

Aspekty metodyczne analiz proteomicznych z wykorzystaniem metod elektroforezy dwukierunkowej i spektrometrii mas

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Methodological aspects of proteomic analyses involving two-dimensional electrophoresis and mass spectrometry

Summary

Proteomics is a scientific discipline that focuses on the large-scale study of proteins, particularly their structures, functions and interactions. The proteome is the full complement of proteins expressed by genome. During the last decade, thanks to subset of proteomic techniques and workflows, it has been possible to identify: diagnostic protein biomarkers, potential therapeutic targets and also biotechnologically important plant proteins, like those that give a plant resistance to drought. Over the last years, proteomics has generated a relatively large number of reviews on technical aspects and concepts. Although total automation and reproducibility are possible, the protocols of protein isolation and separation are sample specific. Moreover, most of them address the development of optimal sample preparation protocols of mammalian cells and tissue. In contrast, plant proteomics is still in its infancy, probably because plant material is very recalcitrant. The objective of this review is to pay attention to some methodological aspects of proteomic analyses using 2DE and mass spectrometry, especially in the case of plant material.

Key words:

2DE, mass spectrometry, sample preparation, proteins

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