i.   Title/Heading

"Rumen Gateway- mitigation through the microbiome"

ii.   Context and rationale

Reductions in anthropogenic greenhouse gases (GHGs) are required[1]. The agriculture sector contributes a significant share (14.5%) to anthropogenic GHGs with ruminant livestock accounting for most of those emissions[2]. Currently, plausible mitigation practices in the agriculture sector are estimated to only deliver 21 to 40% of the needed mitigation[3]. At the same time agriculture needs to produce more food to feed the world's growing population, therefore, new tools and technologies must be developed to achieve this goal without growing GHGs.

Regardless of the ruminant species, the largest source of GHG emissions from ruminant production is methane. Microorganisms located in the fore-stomach (reticulorumen) of ruminant animals have a major influence on feed digestion and the production of methane. Consequently, a range of microbial-based mitigation options with strong potential to reduce methane emissions are being investigated but require further development and/or longer time frames to be viable mitigation options (Table 1).

Table 1.		
Mitigation tool	**Technical reduction potential**	**Time to Impact**
Inhibitors	Up to 30%	3-5 years
Animal breeding	10-20%	>10 years
Low emission feeds	1-10%	1-5 years
Direct-fed microbials	1-10%	2-5 years
Vaccine	Up to 30%	>7 years

The progress to date has been facilitated by new DNA sequencing technologies which have increased our knowledge of the rumen microbiome, but it is clear that these data have barely scratched the surface of the very complex rumen microbiome and a greater understanding of the microbial diversity and function present in the rumen of animals around the world is urgently needed.

iii.   An overview of the contribution.

It is proposed that a global, co-ordinated, cross-disciplinary effort is required to understand, predict, and harness rumen microbiome function to enable the accelerated development of microbiome-based solutions to support sustainable livestock development that underpins food security, resilient economies, livelihoods of farmers, animal health, and a reduced environmental footprint.

What would be done?
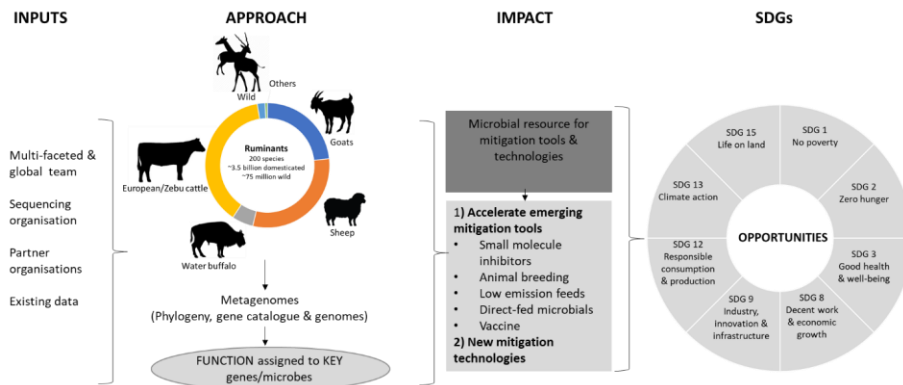
- **Sample.** Samples needed for the initiative will come from the existing Global Rumen Census data and samples[4] and will be used in combination with the Global Research Alliance (GRA) on Agricultural Greenhouse Gases network of scientists to obtain further samples. Building on these existing networks and datasets, a comprehensive census of rumen microbiome samples will be produced.

- **Analyse.** Aligning with a sequencing partner, next-generation DNA sequencing and metagenomic analysis will be performed, allowing a detailed and unprecedented insight into the biodiversity and predicted function of the rumen microbiota. This will be achieved by generating a gene-based view of global rumen communities, to find abundant, common, and unique functions. A comprehensive, open access data resource will be generated which will identify the main genes and pathways operating in the different farmed ruminants around the world.

- **Function**. The expertise contained within the GRA scientific network and the culture resource of the Hungate1000[5] will be used to drive a massive upscaling of detailed microbiological and biochemical characterisation of the key rumen microbiota encoding the most important metabolic pathways identified in the sequencing phase. Assigning and verifying existing biological functions and assigning genes to new functions will allow development of innovative, effective, microbiome-based solutions to reduce GHG emissions from ruminants.

iv. **How the contribution leverages living natural systems as a solution to avert climate change?**

Ruminants are one of the most successful groups of herbivorous mammals on the planet, with around 200 species represented by approximately 75 million wild and 3.5 billion domesticated animals worldwide.

Ruminants are defined by their mode of plant digestion, and have evolved a forestomach, the reticulo-rumen (or, more simply, rumen), that allows partial microbial digestion of feed before it enters the true stomach. Ruminants themselves do not produce the enzymes needed to degrade most of the complex polysaccharides found in plants, and the rumen provides an environment for a rich and dense consortium of anaerobic microbes that fulfil this digestive function. These rumen microbes ferment the released sugars to form volatile fatty acids that are major nutrient sources for the host animal and drive ruminant productivity. The protein in the microbial biomass and unfermented feed components leaving the rumen also contribute to the nutrition of the animal further down the digestive tract.

Ruminants have evolved to thrive on a range of plant species, and this flexibility has enabled them to occupy many different habitats spanning a wide range of climates. These were also important factors in their domestication, allowing conversion of human-indigestible plant material into readily digestible animal products, especially dairy and meat for consumption, the production of useful animal fibres for clothing and materials, and the provision of draft power for transportation and the cultivation of land. Ruminants also have special standing in some religions and often signify wealth status in certain cultures and thus have played an important role in developing and sustaining human societies around the world.

