Ph.D. course: FOOD SCIENCE

Project Title: Ruminant milk's nutraceutical qualities and the genetic component responsible for their synthesis

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Objectives of the research project and interdisciplinary collaborations (max 200 words):
Milk is a complex mixture of lipids, carbohydrates, proteins, and smaller metabolites and thus it is a complete food able to provide nutritional subsistence of infants, healthy growth of children and nourishment of adult humans. Then milk contains a plethora of components that encode functional health benefits to consumers. Considering the increasing demand for healthy products, it is necessary to develop strategies that aim to increase the consumption of functional foods in order to meet the consumer market. Carbohydrates are one of the most predominant solid fractions of milk and besides the main milk sugar, lactose, a number of more complex free oligosaccharides (OS) is also present in milk at lower abundance. Comprehensive studies on human milk OS have elucidated a wide range of beneficial actions of milk OS on improving health. Oligosaccharides exhibit many specific biological functions, they are prebiotics, immune modulators, and pathogen inhibitors and they improve barrier function in the gut. Sialic acids (Sias) include a wide family of monosaccharides with a nine-carbon backbone usually linked, in the terminal position of the carbon chain, to glycoproteins. The most common and abundant Sias in mammalians are the N-acetylneuraminic acid (Neu5Ac) and N-glycolylneuraminic acid (Neu5Gc). They differ by only one hydroxyl group and Neu5Ac which is converted to Neu5Gc by cytidine- 5'-monophosphate-N-acetylneuraminic acid hydroxylase (CMAH). Humans are unable to synthetize Neu5Gc, the small amounts of it, detected in human tissues, either normal (epithelial and endothelial) or malignant (ovarian, breast, colon, and others) lead to the hypothesis of exogenous sources, particularly from food rich in Neu5Gc (Figure 1). The presence of exogenous Neu5Gc in human cells potentially contributes to pathologies associated with chronic inflammation.
Oligosaccharides and sialic acids have been determined in human and other mammals' milk. Research in the field of food science is interested in examining these components in milk that is destined for human consumption, such as those from cows, goats, donkeys, etc.
Due to the beneficial effects of milk OS, and the inflammatory effect of milk Sias, it's important to develop the means to control the concentrations of these nutraceutical compounds in ruminant milk. One of these methods is represented by genomic and transcriptome studies that help us understand the collection of genes that code for OS and Sias. GWAS studies have been performed on cattle and goats of various breeds to identify SNPs associated to milk oligosaccharides and sialic acids contents Transcriptome analyses were also carried out in goats and cattle at various stages of lactation to identify genes that were differently expressed in relation to milk oligosaccharides and sialic acids contents.
Investigating these nutraceutical molecules in buffalo milk is extremely intriguing considering not much is understood about them. In addition, although there are many studies about the effect that the consumption of probiotics has on chronic health conditions, there is hardly any research about probiotics from buffalo milk.
The aim of this work is evaluated buffalo milk prebiotic and probiotic characteristics and its products so to promote commercially feasible applications of buffalo milk
as a functional food to health-related problems.
We propose to

1) Analyze contents of oligosaccharides and sialic acids in buffalo milk and its products
2) Transcriptomic and genomic studies of candidate genes for these molecules
3) Metagenomic study of buffalo milk to determine probiotic microorganisms

Innovation and originality of the project in relation to the state of the art

Although research into the function of the compounds under investigation has moved forward with the development of in vivo and in vitro models, little is known about the genes that synthesize the enzymes responsible for their biosynthesis. Oligosaccharide synthesis is genetically controlled by glycosyltransferase expression and the availability of the sugar nucleotide substrate, but the regulatory mechanisms regulating their expression are unexplored. Some of these genes annotated in the reference species can be found in genetic data databases (Ensemble, NCBI), but no polymorphisms or splice variants associated with the phenotypes of interest have yet been identified, which could be used for selection and other purposes. There are no researches on the CMAH gene in ruminant species in the scientific literature.

Grant availability:

University and Research Ministry, "AGRITECH", National Research Centre for Agricultural Technologies, spoke 1 "Plant, animal and microbial genetic resources and adaptation to climatic changes", WP1 "Plant, animal and microbial genetic resources: mining for resilience" (September 2022-September 2025)

European Project, CE, HORIZON-CL6-2023-FARM2FORK-01-2, Co-funded European Partnership- Animal Health and Welfare (EUP_AHW), proposal n°101136346, WP3 Internal Actions (January 2024-December 2030)

Collaborations with foreign institutions:

Collaboration with international institutes aims to address difficulties and topics that cannot be carried out at CREA, including:

- In vitro bioactivity tests of OS and Sias
- Recovery from dairy industry by-products
- Microencapsulation technologies