

【S2-1】**Proteomics in Nutrition Research**

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The proteome varies with time and is defined as "the proteins present in cell, tissue, and organism at a certain point in time". There is an increasing interest in proteomics technologies now because proteomes provide the various ways in which the life of the cell is a dynamic process.

Proteomics can be used to identify the protein profile of a cell, tissue, or microorganism at different stages of development, and to examine the integrated response to a particular challenge. The challenge may be hormonal, environmental, or nutritional. As well as revealing the presence of novel proteins, a major application of proteomics is in trying to identify at a protein level early changes involved in degenerative diseases. This may be valuable either to provide insights into the causes of a disease, or to identify an early marker of the disease process. For the nutritional scientist this is clearly of special interest in relation to those diseases where diet plays an important role.

The critical pathway of proteome research includes sample collection, handling and storage; protein separation; protein identification; protein characterization; bioinformatics. The separation of the proteins in the solubilized sample is accomplished by a technique called 2-dimensional gel electrophoresis (2DE) where the proteins were first separated according to their electric charge and then by their size in polymer matrix. The utility of the classical 2DE approach is limited by the inability to reliably monitor proteins that are present in very low abundance, as well as proteins that are very hydrophobic or that are very acidic or basic. Low copy number proteins might represent key regulatory molecules within cells or signaling molecules in tissues, and the inability to measure changes in expression levels of these important proteins is an important consideration. As proteomics was coming to the forefront of the life sciences, many researchers had entered the race to develop new technologies such as isotope coded affinity tagging (ICAT).

It is expected that the application of the integrated nutrition researches with proteomics will allow for accelerated implementation of mechanistic knowledge in food.