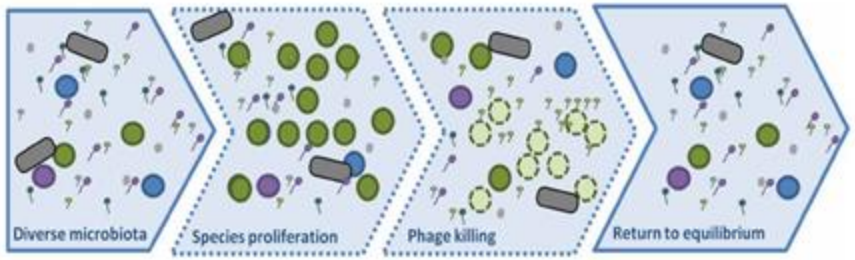
Frost *et al.*, 2005

Alter host metabolism

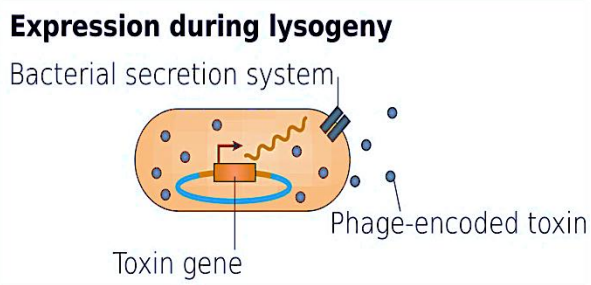


Breitbart *et al.*, 2007

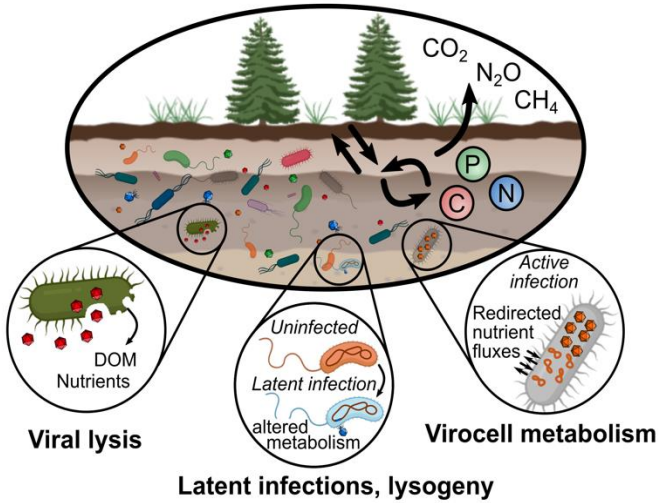
Maintain diversity



De Paepe *et al.*, 2014



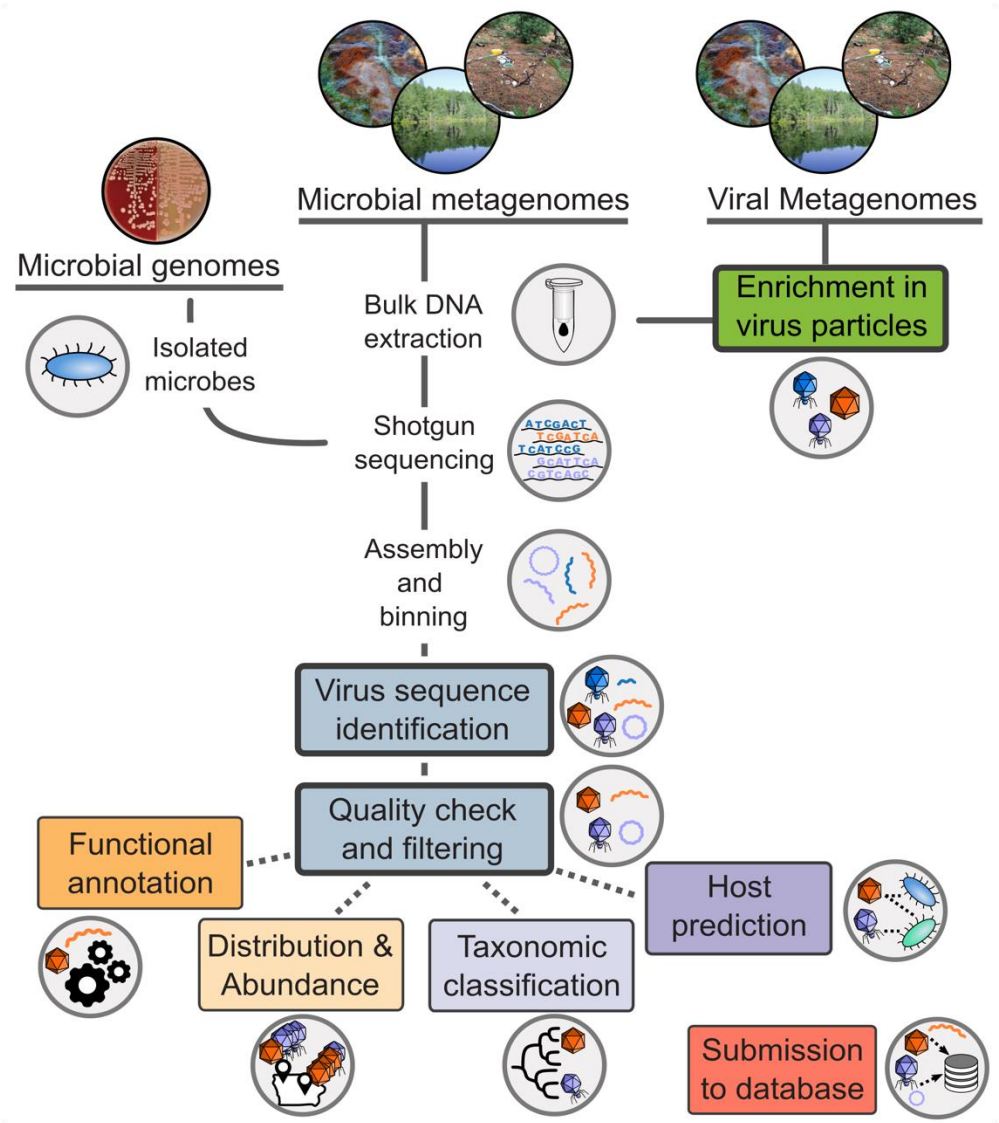
Feiner et al., 2015



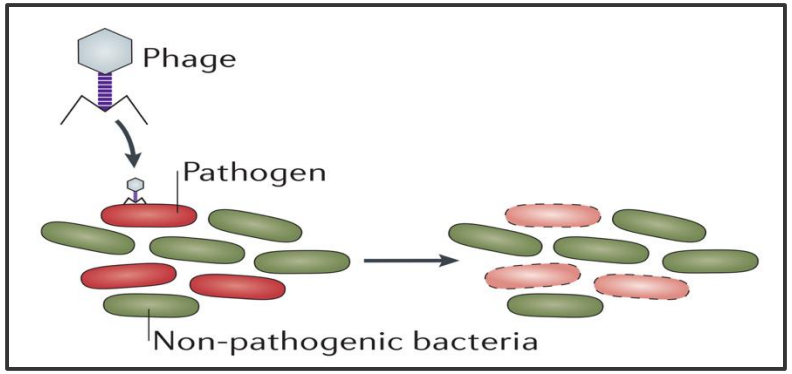
The main approach for exploring viral diversity at scale

