

Summary Report

WDCM Training Course for Microbiome Data Sharing

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Contents

- Personal Information
 - Abstract
 - Key words
1. Brief introduction of your Culture Collection.
 2. Benefit from the training courses.
 3. Suggestion on WDCM work.
 4. Comments or suggestion on the training courses.
 5. Suggestion on further cooperation between WDCM and your collections

BAMIPA: An alternative for animal production and livestock development.

Personal Information

My name is Laura Colomina Alfaro, I am bachelor in Biochemistry and Molecular Biology from University of Havana, 2016. Currently I am working in the Institute of Animal Science of the Republic of Cuba, where I am member of the Biophysiological Science Department, specifically in the Microbiology Group. As Researcher, I am carrying out studies in the fields of digestive physiology of ruminant and non-ruminant animals, microbiology of the gut of these animals and food production.

Bank of Microorganisms of interest for Animal Production. BAMIPA

ABSTRACT

Animal feed is one of the worries in tropical countries due to the lack of raw materials and its high costs. The Institute of Animal Science of the Republic of Cuba have been working in the fields of animal and food production for several years. The production of food and additives by biotechnology is one of the most novel alternatives for food production, and by this way, microorganisms are used as active ingredients or products derived from them. For this reason, we have a collection of

microorganisms isolated from the gut of ruminant and non-ruminant animals and we joined to WDCM in 2015. At moment, we want to characterize buffalo's microbiome and transfer this microbiome to bovine cattle. Also, we are working in isolation of microorganisms from other habitats that may contribute to animal production or other productive areas and incorporate these microorganisms into BAMIPA. The WDCM Training on Microbiome Data Sharing enhances to understanding the WDCM, opportunities existing in the World of Microbiology research, Culture Collection activities and the current state of the research in this field.

Key words: animal production, microbiome, acid-lactic bacteria, yeast, buffaloes, lignocellulolytic enzymes, WDCM

1. Brief introduction of your Culture Collection.

Animal feed is one of the worries not only in Cuba but also at the international level due to the lack of raw materials and its high costs. For this reason, many alternatives are sought and within these one of the most novel is the production of food and additives by biotechnology, where microorganisms are used as active ingredients or products derived from them. Thus, the isolation, identification, characterization and conservation of these microorganisms become fundamental links.

Our research group has been developing, since 2013, the project:

Promotion of a bank of microorganisms to produce food and food additives intended for animal production. The objective is to isolate, identify and preserve microorganisms from the gastrointestinal tract of animals of productive interest.

The development of this project has allowed to have different collections of microorganisms with strong potential for animal feeding. At present, we have a collection of microorganisms isolated from the tract of chickens and ruminal fluid (28 microorganisms between yeasts and lactic acid bacteria).

This collection of microorganisms (BAMIPA, initials in Spanish for Bank of Microorganisms for Animal Production) also has among its goals to provide authentic and viable microorganisms for the development of other research projects or for technological applications, the obtaining of agricultural products, as well as their use in other productive spheres. It also facilitates the exchange of microorganisms between national and international institutions and contributes to teaching with the training of other specialists in the management of collections of microorganisms and in the activities that derive from them. In 2015, our collection of microorganisms joined to WDCM.

In our laboratory we have only used the molecular tools for the identification of these microorganisms. We have the registration of the DNA sequences of some of them. They were carried out in

collaboration with other foreign institutions and were registered at Genbank database (Tables 1 and 2). At present, our institute is evaluating the potential use of some of these microorganisms as probiotics.

Table 1. Molecular identification of acid-lactic bacteria and yeasts isolated from the gut of chickens.

Strain number	Other collection number	Molecular Identification	Genbank accession number
ICA1	LB-12	<i>Pediococcus pentosaceus</i>	FR717460
ICA2	LB-13	<i>Weisella cibaria</i>	FR717461
ICA3	LB-17	<i>Enterococcus hirae</i>	FR717462
ICA4	LB-25	<i>Pediococcus pentosaceus</i>	FR717465
ICA5	LB-27	<i>Enterococcus hirae</i>	FR717463
ICA6	LB-28	<i>Enterococcus hirae</i>	FR717466
ICA7	LB-29	<i>Lactobacillus crispatus</i>	FR717467
ICA8	LB-31	<i>Lactobacillus pentosus</i>	FR717464
ICA9	LB-33	<i>Enterococcus hirae</i>	FR717468
ICA10	LV-2	<i>Trichosporon sp.</i>	FR717637
ICA11	LV3=LV-4	<i>Trichosporon asahii</i>	FR717638
ICA12	LV-6=LV-7	<i>Wickerhamomyces anomalus</i>	FR717639
ICA13	LV-8	<i>Pichia kudriavzevii</i>	FR717640
ICA14	LV-9	<i>Kodamaea ohmeri</i>	FR717641
ICA15	LV-10=LV-11	<i>Trichosporon asahii</i>	FR717642

Table 2. Molecular identification of yeast isolated from ruminal fluid.

