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COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

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INTERGOVERNMENTAL TECHNICAL WORKING GROUP ON ANIMAL GENETIC RESOURCES FOR FOOD AND AGRICULTURE

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STATUS AND TRENDS OF MICRO-ORGANISMS FOR RUMINANT DIGESTION

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STATUS AND TRENDS OF MICRO-ORGANISMS FOR RUMINANT DIGESTION

I. INTRODUCTION

1. At its Twelfth Regular Session, the Commission on Genetic Resources for Food and Agriculture (the Commission) emphasized the need for assessing the status and trends of micro-organisms relevant to food and agriculture. In this context, it requested the Commission Secretariat to prepare for consideration at its Fourteenth Regular Session further analyses and studies on status and trends of micro-organisms, including for ruminant digestion, agro-industrial processes and food processing.¹
2. At its Thirteenth Regular Session, the Commission reiterated the need to continue to advance this work in collaboration with relevant international organizations and scientific institutions and it also requested its Intergovernmental Technical Working Groups to review the relevant assessments within their fields of expertise.²
3. This document introduces and provides a brief summary of the study, *Micro-organisms and ruminant digestion: state of knowledge, trends and future prospects*. The complete version of the study is available as Background Study Paper.³
4. The study provides a historical account of the progress that has been made in rumen microbiology research and gives an overview of the current understanding of the rumen microbial ecosystem. It also addresses the opportunity new DNA sequencing technologies provide for improving productivity of livestock and the impacts of livestock production systems on the environment.

II. MICRO-ORGANISMS AND RUMINANT DIGESTION: STATE OF KNOWLEDGE AND TRENDS

5. During the last decade, an increase in the human population, decrease in arable land due to soil degradation, urbanization, industrialization, and associated increase in the demand for livestock products has brought about dramatic changes in the global ruminant livestock sector (cattle, sheep, goats, buffalos, camels and yak). These changes include a shift in the size of regional livestock populations and in the types of management and feeding systems under which ruminant livestock are held. There will be increased demand of a wider range of quality attributes from animal agriculture, not just of the products themselves but also of the methods used in their production. The livestock sector will therefore need to respond to new challenges of increasing livestock productivity while protecting the environment and human health and ensuring the conservation and sustainable use of natural resources, including of all the components of biodiversity for food and agriculture.
6. The importance of rumen microbial ecology and diversity of microorganisms in the ruminant forestomach has gained increasing attention in response to recent trends in global livestock production. The microorganisms in the digestive tracts of ruminant livestock have a profound influence on the conversion of feed into end-products which can impact on the animal and the environment. As the livestock sector grows in numbers and productivity, particularly in developing countries there will be an increasing need to understand these processes for better management and use of both the feed-base and other natural resources that underpin the development of sustainable feeding systems.
7. Until recently, knowledge of ruminant gut microbiology was primarily obtained using classical culture based techniques which probably only account for 10 to 20% of the rumen microbial

¹ CGRFA-12/09/Report, paragraph 60.

² CGRFA-13/11/Report, paragraph 91.

³ CGRFA Background Study Paper No. 61: *Micro-organisms and ruminant digestion: state of knowledge, trends and future prospects*.

population. The gut microbiota and its collective genomes (termed the microbiome) is estimated to contain 100 times more genes than the host animal and provides the ruminant with genetic and metabolic capabilities that the host has not had to evolve on its own, including capabilities to hydrolyze and ferment inaccessible nutrients and toxins. Such processes require the involvement of diverse rumen microbes that have been redefined into three domains, i.e. bacteria (eubacteria), archaea (methanogens) and eucarya (ciliate protozoa and anaerobic rumen fungi).

8. Advances in molecular microbial ecology based on 16r RNA gene (*rrn*) phylogeny have enabled the identification and quantification of the normal microbiota in the rumen. This system of microbial classification coupled with deep sequencing of DNA from the rumen has revealed the presence of complex communities that have co-evolved with the ruminant host in response to the environmental conditions (feedbase etc) and gut physiology of the animal. While there are differences in gut microbial communities between animal species and breeds⁴ there is also new evidence that the bacterial microbiome and metabolic potentials in the rumen are different between animals of the same breed when fed the same diet and viewed in relation to nutrient utilization.

9. Based on the analysis of global data sets available in public databases, the majority (>90%) of rumen archaea are affiliated with genera; *Methanobrevibacter* (> 60%), *Methanomicrobium* (~ 15%), and a group of uncultured rumen archaea commonly referred to as rumen cluster C (RCC, ~16%) or Thermoplasmatales-Affiliated Lineage (TALC) which are of unknown function. Metagenomic approaches recently enabled to reconstruct the genome of RCC methanogens from a mixed culture without the need to isolate the organism. This revealed a novel metabolic activity by which the RCC methanogens produce greater amounts of methane relative to the autotrophic *Methanobrevibacter*.

