



# COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

## Item 9.2 of the Provisional Agenda

### Nineteenth Regular Session

Rome, 17–21 July 2023

## MICROORGANISMS RELEVANT TO RUMINANT DIGESTION

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## I. INTRODUCTION

1. The Commission on Genetic Resources for Food and Agriculture (Commission), at its Seventeenth Regular Session, adopted its Work Plan for the Sustainable Use and Conservation of Micro-organism and Invertebrate Genetic Resources for Food and Agriculture (Work Plan).<sup>1</sup> The Work Plan addresses microorganisms and invertebrates as functional groups and foresees that the two functional groups considered by the Commission at its Nineteenth Regular Session will be (i) soil microorganisms and invertebrates, with emphasis on bioremediation and nutrient cycling organisms<sup>2</sup> and (ii) microorganisms of relevance to ruminant digestion.
2. The Work Plan foresees that each functional group will be addressed on the basis of:
  - a summary of the status and trends of conservation, use and access and benefit-sharing, based on previous work of the Commission, existing literature and, as appropriate, an open survey that may also compile best practices with respect to their sustainable use and conservation;
  - a mapping of regional and international organizations and other institutions most relevant for the functional group and the identification of strategic areas of possible collaboration; and
  - an analysis of the gaps and needs, and possibilities for the Commission and its Members to address them.<sup>3</sup>
3. In response to the Work Plan, FAO commissioned Queen's University Belfast, United Kingdom of Great Britain and Northern Ireland, to prepare a study on the use and conservation of microorganisms relevant to ruminant digestion. The draft study, as revised in the light of comments received from Members of the Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture (Working Group), is contained in the document, *Draft study on the sustainable use and conservation of microorganisms of relevance for ruminant digestion*.<sup>4</sup> As requested by the Working Group,<sup>5</sup> the comments have been made available in the document *Submissions on the draft study on the sustainable use and conservation of microorganisms of relevance to ruminant digestion*<sup>6</sup> for the information of the Commission.
4. This document draws on the findings of the revised draft study to present an overview of the status of microorganisms of relevance to ruminant digestion and their management, and seeks the Commission's guidance on future work on this group of microorganisms.

## II. BACKGROUND

5. Ruminant livestock production is highly relevant to two of the most important challenges facing the world: improving the food security and nutrition of a growing world population and mitigating climate change. Ruminants can convert plant materials that because of their high fibre content are inedible to humans into edible foods that are rich in protein and micronutrients. However, the ruminant digestive system is a major source of the greenhouse gas methane. Microorganisms, particularly those that live in the rumen – the main compartment of the fore-stomach of ruminant animals – are key both to ruminants' digestive capacities and to their role as emitters of methane.
6. The rumen is a complex, dynamic ecosystem composed of anaerobic bacteria, protozoa, anaerobic fungi, methanogenic archaea and bacteriophages. Carbohydrates eaten by a ruminant animal are broken down by the microorganisms in its rumen, resulting in the production of various volatile fatty acids that are used by the animal as a source of energy. However, the process also produces hydrogen, which is used by the archaea present in the rumen to convert carbon dioxide into methane, which then passes out of the animal's mouth and into the atmosphere.

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<sup>1</sup> CGRFA-17/19/Report, *Appendix E*.

<sup>2</sup> See CGRFA-19/23/9.1; CGRFA-19/23/9.1/Inf.1.

<sup>3</sup> CGRFA-17/19/Report, *Appendix E*, paragraph 7.

<sup>4</sup> CGRFA-19/23/9.2/Inf.1.

<sup>5</sup> CGRFA-19/23/9.1, paragraph 28.

<sup>6</sup> CGRFA-19/23/9.2/Inf.2

7. The characteristics of the rumen microbiome (the assemblage or community of microorganisms within the rumen) affect the supply of nutrients to the animal and the amount of hydrogen available to the methanogenic archaea. This raises the possibility that manipulating the rumen biome could be a means both of improving animal nutrition and of reducing methane emissions. The need to understand the ecology of the rumen and the roles of rumen microorganisms has thus never been greater.

