

The global rumen census and Hungate1000: collaborative research projects targeting rumen microbes

Bill Kelly



New Zealand research is a collaborative partnership funded by



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GLOBAL RESEARCH ALLIANCE

ON AGRICULTURAL GREENHOUSE GASES



Rumen Microbial Genomics Network

GRA Livestock Research Group

- Established 5 years ago
- Purpose - To underpin the development of methane mitigation and rumen adaptation technologies using microbial genomics approaches.
- Two international, collaborative research projects focused on rumen microbes were developed.

A Global Census of Rumen Microbial Diversity

Rumen microbial community composition varies with diet and host, but a core microbiome is found across a wide geographical range.

G. Henderson, F. Cox, S. Ganesh, A. Jonker, W. Young, Global Rumen Census Collaborators & P. Janssen.

Scientific Reports 2015 5:14567.

Global Rumen Census Collaborators

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742 Samples, 32 Animal species, 35 Countries.

Research Questions

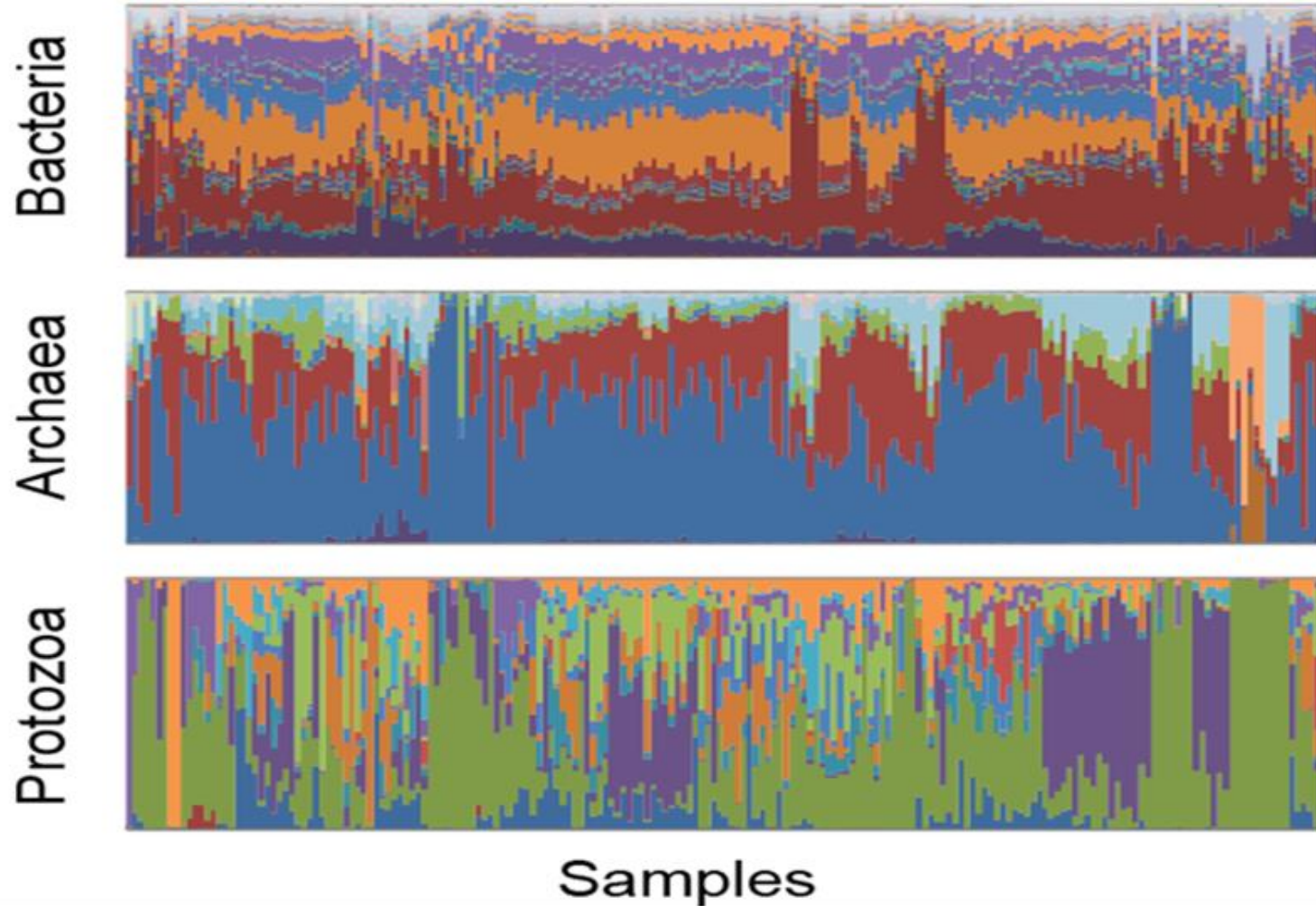
The Global Rumen Census is a culture-independent study based on sequencing ribosomal RNA genes using a standardised pipeline.