LIMITATIONS for DISCOVERY

- ✕ No available cultures
- ✕ No universal viral marker genes
- ✕ Applications – phage therapy



Host specificity can be leveraged for phage therapy



DECEMBER 31, 2024 | 7 MIN READ

Nearly Forgotten 'Phage Therapy' Fights Antibiotic Resistance

In a new book, a science journalist recounts the story of a lifesaving treatment for infection that scientists broadly dismissed until recently

BY SAIMA S. IQBAL EDITED BY TANYA LEWIS

World Health Organization | Health topics | Our work | Newsroom

Latest news

Building evidence for the use of bacteriophages against antimicrobial resistance

Jun 25, 2024, 13:33 PM

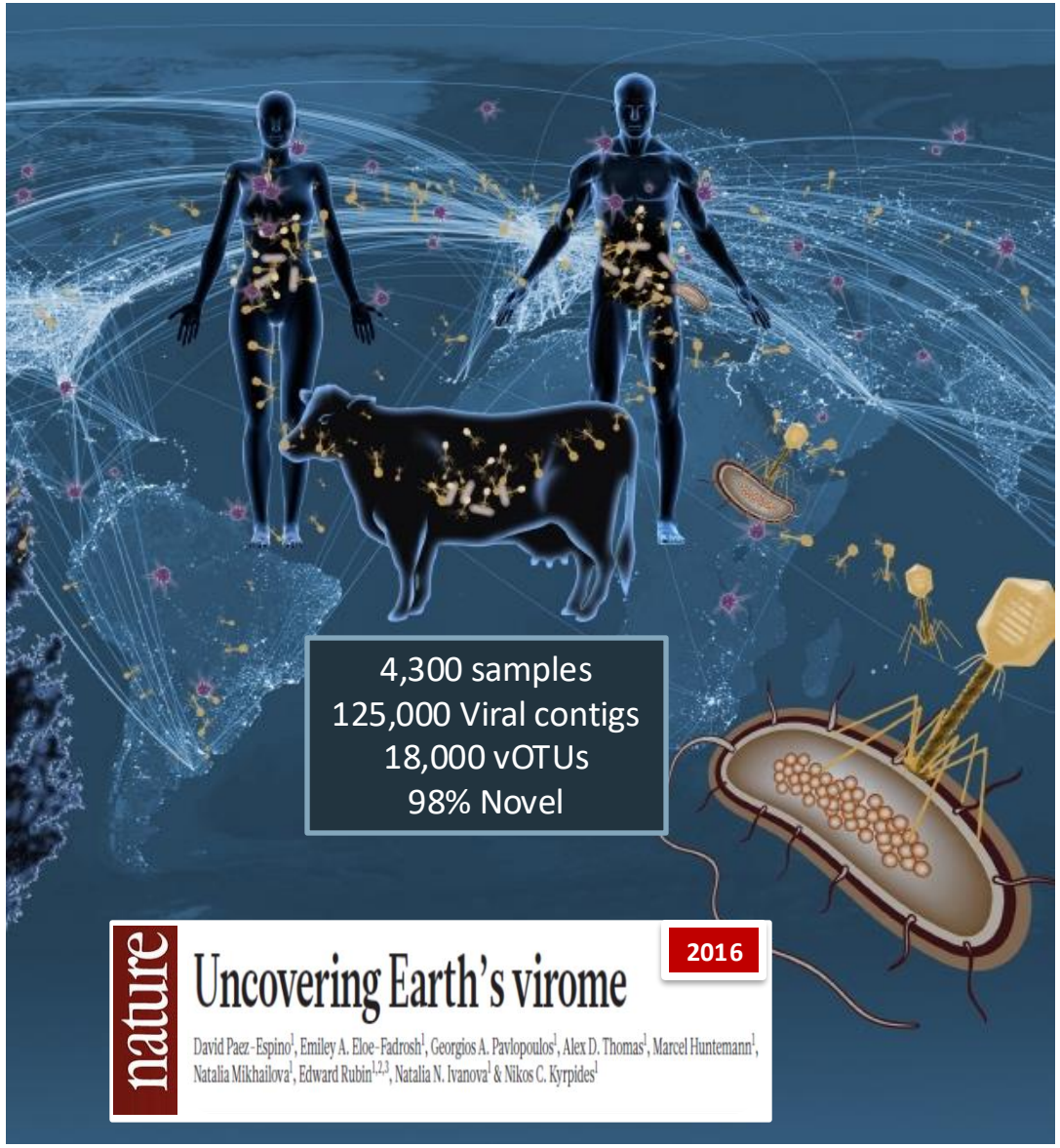
DelveInsight

Phage Therapies Clinical Trial Pipeline Shows Potential with Active Contributions from 20+ Key Companies | DelveInsight

The phage therapy market is experiencing significant growth due to the increasing prevalence of antibiotic-resistant infections and the growing interest in alternative treatments. Advances in biotechnology and ongoing research are driving innovation in phage-based therapeutics, offering a promising solution to combat multidrug-resistant pathogens. Additionally, regulatory support and rising investments in the development of phage therapies are further fueling market expansion. This market is expected to continue growing as healthcare providers seek effective alternatives to traditional antibiotics.

January 23, 2025 13:00 ET | Source: DelveInsight Business Research LLP Follow

Virus Discovery from metagenomes



Nikos Kyrpides

Uncultivated genomes massively expand the known diversity of viruses

Frederik Schulz

Science — Giant viruses with an expanded complement of translation system components — 2017

Simon Roux

nature microbiology — Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes — 2019

Frederik Schulz

nature — Giant virus diversity and host interactions through global metagenomics — 2020