Fundamental gaps in our knowledge of rumen microbial diversity remain. A more complete understanding of this diversity and its function, both *in vitro* and *in situ*, will greatly advance the development of effective technologies or practices that support sustainable livestock development that contributes to food security while reducing its environmental footprint.

v. How might the contribution support both climate, mitigation and adaptation as well as other important co-benefits and social, economic and environmental outcomes in coming years.

The Rumen Gateway would support implementation of a number of SDG 2030 goals and targets, including:

- Promote fair and equitable sharing of the benefits arising from the utilization of genetic resources and promote appropriate access to such resources, as internationally agreed
- Mobilize and significantly increase financial resources from all sources to conserve and sustainably use biodiversity and ecosystems
- By 2030, end hunger and ensure access by all people, in particular the poor and people in vulnerable situations, including infants, to safe, nutritious and sufficient food all year round
- By 2030, double the agricultural productivity and incomes of small-scale food producers, in particular women, indigenous peoples, family farmers, pastoralists and fishers, including through secure and equal access to land, other productive resources and inputs, knowledge, financial services, markets and opportunities for value addition and non-farm employment
- By 2020, maintain the genetic diversity of seeds, cultivated plants and farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks at the national, regional and international levels, and promote access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge, as internationally agreed
- Increase investment, including through enhanced international cooperation, in rural infrastructure, agricultural research and extension services, technology development and plant and livestock gene banks in order to enhance agricultural productive capacity in developing countries, in particular least developed countries

vi. Which countries and organisations are involved in the contribution?

Possible partners include:
- Sequencing centre (e.g. US Department of Energy's Joint Genome Institute (JGI), Beijing Genomics Institute (BGI))

- Collaborators (e.g. GRA network members and partner organisations: http://www.rmgnetwork.org/, http://www.asggn.org/gra-livestock-research-group.html, http://www.methagene.eu/, http://eragas.eu/research-projects/rumenpredict, www.cgiar.org, https://ccafs.cgiar.org/)
- Governments (so far consulted: New Zealand, Australia, Canada, US, EU, France, Germany, UK).

vii.   How have stakeholders (for example local communities, youth and indigenous peoples, where applicable) been consulted in developing the contribution?

Representatives of the relevant scientific community has been consulted to prepare this draft proposal.

viii.   Where can the contribution be put into action?

The project is of global relevance.

ix.   How the contribution will be delivered? How will different stakeholders be engaged in its implementation? What are the potential transformational impacts?

Value for science. A comprehensive public resource that underpins the development of new mitigation tools and technologies but equally can help support the acceleration of the emerging microbiome-based mitigation technologies. A resource that can provide a complete overview of the global biodiversity of the rumen microbiome.

Relevance to many disciplines. The public resource can provide the underpinning knowledge to develop applications within or across animal and human microbiology, food production and safety, biofuel generation and the environment.

x.   Is this initiative contributing to other Climate Action Summit workstreams (industry transition; energy transition; climate finance and carbon pricing; infrastructure, cities and local action; resilience and adaptation; youth and citizen mobilization; social and political drivers; mitigation strategy)?

Rumen Gateway is also of relevance to the resilience and adaptation workstream.

xi.   How does this contribution build upon examples of experience to date? How does the contribution link with different ongoing initiatives?

The Rumen Gateway will build on previous work, as detailed below.

Global Rumen Census

The GRC[4] is the most extensive exploration of rumen microbial communities to date, representing 742 samples from 32 animal species from 35 countries, and supported by 140 scientists from 73 research institutions worldwide. A key finding of the GRC was that similar bacteria and archaea dominated in nearly all samples, and that diet is a key driver of microbial-community structure. This study identified the microbial groups in the rumens, without investigating function.

Hungate1000

Building on the results of the GRC, the Hungate1000 project[5] used the culture resources of multiple rumen microbiology laboratories around the world (57 researchers, from 14 research organizations in nine countries) to develop a reference set of 501 rumen-microbial genome sequences and cultures. The Hungate1000 has captured almost all cultured rumen bacterial and archaeal species that have been taxonomically characterized and several as-yet uncharacterized strains belonging to novel species and genera. It represents the single largest effort to provide a catalogued and curated culture and genome resource for rumen microbes to date. The Hungate1000 data is being used, not just by rumen microbial scientists but also by the wider scientific community. The genome data from one Hungate1000 culture, Lachnospiraceae bacterium ND2006 (LbCpf1) has been used to design an extremely effective CRISPR/Cpf1 system which can modify mammalian cells. This study initiated the investigation of function in cultured rumen microbes but could not capture the global diversity of the metabolic capacity of rumen microbial communities.

Deep sequencing of the high/low rumen microbiome

Researchers in New Zealand have demonstrated that it is possible to breed sheep that naturally produce less methane and have shown a ten per cent difference in methane produced between the average sheep in both the high and low methane breeding lines. To understand the microbial differences between these sheep a deep sequencing approach was applied to the rumen microbiome[6]. The results identified a discrete set of rumen methanogens whose methanogenesis pathway transcription profiles correlated with methane yields and provided new targets for methane mitigation at the levels of microbiota composition and transcriptional regulation which had not been known previously. They also demonstrated that the underlying basis for the different methane emissions were contrasting rumen fermentative communities[7]. This work was made possible by a strong collaboration with the US Department of Energy Joint Genome Institute and the GRA.

xii.   What are the mechanisms for funding (with specific emphasis on potential for partnerships)?

The Rumen Gateway can only be delivered through global collaborative partnerships.

National funding agencies combined with in-kind contributions from scientists all over the world will be required to deliver the project.

xiii.   What are the means of stewardship, metrics for monitoring?
TBC.

xiv.   What is the communication strategy?

TBC

xv.   What are the details of proponents (indicating the degree of commitment among the countries and organizations that are named)

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References

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