1. Which (dominant / novel) microbial groups are present?
2. Is there a “core” microbial community?
3. How much variation is there in rumen microbial communities?
4. What factors might explain differences in microbial communities?
5. Do any microbial groups co-occur?

Outcomes

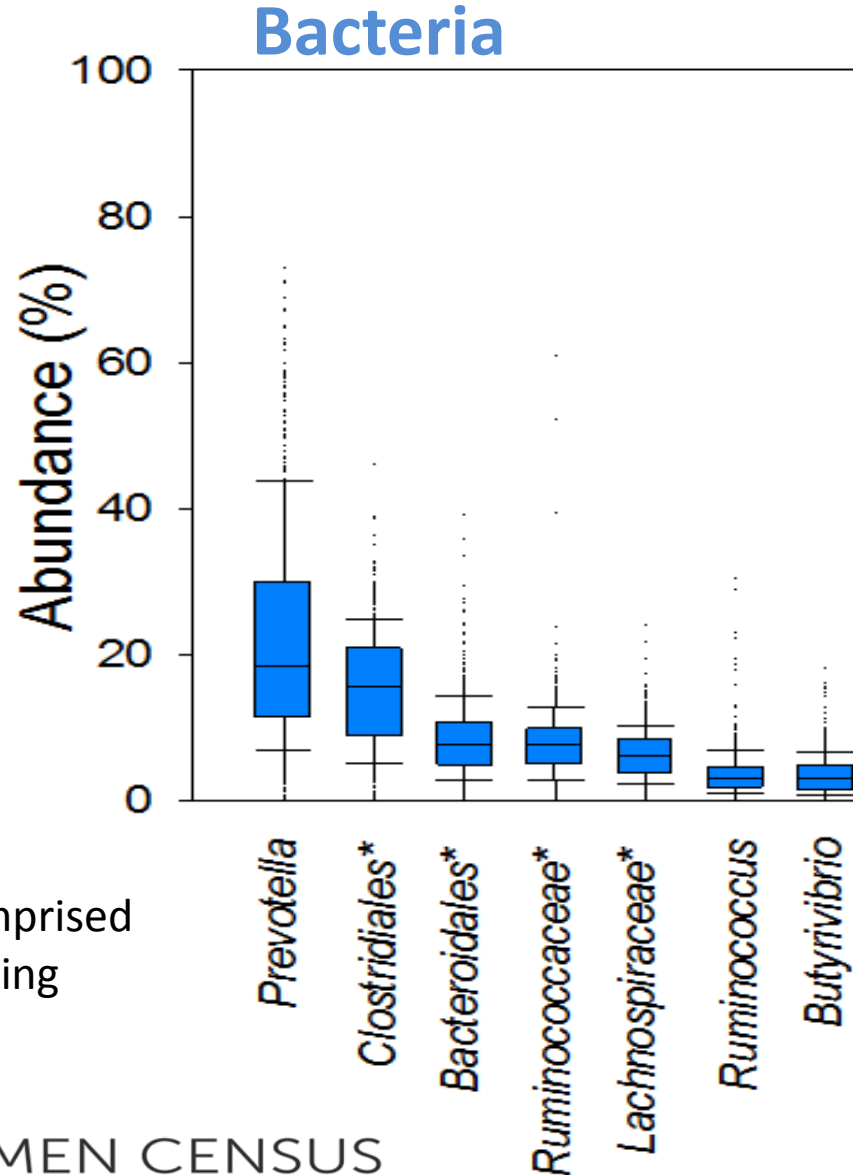
- Reference to compare variability and changes observed in mitigation research programs?
- Universality or regionality of rumen microbial populations?
- Factors that may explain variation of microbial populations?