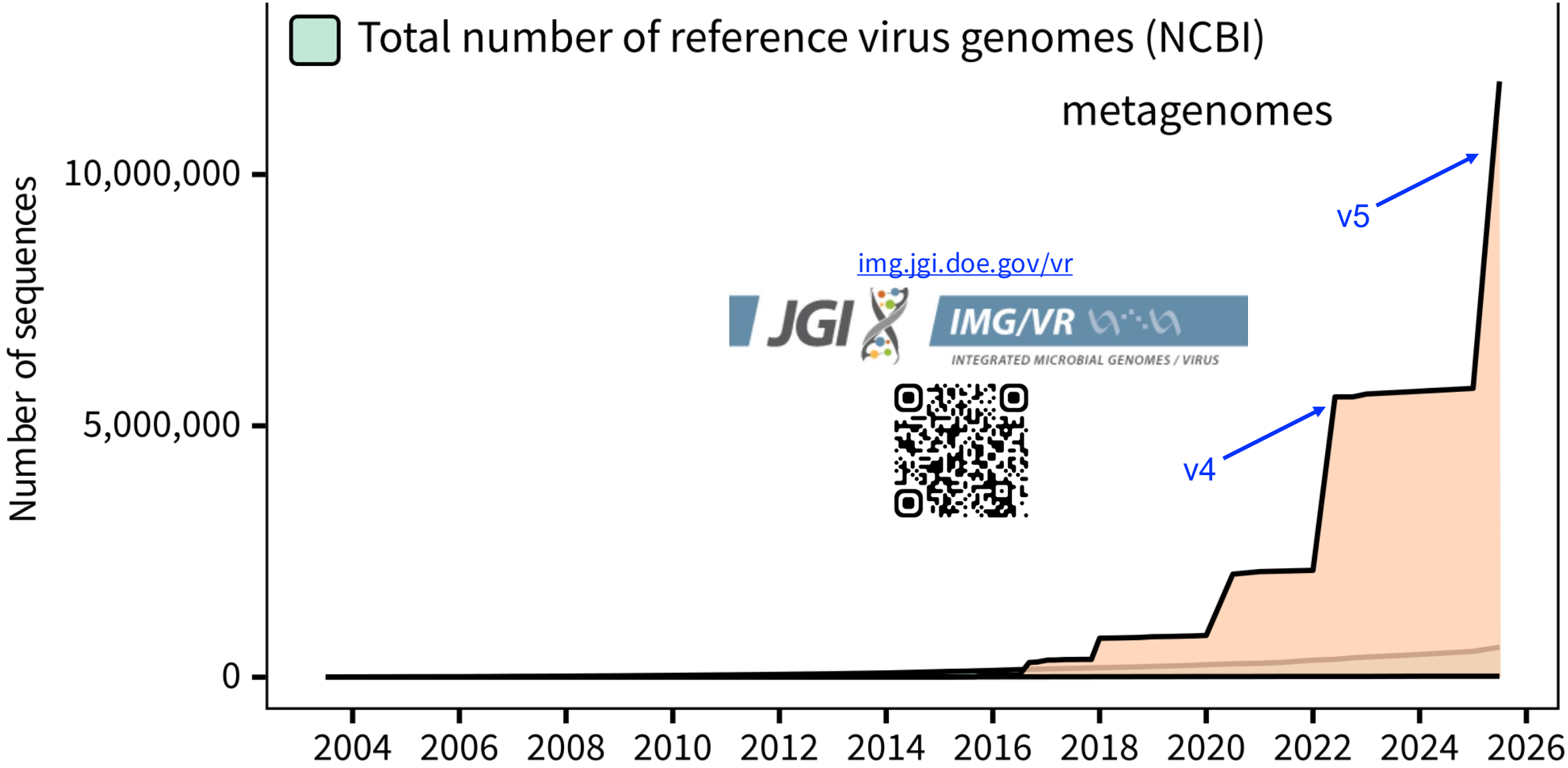
David Paez-Espino

Microbiome — Diversity, evolution, and classification of virophages uncovered through global metagenomics — 2020

Stephen Nayfach

nature microbiology — Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome — 2021

Aggregating global viral genome catalogs



Computational Tools

Tools & Standards for Metagenomics

MetaBAT binning tool (>5,000 citations)

2015

2016

MIMAG standards (>2,000 cit.)

2017

CheckV (>1,400 cit.)

2019

geNomad (>560 cit.)

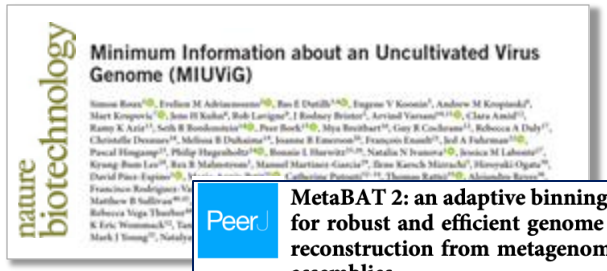
2021

2023

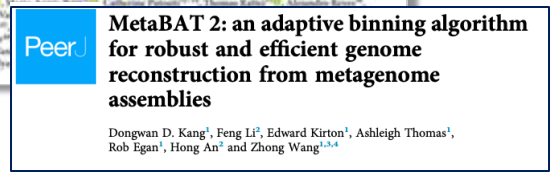
2024

Earth's virome (>1,100 cit.)

MIUViG standards (>600 cit.)



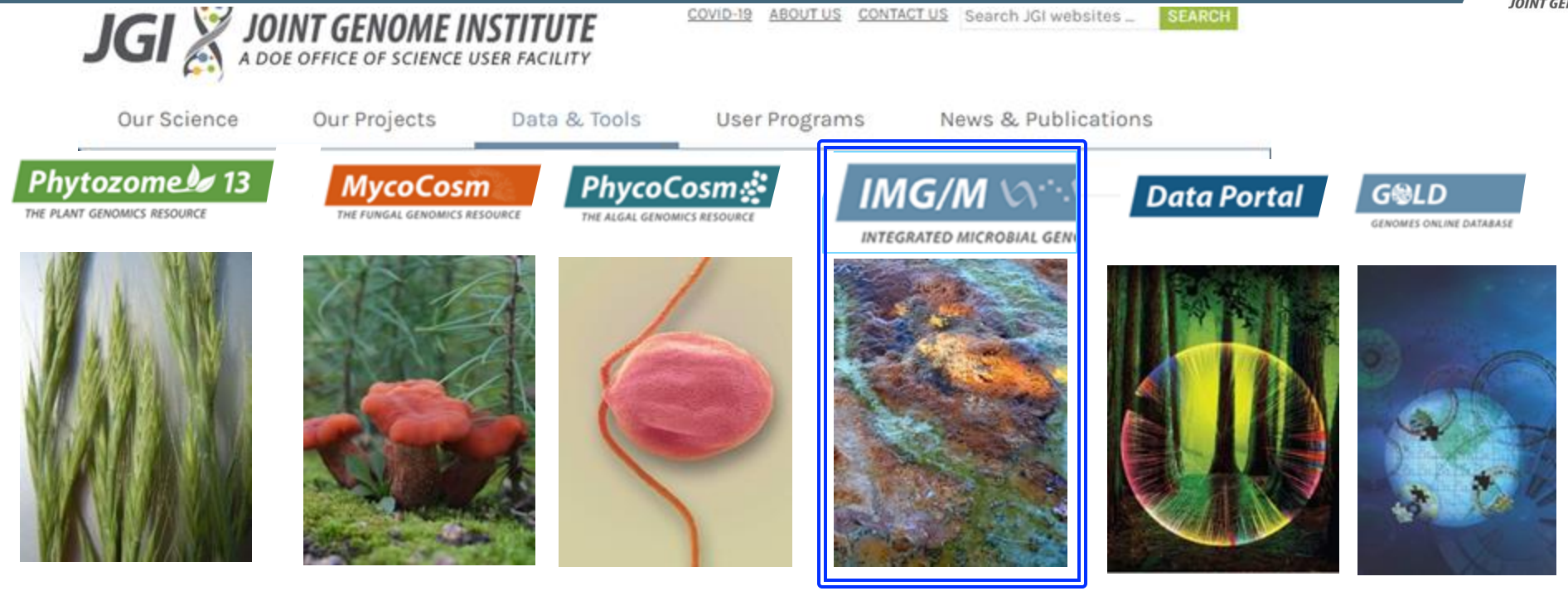
MetaBAT2 (>3,200 cit.)

