Global Census of Rumen Microbial Diversity

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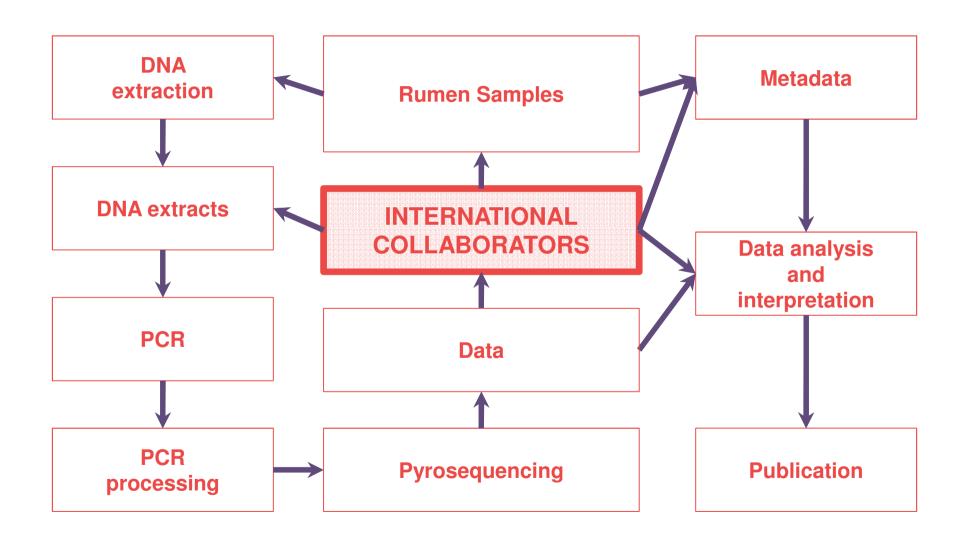
Research Questions

- 1. How much **variation** is there in rumen microbial communities?
- 2. What is the extent of **diversity** in each microbial group?
- 3. What **novel groups** are present?
- 4. Is there a core microbial community?

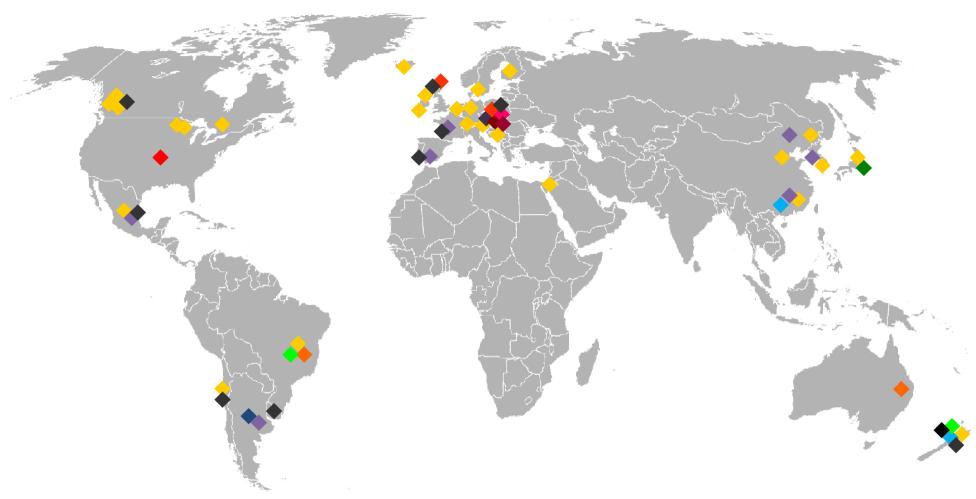
Benefits

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

Approach



Samples provided to date



Status 12/06/2013, map source: Wikimedia Commons by original contributor Roke, accessed on 01/05/2013

- American bison (Bison bison)
- Zebu (Bos indicus)
- Cattle (Bos taurus)
- Bos taurus / indicus hybrid
- Water buffalo (Bubalus bubalis)

- Goat (Capra hircus)
- Steinbock (Capra ibex)
- Roe deer (Capreolus capreolus)
- Red deer (Cervus elaphus)
- Sika deer (Cervus nippon yesoensis) ◆ Alpaca (Vicugna pacos)
- Llama (*Lama glama*)
- Argali (Ovis ammon musimon)
- Sheep (Ovis aries)
- Chamois (Rupicapra rupicapra)