Bacteria and archaea are similar- protozoa are variable



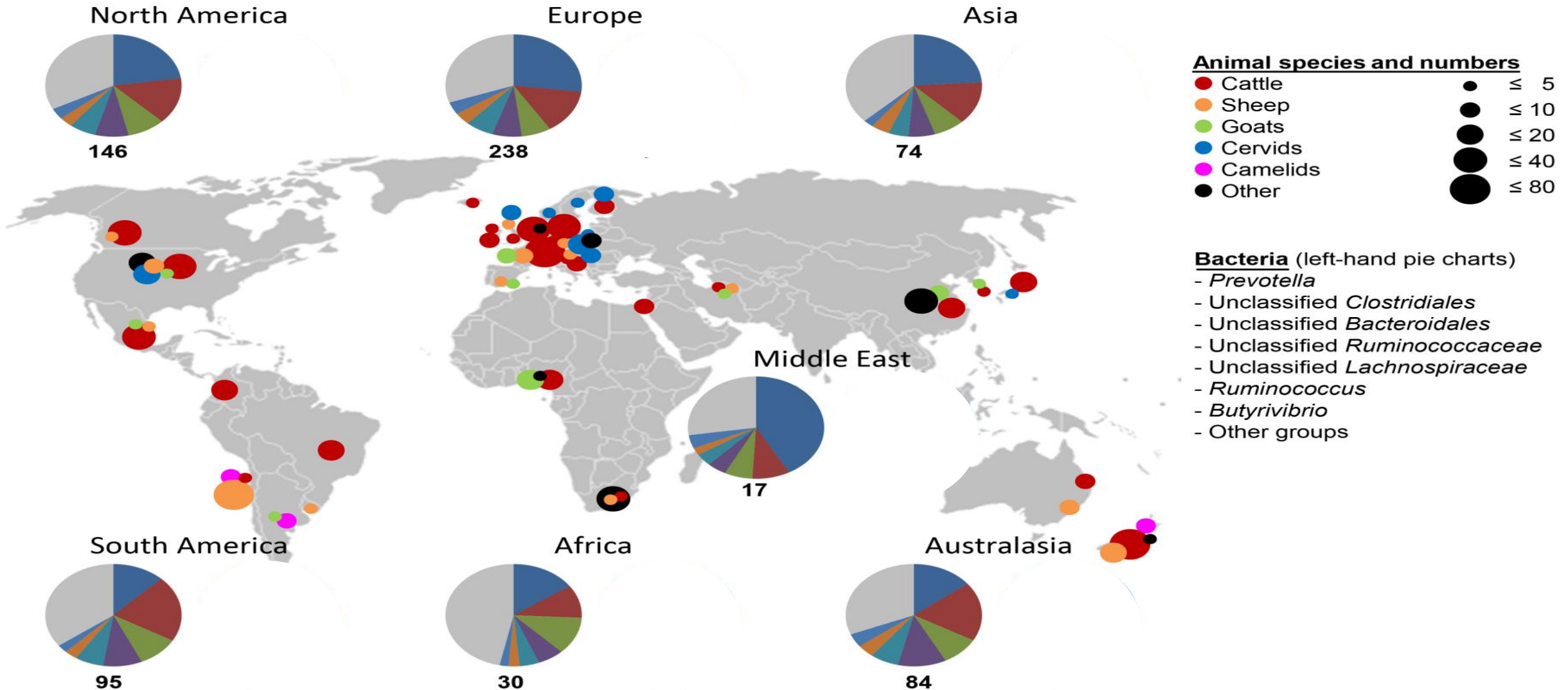
Relative abundances
of microbial groups
in individual samples

Dominant microbial taxa



7 bacteria taxa comprised
2/3 of the sequencing
reads

The global picture



The underlying map was sourced from Wikimedia Commons (original uploader Roke, accessed May 2013)

Summary

- Communities consist of a small number of (dominant) taxa
 - Archaea especially
 - Dominant bacteria responsible for the majority of plant polysaccharide breakdown
- Communities are affected by host and diet
 - Especially bacteria
 - Mainly by diet
- Few strong associations between microbial groups
 - Functional redundancy, multiple species can perform the same function
 - Minor groups, possibly substrate-linked

The Hungate1000-a catalog of reference genomes from the rumen microbiome



Dick Clarke and Bob Hungate,
Palmerston North, NZ, circa 1971.



HUNGATE1000

A catalogue of reference genomes from the rumen microbiome.

Research Aims

The Hungate1000 is a culture-dependent study with the following aims:

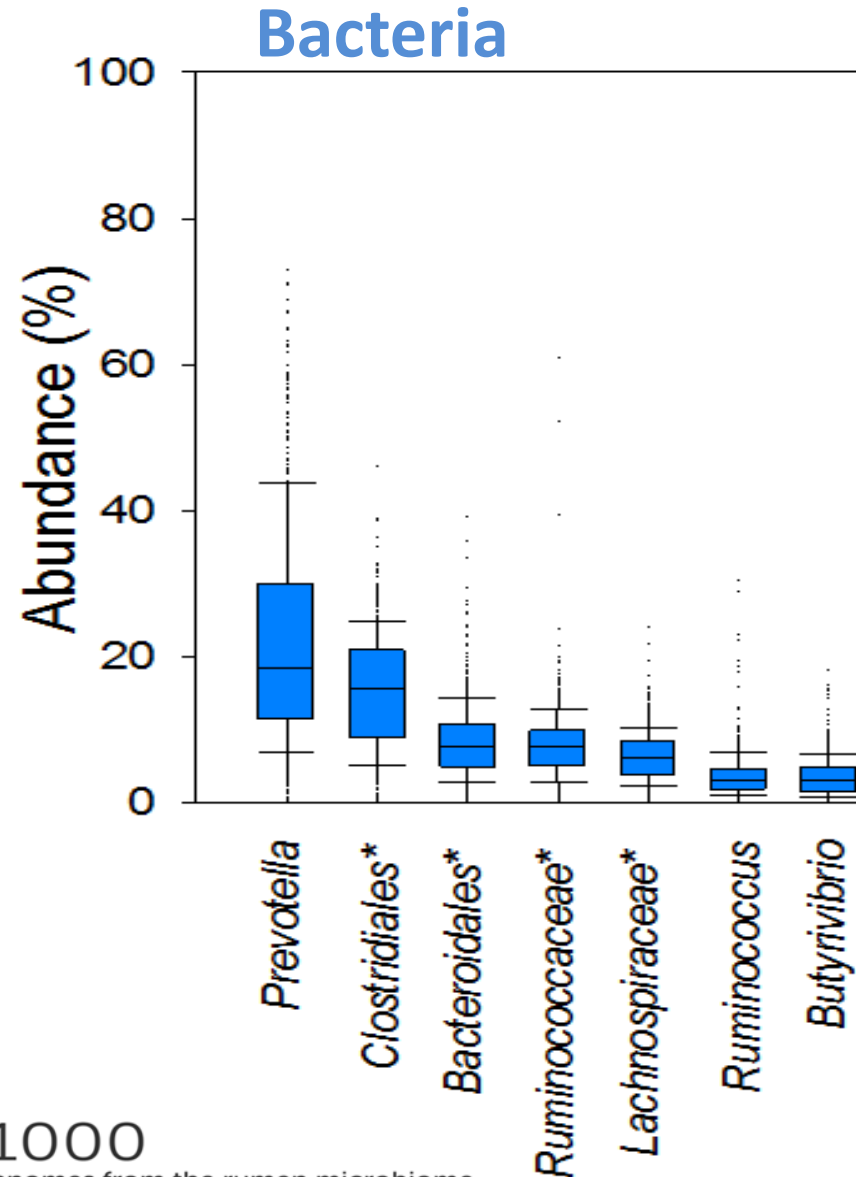
1. To produce a reference set of rumen microbial genome sequences from cultivated rumen microbes including bacteria, methanogens, phage, anaerobic fungi and ciliate protozoa.
2. To support research aimed at understanding rumen function in order to find a balance between increased food production and greenhouse gas emissions.
3. To underpin the analysis and comprehension of metagenomic sequence datasets.

Progress

The Hungate1000 has produced >400 genome sequences from cultivated rumen bacteria, archaea and bacteriophage. Sequencing is supported by the Community Science Program of the US DOE Joint Genome Institute.

~500 genome sequences are now available for rumen microbes (cf 15 when this project started).

Dominant microbial taxa



Functional
redundancy



HUNGATE1000

A catalogue of reference genomes from the rumen microbiome.

* unclassified

Conclusions

The Global Rumen Census has determined the composition of the rumen microbial community across a wide range of countries, animal species and diets, providing information on Who's there?

Although differences are apparent the microbial composition is largely similar overall.

The Hungate1000 is contributing genome sequences for rumen microbes and providing information on What are they doing?

There appear to be few 'key' species and a large supporting cast.

We hope the resource that has been developed will be valuable for researchers interested in the microbiology of the rumen and other gut environments.

This research area is only beginning and the challenge is now to use the knowledge generated.

Acknowledgements

New Zealand Government

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The Global Rumen Census and Hungate1000 projects are team efforts.

From AgResearch:

- Gemma Henderson, Faith Cox, Siva Ganesh, Wayne Young and Peter Janssen contributed to the Global Rumen Census.
- Sinead Leahy, Graeme Attwood, Rechelle Perry, Kenneth Teh, Nick Palevich, Adrian Cookson and Suzanne Lambie contributed to the Hungate1000.
- Sam Noel, Nicki Kenters, Laura Olthof and Garth Peck isolated new bacterial strains.
Chris Creevey (Teagasc/IBERS).
Nicole Shapiro and Tanja Woyke (JGI).

Most importantly these projects would not be possible without the support of the many collaborators who have provided samples and cultures.