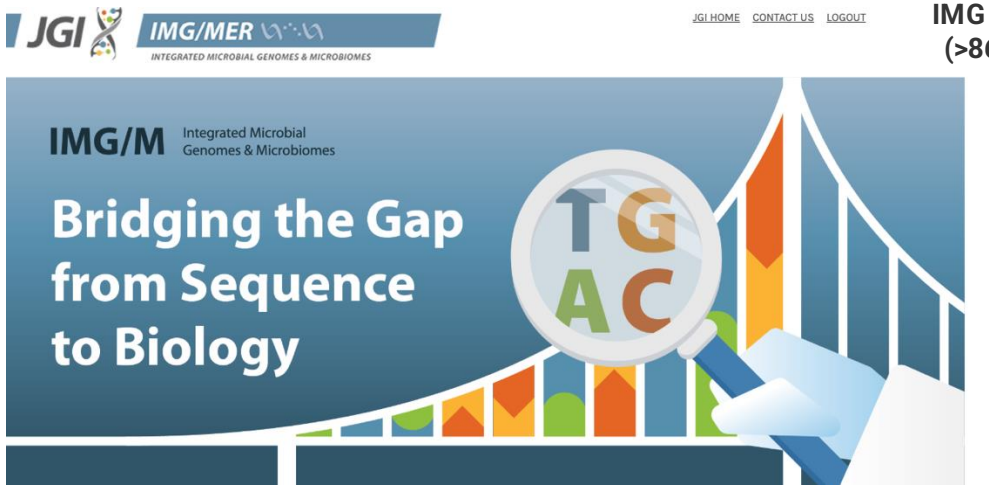


iPHoP: An integrated machine learning framework to maximize host prediction for metagenome-derived viruses of archaea and bacteria

PLOS Biology

Portals for Microbiome Research





IMG Systems (>8600 cit.)

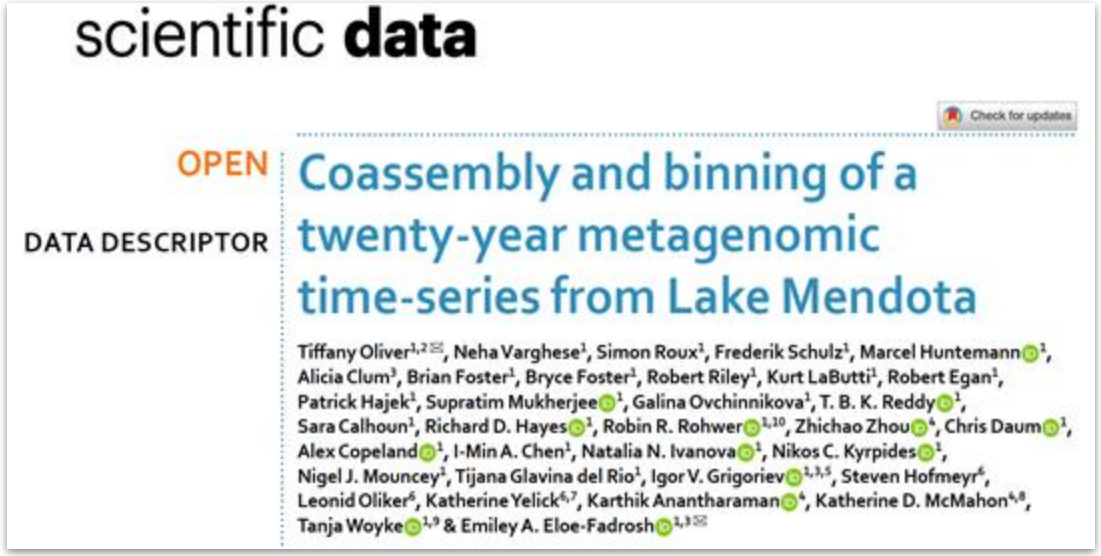
Viral Resource

JGI IMG/VR

Plasmid Resource

JGI IMG/PR

Terabase-scale CO-ASSEMBLY of Metagenomes



scientific data

Check for updates

OPEN

DATA DESCRIPTOR

Coassembly and binning of a twenty-year metagenomic time-series from Lake Mendota

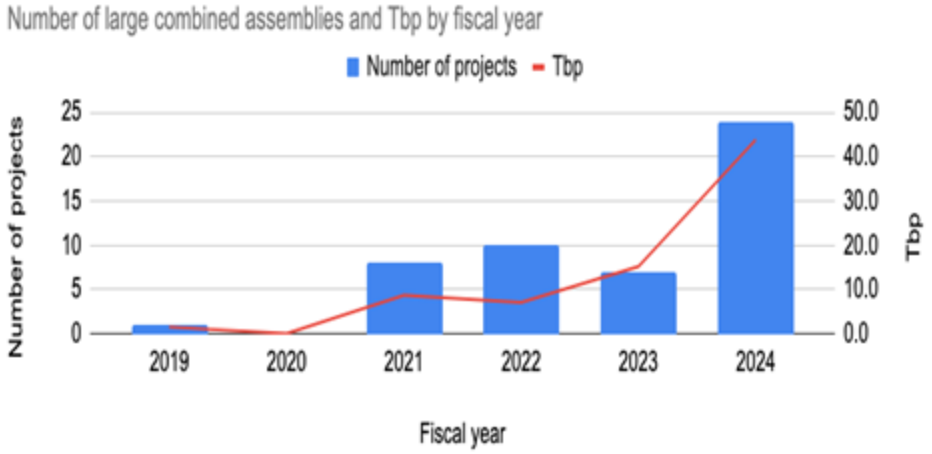
Tiffany Oliver[1,2], Neha Varghese[1], Simon Roux[1], Frederik Schulz[1], Marcel Huntemann[1], Alicia Clum[3], Brian Foster[1], Bryce Foster[1], Robert Riley[1], Kurt LaButti[1], Robert Egan[1], Patrick Hajek[1], Supratim Mukherjee[1], Galina Ovchinnikova[1], T. B. K. Reddy[1], Sara Calhoun[1], Richard D. Hayes[1], Robin R. Rohwer[1,10], Zhichao Zhou[4], Chris Daum[1], Alex Copeland[1], I-Min A. Chen[1], Natalia N. Ivanova[1], Nikos C. Kyrpides[1], Nigel J. Mouncey[2], Tijana Glavina del Rio[1], Igor V. Grigoriev[1,3,5], Steven Hofmeyr[6], Leonid Oliker[6], Katherine Yelick[6,7], Karthik Anantharaman[4], Katherine D. McMahon[4,8], Tanja Woyke[1,9] & Emiley A. Eloe-Fadrosh[1,3]

- Twenty-year time series from Lake Mendota
- Better recovery of low-abundance organisms; longer contigs.

