RUMINANT HOLOGENOME- CHARACTERIZATION OF MICROORGANISM POPULATIONS IN RUMINANTS'DIGESTIVE TRACT AND THEIR IMPACT ON THE HOST'S FUNCTIONAL GENOME, PERFORMANCE, PRODUCT QUALITY AND ENVIRONMENTAL IMPACT

Luciana Correia de Almeida Regitano[1]; Priscila Neubern de Oliveira[2]; Bruno Gabriel de Andrade[2]

1 Empresa Brasileira de Pesquisa Agropecuária – Pecuária Sudeste. 2 Bolsista de Pós-Doutorado FAPESP

The Hologenome is an evolutionary concept where both the host and its associated microorganisms (microbiota) form a cohesive biological entity known as holobiont, whose interaction affects the development and general fitness of the hologenome, considered an independent level of selection, In ruminants, microbial fermentation in the rumen produces methane as a by-product, a greenhouse gas with a high environmental impact. Since feed efficiency is one of the biggest costs of beef production and inversely proportional to the production of methane, the improvement of this characteristic has the potential not only to reduce the cost of production, but also to reduce the territorial expansion of production areas and methane emissions. Reducing production costs and improving product quality while mitigating environmental impacts are key factors in conquering new markets for Brazilian beef.

In a previous project financed by FAPESP, we produced structural and functional genomic data in a reference population of the Nellore breed, thus revealing the main players in the regulation of gene expression and how this expression relates to biological processes relevant to quality characteristics of the beef and feed efficiency in animals raised in confinement.

We are currently dedicating ourselves to data analysis to further integrate the different levels of genomic and phenotypic information, investigating genetic variations that explain the differences observed in gene expression.

In addition to the host's functional genome, we will investigate the profile of microorganisms and rumen metabolites in a new sample of Nellore cattle, raised on pasture and finished in confinement, contrasting animals fed with a traditional diet and those with a by-product diet, the latter aiming at alternatives that reduce environmental impacts.

Adding information regarding microbiota in the host's functional genomics data will answer crucial questions about the relationship between the microbiota's functional diversity and the host environment, also contribute to the design of selection and management strategies aimed at the efficient production of higher quality beef. This information can assist in the estimation of the breed's genetic value for these traits, contributing to improve the reliability of genetic evaluations in breeding programs.

RESULTS

So far. we have identified genes and regulatory elements (miRNA molecules. regions of DNA) that contribute to variations in feed efficiency and to the quality of Nellore carcass and meat, including characteristics that are not normally evaluated in breeding programs. such as tenderness, fat composition and the amount of minerals in the meat (Table 1). We also relate the level of expression of thousands of genes to the various performance and product quality characteristics.

NEXT STEPS AND RECOMMENDATIONS

For this body of information about the functioning of the genes to discriminate the best animals in the breeding routine to be useful, we still need to find the DNA variations that cause a gene to be more or less expressive, which is why we are reassessing the data, integrating the information of DNA, RNA, miRNA and proteins with the production measurements of each animal. In addition, we are investigating the relation between the individual microbiota and metabolite profile with the same measurements (feed efficiency. carcass. and beef quality). in order to develop methods to identify animals that produce better and more efficiently. Another purpose is to provide the knowledge bases for the development of methods that aim to control the composition of the microbiota. aiming at improving animal performance.

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Continued in Annex

PROJECT COORDINATORS

Dra. Luciana Correia de Almeida Regitano

Empresa Brasileira de Pesquisa Agropecuária – Pecuária Sudeste.

e-mail: luciana.regitano@embrapa.br.

Table 1: Genome regions in which DNA base variations (Single Nucleotide Polymorphism – SNP) were associated with feed efficiency traits in Nellore cattle. The candidate genes column describes the genes found in the region associated with food efficiency characteristics.

Characteristics	SNP window	No. of SNPs in window	Explained % variability	Cr.	Candidate genes
CAR	rs132846819-rs136767848	217	1.50	8	
	rs109535395-rs134508640	50	1.42	18	DEPP1. TUBB3
	rs109365529-rs132654030	186	1.12	11	PTGS1
	rs136295413-rs41980878	260	1.12	21	-
CMS	rs133031353-rs42739324	237	3.76	24	HRH4. ZNF521
	rs134105133-rs133615999	161	2.00	13	-
	rs133460769-rs109902312	255	1.29	9	-
CA	rs110424374-rs133308150	73	6.06	12	-
	rs41942246-rs134122046	191	5.99	20	GDNF
	rs42594525-rs109404921	182	1.52	15	LIN7C
	rs109105703 -rs136356118	189	1.40	18	-
EA	rs133645581-rs137479730	231	2.58	9	-
	rs134914044-rs42277860	203	2.30	1	-
	rs136028559-rs110570158	250	1.04	14	-
	rs109171156-rs42987702	255	1.03	2	-

Caption: Residual Food Consumption (CAR). Food Conversion (AC). Dry Matter Intake (DMI). Average Daily Gain (ADG) and Food Efficiency (EA).

(Source: Own authorship).