

Biomarkers or Proteomics in milk

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EDITORIAL

Proteomics

Milk is a complex fluid with a proteome that includes highabundance caseins and medium- to low-abundance whey proteins such ß-lacto-globulin, lacto-ferrin, immunoglobulin, glycoproteins, peptide hormones, and enzymes, among others. In order to accurately detect proteins present or proteins responding to factors such as nutrition, health, or genetics, a sample preparation process with high reproducibility and throughput is required. Proteomics is a branch of biology that arose as a result of the human genome's discovery. This statement was first coined in the mid-1990s in response to a requirement for a precise vocabulary to characterise the work being done at the time, which was proteome research. This research looks at all of the proteins in a single cell, including all of their isoforms and alterations, as well as their relationships, structure, and higher-order complexes. Proteomics early efforts were concentrated in the realm of medicine, where significant advancements in illness diagnosis were made.

Milk is a fluid that contains several low-abundance proteins (5 percent of the total protein fraction), which are found in the whey or the membrane of the milk fat globule (MGMF). Milk can be defined as the liquid excreted by mammals' mammary glands in order to feed their new-borns. Milk, on the other hand, has long been regarded as a significant resource by humans due to its nutritional composition and ease of access. Milk's significance has shifted as a result of this contextualised view of it as an exploitable product to meet a demand. As a result, a more consistent technological definition of milk would be the product obtained by milking mammals reared solely for the purpose of producing milk.

Due to the balance of its various components, milk is a nutritionally highly complete diet. These components do not have a set proportion, but rather vary based on factors such the animal species, breed, lactation duration, and food. Buffalo and sheep milks, for example, contain more fat (7.5 percent and 6.4 percent, respectively) than cow milk (3.3 percent) as well as goat milks (3.9 percent).

Proteomics is a term coined in the mid-1990s to describe a field of knowledge framed within the field of biology formed by the combination of the words "protein" and "genomics." The concept was first proposed in 1979 by Anderson and Leigh in a presentation titled "Human Proteins Index Project," in which they hoped to unlock the genome by identifying the respective proteins using the newly developed technique of 2DE. Proteomics, also known as proteome analysis, was first defined by Wilkins. As the separation, identification, and quantification of the set of proteins expressed by a genome, cell, or tissue.

Proteomics refers to the collection of proteins encoded by the genome, and proteomics refers to the study of these proteins. However, this is an oversimplification of the term, as proteomics encompasses not only all of the proteins in a cell, but also all of their isoforms and modifications, as well as their interactions and descriptions of their structures and higher-order complexes.

Given the huge variety of forms in which proteins can arise, characterisation of proteomes is a difficult and complex undertaking. Unfortunately, there are currently no methodologies that allow for the entire examination of proteomes in a single, easy step.

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