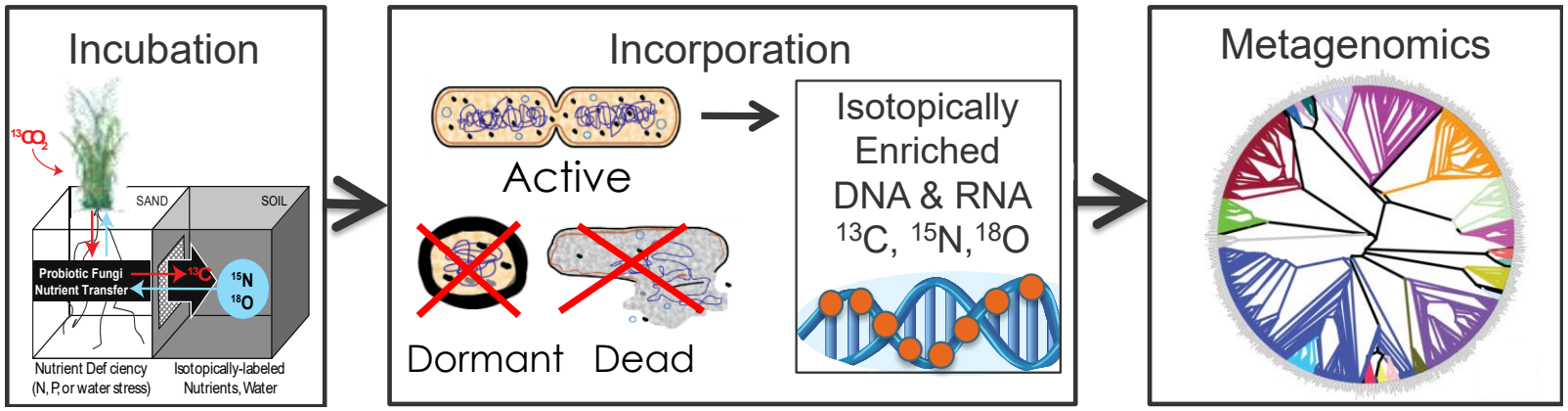
MetaHipMer scales to run on supercomputers

Emiley Eloe-Fadrosh

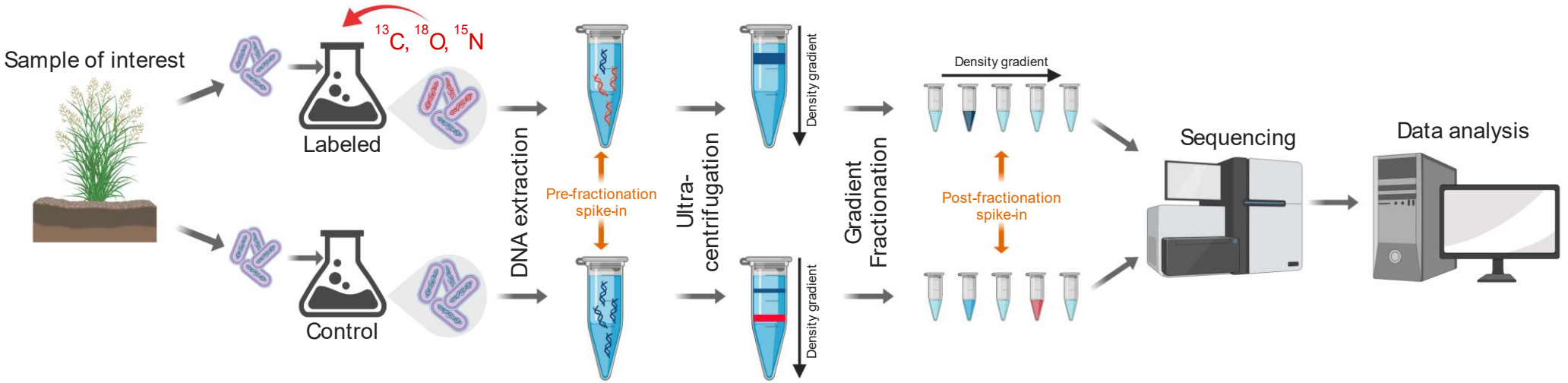
- Input Data: >10 Tbp from 471 individual metagenome samples
- Largest environmental metagenome assembly
  - Staggering 95,523,664 contigs assembled
- 1,894 non-redundant prok MAGs, 9 euk MAGs, 6,350 HQ viruses



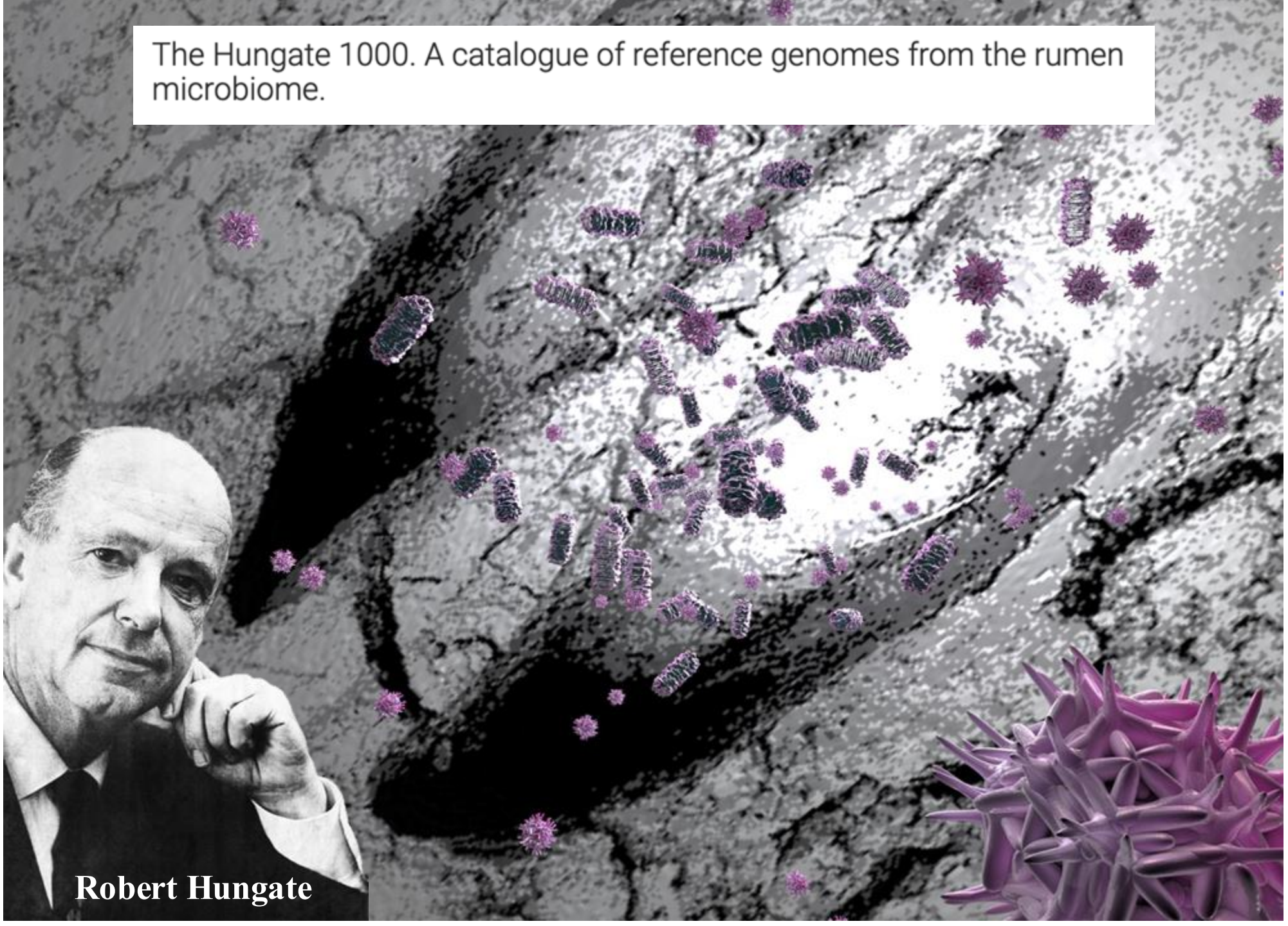
Accessing active populations with qSIP-Metagenomics



