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Editorial OMICS International

Organellar Proteomics: Tissue Specificity, Absolute Quantity, Post-translational Modifications and Protein-Protein Interactions

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Editorial

Organellar proteomics combines subcellular fractionation and mass spectrometry-based protein identifications. In the past decades, organellar proteomic analysis has been carried out for virtually every subcellular compartment in mammalian cells and tissues [1-4]. While conventional biochemical and biophysical approaches study the structures and functions of individual proteins, mass spectrometry-based proteomic studies allow us to understand the entire proteome or sub proteome systematically by: (i) Identifying proteins present in each subcellular organelle; (ii) Quantifying their expression levels; and (iii) Characterizing their posttranslational modifications and protein-protein interactions. All of the above determines the protein's function and activity.

Mass spectrometry analyses of different cell lines and multiple tissues have been carried out to address how tissues differ in gene and protein expression and how this contributes to tissue-specific biological functions [5-7]. Particularly important to subcellular organelles, existing proteomics studies indicated that mitochondria are functionally specialized in different tissues, which is crucial to its involvement in normal physiology and diseases [8-10]. Our results also indicated that the endoplasmic reticulum, another important organelle, expresses unique proteins to accommodate its tissue-specific functions [11,12]. In order to comprehensively unveil the tissue-specific and species-specific organellar markers, we will need to perform more quantitative organellar proteomics analyses. It is of equal importance that we will need the bioinformatics tools to mine the existing proteomics data sets to discover such markers.

Nowadays, quantitative mass spectrometry-based technologies have been widely used to compare relative protein abundances in different samples. Such examples include several of our studies on organellar protein changes in different cellular or diseased states [13-15]. More recently, Selected Reaction Monitoring (SRM)-based targeted proteomics approaches have been used to obtain absolute quantities and copy numbers of cellular proteins [16-18]. Due to the high cost of the stable isotope labeled synthetic peptides, it is not yet feasible to obtain such absolute quantification for the entire cellular proteome or a sub proteome of a given organelle. Therefore, computational methods are needed and several have already been developed to overcome these limitations [18-20]. By quantitatively determining protein copy numbers, proteomics studies can lead to a deeper understanding of protein stoichiometry and cellular functions of a specific organelle.

In addition to tissue specificity and quantitative measurements, proteomics can also help to identify the role of multiprotein complexes in exerting specific organellar functions. The biological function of proteins often relies on the association and dissociation of protein complexes. These complexes are dynamic in nature, often controlled by posttranslational modifications such as acetylation, phosphorylation, and ubiquitination [4]. Modern proteomics technologies have made it feasible to detect and quantify changes of protein modifications, protein conformations and protein interactions. Other biochemical approaches such as native gel electrophoresis and chemical crosslinking are often utilized in combination with mass spectrometry [4,21]. Such proteomic studies are expected to advance our understanding of the function and protein composition of each subcellular organelle in normal and disease states.

Our deeper understanding of biological functions of subcellular organelles will rely on a comprehensive characterization of their tissue-specific protein compositions, determination of protein copy numbers and dynamic protein-protein interactions. Proteomic technology developments in the past years have made such tasks feasible. Major advances in this area are expected in near future. Advances in bioinformatics and machine-learning technologies will also facilitate us to obtain a systematic understanding of how organellar sub proteome functions in a systematic manner.

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