8. Previous work on microorganisms of relevance to ruminant digestion undertaken under the auspices of the Commission include the publication, in 2012, of Background Study Paper No. 61 *Microorganisms and ruminant digestion: state of knowledge, trends and future prospects* and, in 2019, of Section 5.8 “Rumen microbial diversity” of *The State of the World’s Biodiversity for Food and Agriculture*.<sup>7</sup>

### III. OVERVIEW, STATUS AND TRENDS

9. The rumen microbiome has been studied for many decades. Rumen **bacteria** are the most abundant and diverse group of rumen microorganisms and they perform a multitude of functions, including breaking down starch, cellulose, proteins and fats. Many are regarded as generalists (having a broad range of functions) and others as more specialist. Although there have been significant technological advances during the last decade, the functions of rumen bacteria and their interactions with the host and other members of the rumen microbiome are still poorly understood. The taxonomy of rumen bacteria remains a major challenge. Some bacterial taxa dominate numerically, but studies have shown that those present in smaller numbers can nonetheless have a major influence on the rumen ecosystem.

10. In recent years, sequencing-based approaches have provided insights into the functions of rumen bacteria and into the effects of factors such as host genetics, host diet and the use of feed additives. They are also key tools in the identification of bioactive substances within the rumen for potential use in the biotechnology industry. The ability to culture rumen bacteria has improved markedly in recent years.

11. Given their above-noted role in methanogenesis, the rumen **archaea** are a key target of rumen-microbial research. These organisms are strict anaerobes, and growing them outside the rumen is therefore challenging. Nonetheless, it is possible to culture them in the laboratory, and progress has been made in terms of improving knowledge of their taxonomy, the pathways through which they produce methane and their interactions with other types of rumen microorganisms, such as protozoa and fungi.

12. While bacteria are the most numerous group of rumen microorganisms, **protozoa** occupy the most space within the rumen (up to 50 percent). Rumen protozoa remain understudied because of the challenges involved in culturing them and because their complex genetic structure makes genomic studies difficult. Because of the latter issue, until recently, only one rumen protozoan (*Epidinium caudatum*) had had its genome sequenced. The function of the rumen protozoa remains somewhat controversial. Some of them are fibrolytic, while others utilize “simple” carbohydrates. These processes aid forage breakdown and improve the availability of nutrients to the host animal. However, protozoa are also linked to methanogenesis. Methane emissions from animals whose rumens have been defaunated (have had their protozoa removed by chemical means) have been found to be lower than those from animals whose rumens have not been defaunated. Defaunated animals are also more productive in terms of average daily weight gain or milk production. However, rumen protozoa vary substantially in their contributions to plant degradation and methane production, and thus total defaunation may not be the optimal strategy. Selectively removing particular types of protozoa from the rumen, however, remains challenging.

13. Anaerobic rumen **fungi** are potent fibre degraders thanks to their extensive repertoire of carbohydrate-degrading enzymes and their ability to physically penetrate plant cell walls. The latter

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<sup>7</sup> FAO. 2019. *The State of the World’s Biodiversity for Food and Agriculture*, J. Bélanger & D. Pilling (eds.). FAO Commission on Genetic Resources for Food and Agriculture Assessments. Rome. <https://doi.org/10.4060/CA3129EN>.

action benefits other rumen microbes by increasing the surface area available for colonization. The activity of anaerobic fungi is enhanced by methanogenic archaea, which are known to physically attach to anaerobic fungal biomass. It has been shown that anaerobic fungi can be used to improve feed intake, feed digestibility, feed efficiency, daily weight gain and milk production. However, they are not routinely studied despite the availability of suitable cultivation methods.

14. **Viruses**, including bacteriophages (viruses that use bacteria as their hosts), also form part of the rumen microbiome. Bacteriophages were isolated from the rumen as long ago as the 1960s. Some research on them was carried out during the 1970s and 1980s, but only those with potential biotechnological applications were further characterized and kept in culture collections. Recent years have seen some studies that have isolated additional bacteriophages and sequenced their genomes. It is known from other contexts that bacteriophages alter the ecology of microbiomes. However, little is known about their roles in the rumen.