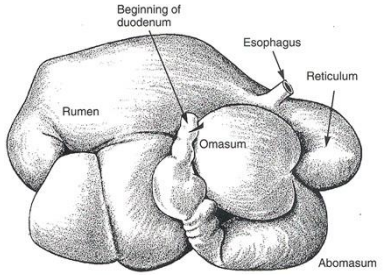
Rex Malmstrom



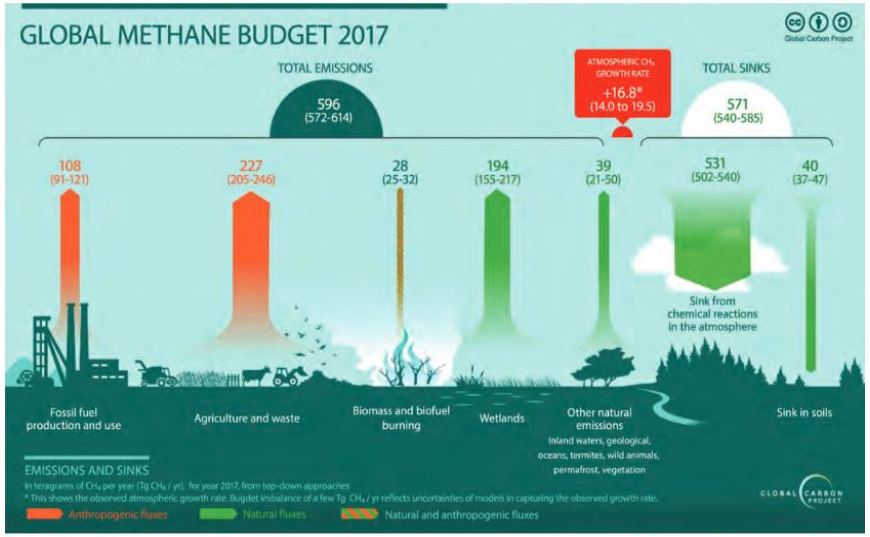
The Hungate 1000. A catalogue of reference genomes from the rumen microbiome.



Why the Rumen



- World's largest commercial fermentation chamber
- Dense microbial habitat - ***symbiotic*** bacteria, archaea, fungi, protozoa & viruses
- 2-12% feed energy loss from via CO2 and CH4 - 1/3rd of human-made emission
- Goal - Modify rumen microbiome to reduce CH4, improve animal health and nutrient utilization!



Jackson etal, 2020

Figure 4. The global CH_4 budget for year 2017 based on natural sources and sinks (green), anthropogenic sources (orange), and mixed natural and anthropogenic sources (hatched orange-green). Image from Jackson et al. 2020.

Rumen Model System
Direct access to site (cannula)
Large (liters), allows comprehensive multi-omics.
High control over diet, environ; isolate variables
Low; use of specific breeds
Can ethically induce and study states of dysbiosis (e.g., acidosis).

Monensin and Nisin Affect Rumen Fermentation and Microbiota Differently *In Vitro*

Junshi Shen[1,2] Zhuang Liu[1] Zhongtang Yu[2*] Weiyun Zhu[1*]

Epub 2015 May 23.

Effect of Probiotics/Prebiotics on Cattle Health and Productivity

Yutaka Uyeno [1], Suguru Shigemori, Takeshi Shimosato

Methane production and digestion of different physical forms of rapeseed as fat supplements in dairy cows

M. Brask *, P. Lund *, M.R. Weisbjerg *, A.L. F. Hellwing *, M. Poulsen *, M.K. Larsen †, T. Hvelplund *

> PLoS One. 2017 Aug 16;12(8):e0182235. doi: 10.1371/journal.pone.0182235. eCollection 2017.

> Appl Environ Microbiol. 2009 Apr;75(7):1860-6. doi: 10.1128/AEM.02453-08. Epub 2009 Feb 6.

A vaccine against rumen methanogens can alter the composition of archaeal populations

Yvette J Williams [1], Sam Popovski, Suzanne M Rea, Lucy C Skillman, Andrew F Toovey,

208 Effects of bacteriophages, their bacterial hosts, and combined phage-bacteria inoculations on *in vitro* ruminal fermentation and methane production FREE

Gabriela Magossi, Godson Aryee, Kendall C Swanson, Samat Amat

Journal of Animal Science, Volume 103, Issue Supplement_1, May 2025, Pages 43–44,

Natural and artificial feeding management before weaning promote different rumen microbial colonization but not differences in gene expression levels at the rumen epithelium of newborn goats

Effects of active dry yeasts on the rumen microbial ecosystem: Past, present and future ☆

The role of probiotics, prebiotics and synbiotics in animal nutrition

Paulina Markowiak [1], Katarzyna Śliżewska [1]

Exploitation of dietary tannins to improve rumen metabolism and ruminant nutrition

Amlan K Patra, Jyotisna Saxena

First published: 02 September 2010 | https://doi.org/10.1002/jsfa.4152 | Citations: 558

Application of Bacteriophages To Control Intestinal *Escherichia coli* O157:H7 Levels in Ruminants

Authors: Haiqing Sheng, Hannah J. Knecht, Indira T. Kudva, Carolyn J. Hovde | AUTHORS INFO & AFFILIATIONS

J. Dairy Sci. 92:2118–2127
doi:10.3168/jds.2008-1903
© American Dairy Science Association, 2009.

Crushed sunflower, flax, or canola seeds in lactating dairy cow diets: Effects on methane production, rumen fermentation, and milk production

K. A. Beauchemin,*[1] S. M. McGinn,* C. Benchaar,† and L. Holtshausen*
*Agriculture and Agri-Food Canada, Lethbridge, Alberta, T1J 4B1, Canada
†Dairy and Swine Research and Development Centre, Sherbrooke, Quebec, J1M 1Z3, Canada

Meta-analysis on Methane Mitigating Properties of Saponin-rich Sources in the Rumen: Influence of Addition Levels and Plant Sources

Anuraga Jayanegara[1,*], Elizabeth Wina[2], and Junichi Takahashi[1,3]

Red seaweed *(Asparagopsis taxiformis)* supplementation reduces enteric methane by over 80 percent in beef steers

Breanna M. Roque, Marielena Venegas, Robert D. Kinley, Rocky de Nys, Toni L. Duarte, Xiang Yang, Ermias Kebreab

An inhibitor persistently decreased enteric methane emission from dairy cows with no negative effect on milk production

Alexander N. Hristov, Joonpyo Oh, Fabio Giallongo, Tyler W. Frederick, Michael T. Harper, Holley J. Weeks, Antonio F.