Strain number	Other collection number	Molecular Identification	Genbank accession number
ICA16	23	<i>Issatchenkia orientalis</i>	JF894138
ICA17	24	<i>Issatchenkia orientalis</i>	JF894147
ICA18	29	<i>Issatchenkia orientalis</i>	JF894140
ICA19	33	<i>Issatchenkia orientalis</i>	JF894146
ICA20	13	<i>Pichia guillermondii</i>	JF894136
ICA21	15	<i>Pichia guillermondii</i>	JF894141
ICA22	17	<i>Pichia guillermondii</i>	JF894137
ICA23	22	<i>Pichia guillermondii</i>	JF894139
ICA24	27	<i>Pichia guillermondii</i>	JF894143
ICA25	28	<i>Pichia guillermondii</i>	JF894145
ICA26	32	<i>Pichia guillermondii</i>	JF894142
ICA27	25	<i>Candida Tropicalis</i>	JF894135
ICA28	18R	<i>Rhodotorula mucilaginosa</i>	JF894148

2. Benefit from the training courses.

Knowledge and tools that I acquired in this training course of MICROBIOME will be very useful for our laboratory to achieve all its goals in the fields of identification, characterization and preservation of

microorganism isolated from the gut of animals of productive interest. It also allowed us to exchange with other professionals who work on the topic of collections of microorganism and know about their research projects. This training provided complete information related to bacteria, fungi and database development. The professors gave us a lot of information related to general application policies for international student and collaborations, and they showed us the current state of the research about microbiome, opportunities existing in the World of Microbiology research and Culture Collection activities.

3. Suggestion on WDCM work.

The work of WDCM is impressive and admirable. I am very glad to participate in this training and to know about its work, this is an important experience for me and my institute.

4. Comments or suggestion on the training courses.

I think the WDCM training Course for Microbiome Data Sharing was very interesting and I just want to suggest something related to the database practices, and it is that to do some practices we need to have some additional materials or be registered on some websites. I think we need know about this before coming to the training to bring the necessary information and be registered on the websites that we will use and so have a good database practice.

5. Suggestion on further cooperation between WDCM and your

collections.

The buffaloes are ruminant animals with productive and reproductive indicators higher than those of the bovine cattle because they have more rusticity, longevity and capacity to convert the fiber of the vegetables into meat and work. In the American tropics, it has been reported that Buffaloes have a higher conversion of dietary nitrogen in rumen protein and a better use of fiber, compared with other ruminant species. They produce a higher concentration of AGV and usually have higher ruminal pH than bovine cattle fed with equal diets.

This specie was introduced in Cuba in 1983 and now, our research group is interested in elaborate research projects that allow us to characterize the microbiome in the buffalo rumen and to compare it with the bovine cattle. By this way, we would contribute to elucidate the superiority that the buffalo has for use the fibrous materials and we would use this superiority to improve bovine cattle performance. The sequencing of the genes of microorganisms responsible for the degradation of the fiber will allow the identification of the genes that give the microorganism this superiority and thus we would insert these genes, by recombinant technology, in other microorganisms that do not have this capacity and thus to enhance the degradation of the fiber in the rumen or we would inoculate directly the microorganisms into the rumen (by catheter or direct puncture in the rumen) of bovine cattle just before de birth and

monitor the microbiome until the calf became in adult.

We want to establish alliances with other groups of researchers working in the microbiology of the rumen to create a database of DNA sequences of rumen microorganisms that allows to deepen their genes and their functions, in addition to facilitating the work of researchers working this topic.

Microorganisms identified and characterized would be use as microbial additives (probiotics and microorganisms activating the ruminal fermentation) for animal feeding and by this way contribute to improved health and greater use of food, which allows to increase productive yields and consequently, the availability of milk, meat and eggs for human feeding.

Others future projections include isolating, characterizing, identifying and preserving microorganisms from other habitats that may contribute to animal production or other productive areas and incorporate these microorganisms into BAMIPA. We have in execution a new project that has as main objective the obtaining and evaluation of an enzymatic product with fibrolytic activity for the cattle sector and the bioindustry. The production of fibrolytic enzymatic extracts for other industrial sectors, would also ensure benefits, in the quality of products obtained in the textiles, paper, leather and pharmaceutical industry and for food production. We want to stablish alliances with others research teams to

carry on the molecular identification and characterization of the strains isolated.