15. Analysis of rumen microbiomes from different host species and different parts of the world has revealed that they are dominated by a core community of microorganisms. Variations are driven primarily by host diet, but they are also influenced by the species, breed and individual genetics of the host. The presence of geographically specific minor groups of rumen organisms is probably linked to climate-related variations in the plant material consumed or to the presence of locally adapted breeds of ruminants. It is likely that the microorganisms in such “minor” groups play important roles in allowing their hosts to cope with local environmental conditions and represent pools of genetic diversity that need to be maintained and might be further exploited.

16. The rumen microbiome is not static across the lifetime of the animal. Newly born calves are usually described as “preruminants”, and their digestive systems function in a manner more similar to those of young monogastric animals than those of adult ruminants. The transition from preruminant to ruminant occurs between four and eight weeks of age and is tightly linked to the colonization and establishment of an early-life microbiome. Evidence suggests that a core group of microbes establishes early on and persists until adulthood, although their numbers change over time. However, different studies have observed different microbial assemblages in early life. These differences may be caused by differences in management approaches. There is evidence that factors such as birthing method, preweaning feeding, weaning age, early-life diet and inoculation with rumen fluid can affect the early-life microbiome.

17. Trends towards the industrialization and homogenization of animal management practices globally mean that the risk of losing the localized diversity of rumen microorganisms is high. For instance, diet supplementation with easily digestible carbohydrates, as is common in more industrialized systems, has been observed to be associated with a simplification of the rumen microbial community, resulting in lower bacterial diversity and lower concentrations of fibrolytic microbes. Similarly, increased feed efficiency in ruminants (a key goal in ruminant agriculture given the need to sustainably feed a growing world population) has been linked to a reduction in the diversity of the rumen microbiome. Strategies involving the use of feed additives to reduce methane production from ruminants have been linked to alterations in ruminant microbiomes that may drive their further homogenization globally.

#### IV. CHARACTERIZATION AND CONSERVATION

18. The trends described at the end of the section above highlight the need to capture and catalogue communities of rumen microorganisms. The Hungate Collection,<sup>8</sup> a recent flagship project for the Global Research Alliance on Agricultural Greenhouse Gases (GRA), which provided 501 rumen bacterial and archaeal genomes, was a major step forward in this regard. However, the project has now ended because of a lack of funding, and many rumen microbial genomes remain unavailable. Certain bacterial taxa are underrepresented in the Hungate Collection relative to their representation in the Global Rumen Census dataset (a previous GRA flagship project) and genomes from so-called unculturable rumen bacteria and metagenomically assembled genomes are hugely underrepresented.

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<sup>8</sup> <https://genome.jgi.doe.gov/portal/HungateCollection/HungateCollection.info.html>

19. There have been significant technological advances in rumen science during the last decade, particularly with respect to “omic” technologies. However, while this has been useful in terms of correlating the rumen microbiome to the host phenotype, it has not resulted in major progress in terms of confirming the functions of particular microorganisms. Progress in this regard will require an enhanced catalogue of pure rumen microbial cultures.

20. Openly accessible culture collections, such as those of Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures<sup>9</sup> in Germany and the American Type Culture Collection<sup>10</sup> in the United States of America, are pivotal to the maintenance of global microbial genetic diversity and in ensuring open access for stakeholders. However, many isolates are not deposited in culture collections, as there is no legal obligation to do so. Concerns about intellectual property mean that many microbes that have potential commercial use remain in individual storage facilities even after patenting and publication.

21. There is a general lack of knowledge of rumen microorganisms associated with particular local areas, and very few of them are in culture.

## V. SUSTAINABLE USE

22. As noted above, effective management of the rumen microbiome can contribute to the mitigation of methane emissions from ruminant production systems. Changing the host animal’s diet is the easiest way to bring about an immediate change in the rumen microbiome and the amount of methane produced. Potential interventions include those that decrease emissions per unit of product and those that lead to absolute decreases in emissions. The former include increasing feeding levels, reducing the maturity and increasing the digestibility of the forage fed, and decreasing the ratio of forage to concentrate in the diet. The latter include supplementing the diet with methane inhibitors (e.g. 3-nitrooxypropanol [3-NOP, commercially known as Bovaer<sup>®</sup>], which inhibits the last step in rumen methanogenesis), tanniferous forages, electron sinks (chemicals or microbes that utilize hydrogen so that there is less available for methanogenesis), oils and fats, or oilseeds. While promising results have been obtained, the mechanisms through which many dietary approaches operate remain unclear.