Ruminal Fluid Transplantation Accelerates Rumen Microbial Remodeling and Improves Feed Efficiency in Yaks

Yan Li [1,2,3], Yingkui Yang [1,2,3], Shatuo Chai [1,2,3], Kaiyue Pang [1,2,3], Xun Wang [1,2,3], Linpeng Xu [1,2,3], Zheng Chen [1,2,3],

Strategy/Intervention	Primary Objective(s)	Mechanism & Description	Status & Practicality	Key References
Dietary & Feed Additive Strategies				
Seaweed (*Asparagopsis*)	**Methane Mitigation**	bromoform, potently inhibits key enzyme in the final step of methanogenesis.	Highly effective (>80% reduction). Commercially available	Roque, B. M. et al. (2021). *PLOS ONE*
Chemical Inhibitors (3-NOP)	**Methane Mitigation**	A synthetic molecule that directly inhibits methyl-coenzyme M reductase	Highly effective and commercially approved in many regions. **A leading practical solution.**	Dijkstra, J. et al. (2018). *PNAS*.
Lipid Supplementation	**Methane Mitigation**	Adds fats/oils to diet, toxic to methanogens and protozoa, and also acts as a sink for hydrogen.	Moderately effective, widely practical. Can impact feed costs and other production aspects	Beauchemin, K. A. et al. (2008). *Journal of Dairy Sci*.
Ionophores (e.g., Monensin)	**Production Efficiency**, Methane Mitigation	Antibiotics that select against certain bacteria, shifting fermentation to propionate production, using up hydrogen.	Widely used for decades. Regulatory approval varies globally (banned as a feed additive in the EU).	Russell J.B. Strobel H.J. (1989). Appl. Environ. Microbiol. 55, 1–6.
Plant Bioactives (Tannins, etc.)	**Methane Mitigation**, Improved Protein Utilization	Natural plant compounds with antimicrobial properties that suppress protozoa and methanogens. (also protect protein)	Variable effectiveness. An active area of research for natural, sustainable solutions.	Patra, A. K., & Saxena, J. (2011). *Advances in Agronomy*.
Probiotics (Direct-Fed Microbials)	**Animal Health**, Production Efficiency	Beneficial microbes (e.g., *Saccharomyces cerevisiae*, *Lactobacillus*) to stabilize rumen, improve digestion, and outcompete less desirables	Commonly used to improve gut health and feed digestion. Effects on methane are generally minor and inconsistent.	Chaucheyras-Durand, F. et al. (2008). *Animal Feed Science and Tech*. Uyeno, Y. et al. (2015). *Animal Sci*.
Prebiotics	**Animal Health** (e.g., pH stability), Production Efficiency	Provides fermentable substrates (e.g., Fructo-oligosaccharides [FOS], Galacto-oligosaccharides [GOS], Xylo-oligosaccharides [XOS]) to selectively stimulate beneficial microbes.	Used to promote a healthy microbial balance. Effectiveness can be variable due to the complexity of the rumen ecosystem.	Markowiak, P., & Śliżewska, K. (2018). *Animals*.
Host & Advanced Strategies				
Early-Life Programming	**All Three** (Long-Term)	Manipulating diet, environment of young to establish beneficial biome that persists in adult.	Experimental but promising. set a permanent beneficial trajectory for the animal's life.	Yáñez-Ruiz, D. R. et al. (2015). *Front in Microbiology*.
Rumen Transfaunation	**All Three** (Corrective)	Transferring rumen fluid from a "donor" animal with a desirable microbiome to a "recipient" animal.	Highly effective for research and treating digestive upset. Long-term stability for production traits is still being studied.	Weimer, P. J. (2015). *Front. Microbiol.*
Vaccines & Phage Therapy	**Methane Mitigation** (Highly Targeted)	Developing vaccines to target methanogens or using viruses (phages) to specifically kill them.	Highly experimental early research stages. Significant technical, immunological challenge.	Magossi G (2025) J Anim Sci. Gilbert, R. (2020). *Front in Microbiol*.