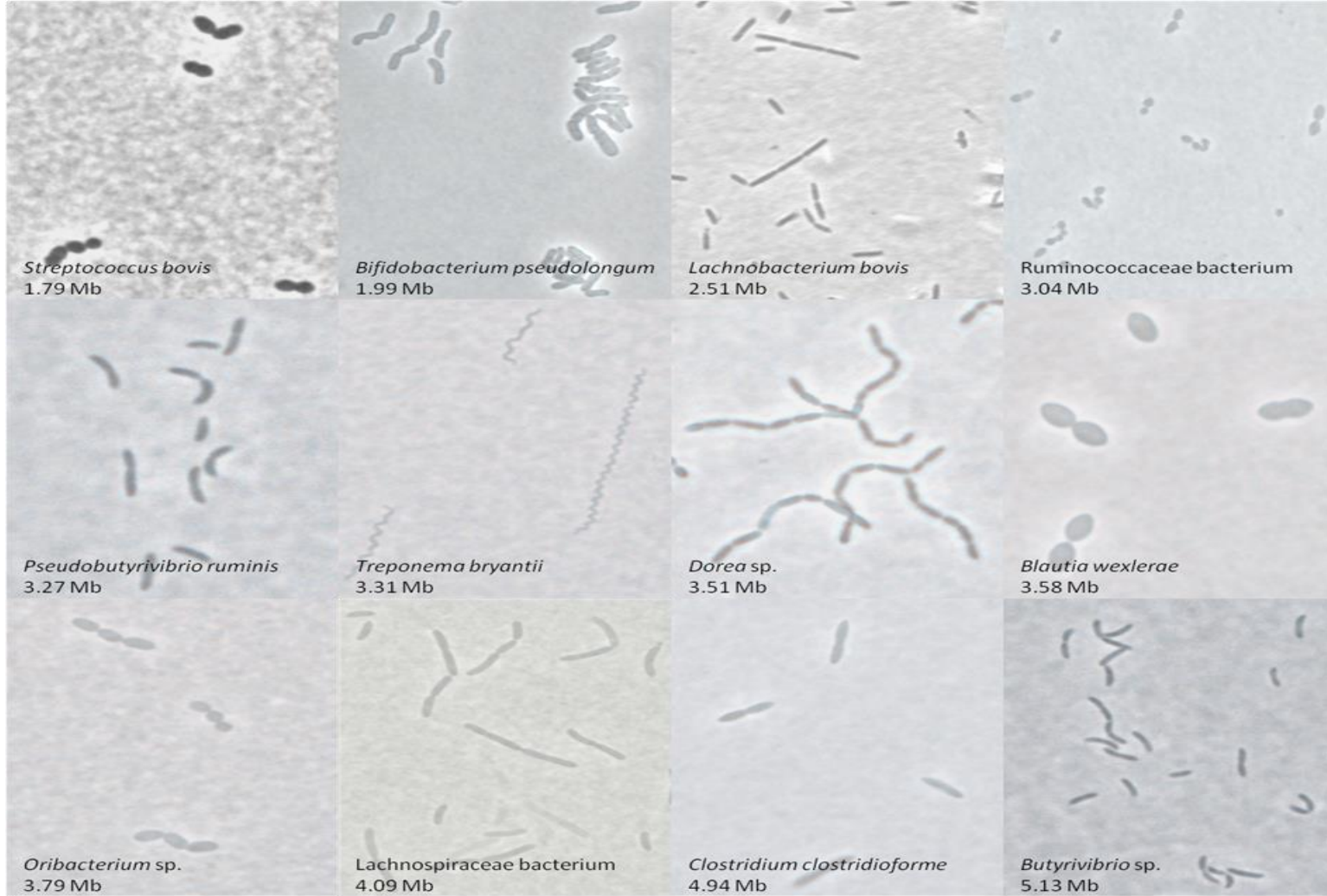
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HUNGATE1000

A catalogue of reference genomes from the rumen microbiome.



GLOBAL RUMEN CENSUS



RMG NETWORK

RUMEN MICROBIAL GENOMICS NETWORK

Factors affecting microbial community composition

- **Animal**
 - Species, breed, gender, age, condition, modification, treatment
- **Diet**
 - Forage / browse to concentrate ratio, forage type, forage plant, starch, pectin
- **Location**
 - Country, region, latitude, longitude, elevation, climate, season, (farming) system, contact with other animals
- **Sample processing**
 - Sampling method, sample composition, time to freezer, sample format provided, DNA extraction
 - Reproducibility of the pipeline
 - DNA extraction, PCR, sequencing, etc.

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