23. The host genome has been shown to influence the rumen microbiome, and recent global data show the potential to breed ruminants with decreased methane emissions. Such an approach can potentially reduce methane emissions by up to 30 percent based on daily methane emissions (g/day), methane yield (g/kg of dry matter intake) and methane intensity (g/kg or litre of product produced). Again, further work is needed to confirm the potential of breeding low methane emitting ruminants and indeed to clarify the mechanisms underlying the effects observed.

24. In addition to its significance to climate change mitigation, the rumen microbiome (and the microbiome of the ruminant gastrointestinal tract more generally) is also significant to efforts to implement the One Health approach.<sup>11</sup> The interconnectedness of human, animal and environmental microbiomes has been demonstrated in many studies, and this underlines the need for an integrated approach to issues such as the spread of antimicrobial resistance. Rumen bacteria have antimicrobial resistance genes that can easily transfer to other bacteria. Rumen microbes also offer novel bioactive compounds that can be used to enhance human, animal and environmental health, for example in development of novel antimicrobials or in biorefining.

25. For many years antibiotics were used as growth promoters in animal feeds because of the benefits they can provide in terms of animal health and feed efficiency. With the banning of use of antibiotics as prophylactics and growth promoters in many countries, alternative approaches have

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<sup>9</sup> <https://www.dsmz.de/>

<sup>10</sup> <https://www.atcc.org/>

<sup>11</sup> “One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals, and ecosystems. It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and interdependent.” One Health High-Level Expert Panel (OHHLEP), Adisasmito, W.B., Almuhairi, S., Behravesh, C.B., Bilivogui, P., Bukachi, S.A. *et al.* 2022. One Health: A new definition for a sustainable and healthy future. *PLoS Pathogens*, 18(6): e1010537. <https://doi.org/10.1371/journal.ppat.1010537>

risen to prominence, including the use of direct-fed microbials (sources of live naturally existing microorganisms). While the use of this approach in ruminants is still under development, it has been linked with improvements in the health of young animals, increased milk production and enhanced growth, suggesting that it may be a viable alternative to the use of antimicrobials.

## VI. POLICY, LEGAL AND INSTITUTIONAL FRAMEWORKS

26. Policy and legal frameworks of relevance to the management of rumen microorganisms include those related to climate change, those related to the conservation, use and exchange of biodiversity for food and agriculture, those related to food and feed safety, and those related to marketing.

27. Climate-related policies are increasingly influencing the availability of funding for work on rumen microorganisms, with many funders prioritizing efforts to optimize the rumen microbiome to achieve reductions in methane emissions. However, regulatory frameworks can act as a barrier to the adoption of such technologies because of the time required to obtain approval for their release. Labelling of products as having been produced with reduced methane emissions is often a grey area in regulatory terms. Where consumers are unable or unwilling to bear the costs of such innovations via increased market prices, there may be a need for governmental intervention to support them or make their introduction mandatory. The cost implications of policies for the approval and use of feed additives may be a deterrent in some countries. Strategies such as promoting the use of legumes and tanninous forages as animal feed may be less costly alternatives but have less impact on emissions.

28. The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity (Nagoya Protocol) has increased the level of bureaucracy involved in the exchange of ruminant microorganisms and this has raised concerns among those involved in their use and conservation globally.

29. Most funding agencies and journals have an open-access policy that ensures that when articles are submitted for review, all the data on which they are based must have been made publicly available. However, publications involving research on novel microbial isolates do not have to ensure open access to the isolate through deposition in a culture collection before publication. This means that open-access sharing of isolates for continued research and societal benefits is limited. This is a major challenge, and changes are needed. However, it also needs to be noted that such changes will require enhanced infrastructure for existing culture collections to enable the organizations responsible for them to maintain and make available the increased number of isolates.