10. Importantly, the RCC methanogens were the predominant population in several ruminant species, like for example yak, cattle and sheep, raised in a unique agro-economical region of central China. The methanogen population in these animals were more similar to each other compared with the structure expected in ruminants on conventional production diets in industrialized countries. This provides further evidence of the interplay between the environmental conditions and physiology of the animal which governs the acquisition, colonization and ultimate structure of the microbiome in the mature animal. The composition of the methanogen population in the maturing rumen is of significance to the amount of methane (greenhouse gas) emitted since some methanogens produce more methane depending on the metabolic pathway that is encoded by their genome. Therefore environmental conditions may dictate the populations of methanogens that are acquired at birth which imprint the structure of the methanogen community in the mature animal and hence methane producing potential.

11. Furthermore it is also evident that there is genetic diversity within rumen bacterial species of practical and economic importance. For example, studies are demonstrating that the rumen bacterium *Synergistes jonesii*, which detoxifies forage from the economically important leucaena tree legume, is genetically diverse based on geographic region. This bacterium was introduced from overseas ruminants into Australian cattle because they lacked the bacterium and were susceptible to intoxication to mimosine present in leucaena. The genetic diversity resident in this species provides further opportunity to introduce more potent detoxifying strains into ruminants in regions dependent upon leucaena production systems for sustainable production.

III. FUTURE POSSIBLE RESEARCH AND INNOVATIONS

12. Major innovations in the field such as metagenomics have arisen in the last decade with the advent of affordable nucleic-acid based-technologies and rapid evolution of DNA sequencing platforms that are culture independent for studying diversity of complex microbial ecosystems. These technologies have the potential to capture and study the entire microbiome (the predominant genomes)

⁴Recent data from Asian breeds of cattle show a distinctive rumen bacterial community compared with Holstein cattle, supporting the notion of host genotype as an important factor shaping the composition.

from the complex microbial community in the rumen and to determine function (“what they are doing”) in addition to structure (“who’s there”) of the community.

13. Rapid advances in the development of publically available annotation tools and computing platforms for assigning function to genes has also made the genome-sequencing of individual microorganisms and interpretation both affordable and available to the broader research community. This has led to an increase in the number of rumen microorganisms (>20) that have sequenced genomes which are publically available, but there is little information available on the genomic make-up of rumen anaerobic fungi and ciliate protozoa and no genomes from these organisms have been published.

14. To address these issues, a Rumen Microbial Genomics (RMG) Network has been formed comprising a consortium of advanced rumen microbiology laboratories, large publicly funded DNA sequencing institutions and curators of international public culture collections. The consortium will facilitate the sequencing and development of rumen microbial genomics approaches for access to methods, genome sequences and metagenome data relevant to the rumen microbial community. The reference genome information of more than 1000 rumen microbial isolates will establish a publicly accessible catalogue (database) of rumen microbial genes and assign function to these genes as a framework for characterizing the rumen microbiome in different ruminant genotypes and under varying dietary and environmental conditions. This information will be used to support international efforts to initiate genome-enabled research aimed at understanding rumen function in order to find a balance between food production and green house gas emissions. It is possible that this reference collection will be biased towards micro-organisms from ruminants in industrialized production systems unless a coordinated effort is initiated to engage laboratories from countries and regions where the animals have evolved and adapted to natural environment, particularly in tropical regions.

15. An opportunity exists for ruminant laboratories in emerging and developing countries to provide DNA from rumen samples and cultures of rumen isolates from local adapted breeds as contributions to this catalogue which will then represent a broader geographical census of micro-organisms that are relevant to many agro-economic zones and environment conditions. In addition, nutrition laboratories in developing countries with an interest in rumen microbiology would benefit from future interactions with the advanced labs, where local scientists are advised and trained in the latest techniques in molecular microbial ecology.

IV. GUIDANCE SOUGHT

16. The Working Group may wish to recommend to the Commission to:

- Welcome the study, *Micro-organisms and ruminant digestion: state of knowledge, trends and future prospects*, and to emphasize the importance of rumen microbial diversity in the light of breed and dietary diversity and of global livestock production and environmental and health related challenges;
- Request FAO to report on relevant developments in this field at its Fifteenth Regular Session, when it will review the work of the Intergovernmental Technical Working Groups on the application and integration of biotechnologies for the conservation and sustainable utilization of genetic resources for food and agriculture; and
- Request FAO to continue to monitor and report on developments in this field, possibly by addressing this issue in The Second Report of the State of the World’s Animal Genetic Resources for Food and Agriculture or in The State of the World’s Biodiversity for Food and Agriculture.