Hungate Isolates & Reference Genomes

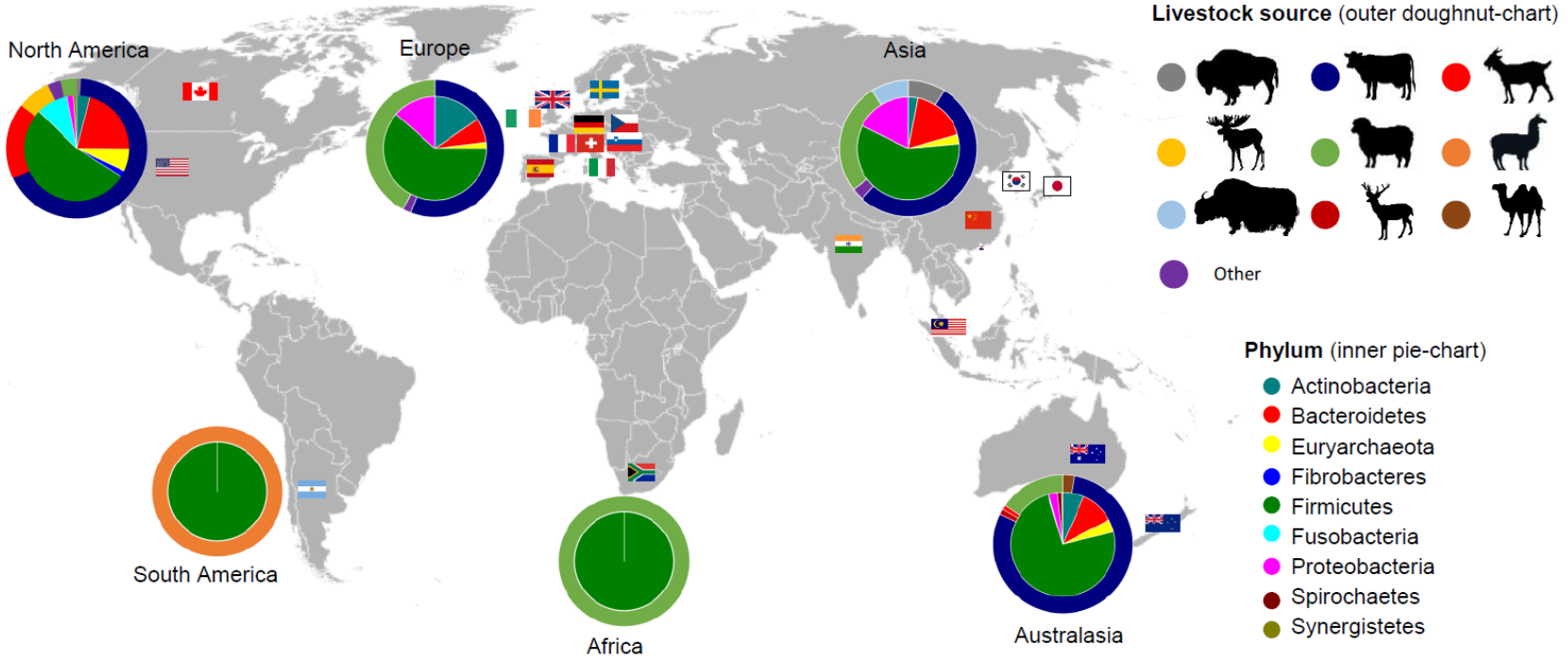
nature biotechnology

Cultivation and sequencing of rumen microbiome members from the Hungate1000 Collection

Rekha Seshadri, Sinead C Leahy, Graeme T Attwood, Koon Hoong Teh, Suzanne C Lambie, Adrian L Cookson, Emiley A Eloe-Fadrosh, Georgios A Pavlopoulos, Michalis Hadjithomas, Neha J Varghese, David Paez-Espino, Hungate1000 project collaborators, Rechelle Perry, Gemma Henderson, Christopher J Creevey, Nicolas Terrapon, Pascal Lapebie, Elodie Drula, Vincent Lombard, Edward Rubin, Nikos C Kyrpides, Bernard Henrissat, Tanja Woyke, Natalia N Ivanova & William J Kelly

Nature Biotechnology **36**, 359–367 (2018) | Cite this article

- 410 genomes contributed (15 at inception)
- Study total - 481 Bacteria & 21 Archaea

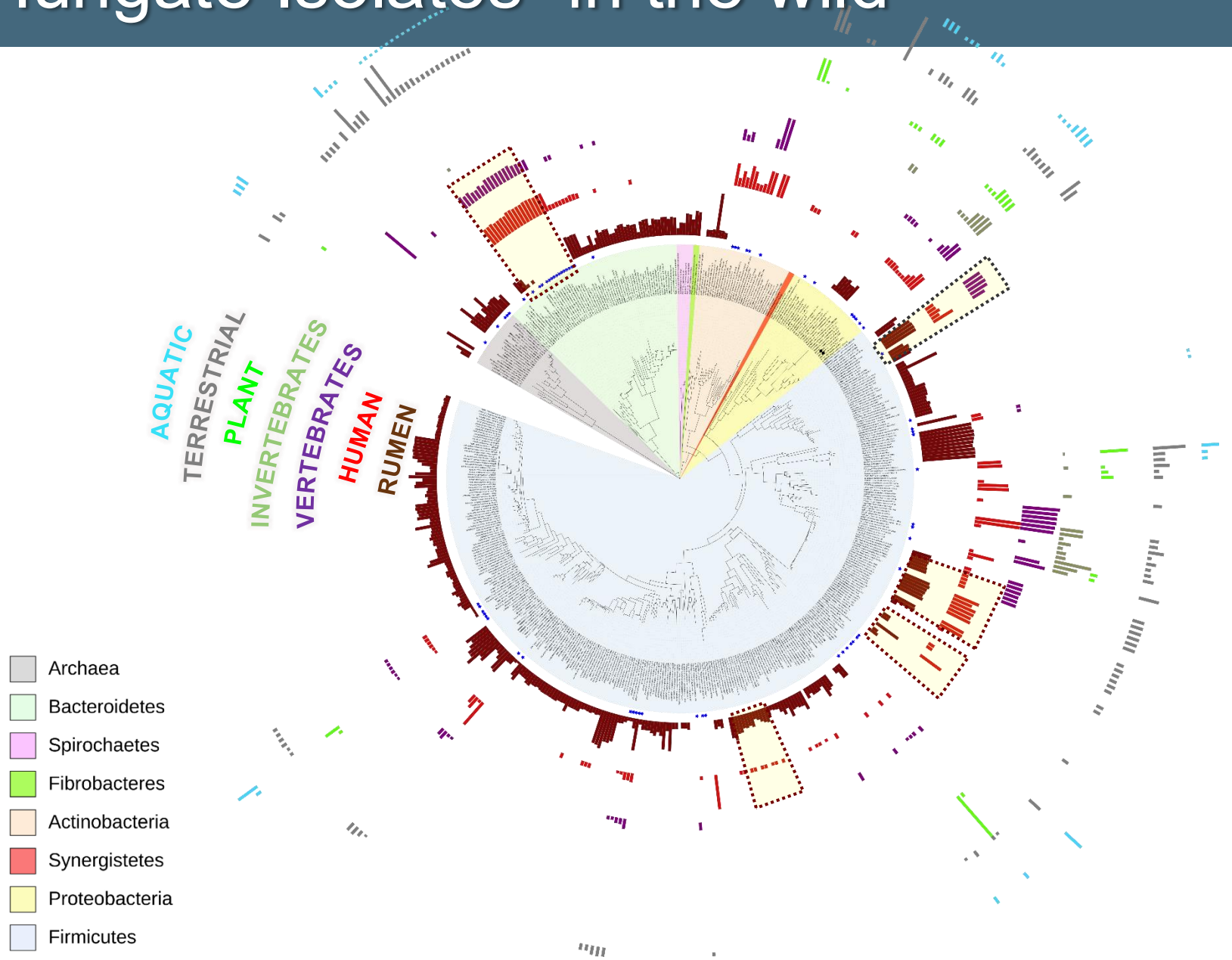


William Kelly

agresearch

RMG NETWORK
RUMEN MICROBIAL GENOMICS NETWORK

Hungate Isolates “in the wild”



- Comparing 500 ISOLATES against >8,200 metagenomes in IMG/M
- 400 isolates in **only 40** rumen samples
- 130 overlapping species with human G.I., e.g.,
  - *Megasphaera elsdenii*
  - *Prevotella bryantii*
  - *Streptococcus gallolyticus, S. equinus*
  - *Ruminococcus flavefaciens*
  - *Dorea spp.*
  - *Blautia spp.*

Save the Date: Sequences to Cultures Jamboree (Nov 6-7)

2025 NeLLi Symposium

Nov 4-7, 2025 @ UNLV & DRI

Hosted by the JGI, University of Nevada, Las Vegas, and the Desert Research Institute

Take part in the "Sequences to Cultures" Jamboree!

Immediately following the NeLLi Symposium, join us for a 1.5–day jamboree on November 6–7 focused on improving cultivation and genomic coverage. Experts in cultivation and environmental genomics will work together to develop recommendations for cultivating new bacteria and archaea revealed by a recent genome census. A key outcome will be a a compelling position paper, and we are pleased to have *Nature Microbiology* editor Kyle Frischkorn joining us to contribute to discussions and provide an editorial perspective.