30. Key institutions and networks related to the conservation and sustainable use of microorganisms of relevance to ruminant digestion include the culture collections discussed in Section IV, the GRA (also discussed in Section IV), the GRA's Livestock Research Group and Rumen Microbial Genomics Network, and a number of universities and research institutes around the world that have major capacity to isolate and maintain ruminant microbes and have their own collections. The private sector probably also holds collections, but details of these are not publicly available. In addition to the GRA projects mentioned above, a number of other major projects promote stakeholder collaboration internationally, including the EU Horizon 2020 projects MASTER (Microbiome Applications for Sustainable food systems through Technologies and EnteRprise)<sup>12</sup> and Holoruminant.<sup>13</sup> Some stakeholders from developing countries report that a lack of funding is a constraint to their participation in collaborative activities.

## VII. GAPS, NEEDS AND POTENTIAL ACTIONS

31. Based on a review of the literature and responses to an informal questionnaire sent to members of the Rumen Microbial Genomics Network of the GRA, the following gaps and needs can be highlighted:

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<sup>12</sup> <https://www.master-h2020.eu/>

<sup>13</sup> <https://holoruminant.eu/>

- *Research.* Much still needs to be done to improve knowledge of the rumen microbiome and its functions. Priorities include improving techniques for culturing rumen microorganisms and exploring the potential for using isolates as direct-fed microbials to reduce methane emissions.
- *Culture collections.* There is a need for journals to insist that microorganisms used in the research they publish are deposited in open-access culture collections. The capacity of culture collections needs to be improved, so that they can accommodate the additional deposits.
- *Policy frameworks.* Relevant policies, legislation and institutional arrangements, including those related to access and benefit-sharing and to intellectual property, need to be reviewed, and where necessary updated, with a view to ensuring an appropriate enabling framework for research and collaboration on rumen microorganisms and their management. There is also a need to put in place policies that will promote the uptake of innovations emanating from research in this field that can help reduce methane emissions.

32. The following actions could be taken to improve the sustainable use and conservation of rumen microorganisms at global and national levels, including potentially by the Commission and its Members:

- establishing a global expert group to work on the prioritization of activities related to the management of microorganisms of relevance to ruminant digestion and on the identification of threats to the sustainable use and conservation of these organisms;
- ensuring adequate resourcing for global research initiatives related to the culture, cataloguing, characterization and management of rumen microorganisms;
- promoting policies that ensure that all pure culture microbial isolates are deposited in open-access culture collections prior to the publication of any data related to the respective organism(s);
- enhancing the capacity of the organizations managing publicly accessible culture collections so that they are able to deal with the increased demand that a policy requiring isolate deposition would bring;
- promoting the funding of research on the management of the rumen microbiome, particularly with respect to ruminant breeding and dietary innovations;
- promoting policy and legal innovations that facilitate the exchange of rumen microbial samples globally; and
- providing stimulus to encourage global collaboration, especially collaboration involving low- and middle-income countries.

## VIII. GUIDANCE SOUGHT

33. The Commission may wish to:

- (i) take note of and provide comments on the draft study;
- (ii) recommend that the study be finalized and disseminated;
- (iii) consider how it can respond to the findings and recommendations of the study and what follow-up actions are needed to ensure that the Commission and its Members continue to strengthen their work on microorganisms of relevance to ruminant digestion;
- (iv) recommend that FAO take the findings of the study into consideration in its work relevant to the sustainable use and conservation of microorganisms of relevance to ruminant digestion, as appropriate;
- (v) invite Members to promote the sustainable use and conservation of microorganisms of relevance to ruminant digestion and ensure they are given due consideration in local, national, regional and international policies and policy-development processes;
- (vi) invite Members to manage and conserve the genetic diversity contained in local breeds, feeds and rumen microbes in an integrated manner;
- (vii) encourage relevant stakeholders, including scientific institutions, to collaborate on the sustainable use and conservation of microorganisms of relevance to ruminant digestion,

especially on capacity development in developing countries and countries with economies in transition;

- (viii) invite Members and stakeholders to intensify research on rumen microbiome management, in particular in relation to ruminant breeding and husbandry, production efficiency, disease resistance and resilience to changing environmental conditions as well as on the potential effects of relevant microorganisms on animal and human health, but also on feed innovations for climate mitigation; and
- (ix) request the Secretariat to collaborate with relevant experts in the drafting of specific recommendations on microorganisms of relevance to ruminant digestion for further consideration by the Commission at its next Session.