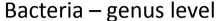
Progress so far

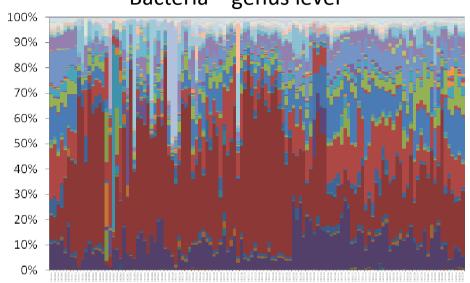
- Received
 - > 500 samples
 - 26 countries
 - 15 species
 - · Several sheep and cattle breeds
 - Sheep
 - » Blackbelly, Canadian Arcott, Chilota, Corriedale, Dorper x Mongolian, Jezersko Solcavska, Suffolk, Texel
 - Cattle
 - » Angus x, Belgium Blue, Belted Galloway, British x Continental, Chinese Holstein, Cika, Danish Shorthorn, Finnish Ayrshire, Friesian, Friesian x Hereford x Holstein, Friesian x Jersey, Hereford, Highland, Holstein, Holstein x Simmental, Icelandic, Japanese Black, Jersey, Jutland, Korean Native, Limousin, Limousin x, Nordic Red, Simmental, Western Finncattle
 - Zebu
 - » Nelore
 - Variety of ~100 diets
- Processed
 - 1st round of sequencing 120 samples (data received)
 - 2nd round of sequencing 260 samples (sent for sequencing)
- Breeds in data analysed to date (next slides)
 - 11 cattle, 5 sheep, 1 zebu, 1 water buffalo, 3 goat, 1 llama and 1 alpaca breeds





Bacteria and fungi





Succinivibrio

63% prevalence, Ø abundance 1.1%

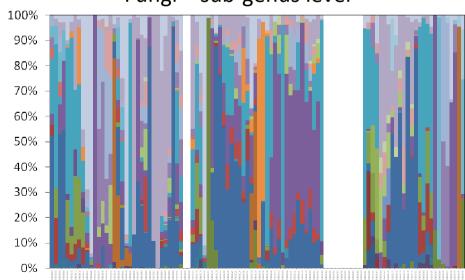
Butyrivibrio

100% prevalence, Ø abundance 3.7%

Prevotella

100% prevalence, Ø abundance 32.8%

Fungi – sub-genus level



SK3

70% prevalence, Ø abundance 10.6%

Neocallimastix 1

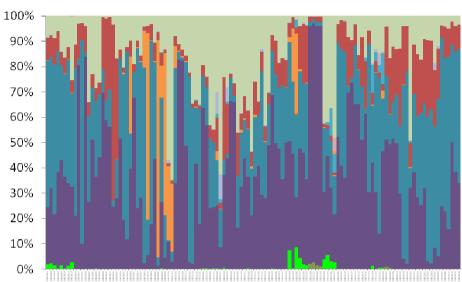
55% prevalence, Ø abundance 13.3%

Caecaomyces 1

59% prevalence, Ø abundance 15.9%

Archaea and protozoa

Archaea – mixed taxonomic ranks



Mbb. ruminantium

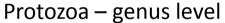
100% prevalence, Ø abundance 30.4%

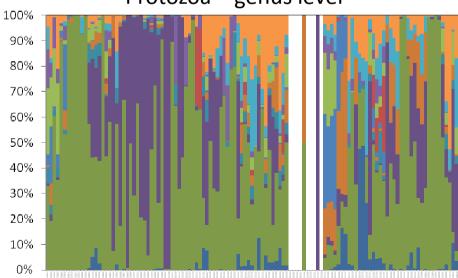
Mbb. wolinii

40% prevalence, Ø abundance 3.5%

Methanobacterium

37.5% prevalence, Ø abundance 0.48%





Isotricha

77.5% prevalence, Ø abundance 7.1%

Entodinium

92.5% prevalence, Ø abundance 42.3%

Next steps

- 3rd and FINAL round of sequencing
 - Deadline for sample submission JUNE 2013
 - Especially interested in samples from India and Africa
- Data analysis
 - Variation
 - Diversity
 - Novel groups
 - Core community
 - Metadata
 - Etc.

Acknowledgements

Global Rumen Census Collaborators

www.globalrumencensus.org.nz/samples

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