

# Translation Proteomics on Translational Research

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## Introduction

Translational proteomics is an emerging sub-discipline of the proteomics field in the biological sciences. Translational plant proteomics aims to integrate knowledge from basic sciences to translate it into field applications to solve issues related but not limited to the recreational and economic values of plants, food security and safety, and energy sustainability. In this review, we highlight the substantial progress reached in plant proteomics during the past decade which has paved the way for translational plant proteomics.

Increasing proteomics knowledge in plants is not limited to model and non-model plants, proteogenomics, crop improvement, and food analysis, safety, and nutrition but to many more potential applications. Given the wealth of information generated and to some extent applied, there is the need for more efficient and broader channels to freely disseminate the information to the scientific community. Identifying aggressive cancers early on requires improved sensitivity and implementation of biomarkers representative of tumor heterogeneity. During the last decade of genomic and proteomic research, significant advancements have been made in next generation sequencing and mass spectrometry techniques. This in turn has led to a dramatic increase in identification of potential genomic and proteomic cancer biomarkers. However, limited successes have been shown with translation of these discoveries into clinical practice. We believe that the integration of these omics approaches is the most promising molecular tool for comprehensive cancer evaluation, early detection and transition to Precision Medicine in oncology. Proteomics provides powerful tools for the study of clinically relevant samples in the context of translational cancer research.

Here we briefly review applications of gel-based proteomics for the study of bladder and lung cancer using fresh tissue biopsies. In general, these studies have emphasized the potential of the technology for biomarker discovery, as well as for addressing the issue of cancer heterogeneity. The sequencing of the human and other important genomes is only the beginning of the quest to understand the functionality of cells, tissues, and organs, both in health and disease. Together with advances in bioinformatics, this development has paved the way to the revolution in biology and medicine that we are experiencing today. We are rapidly moving from the study of single molecules to the analysis of complex biological systems, and the current explosion of emerging technologies within proteomics and functional genomics promises to elicit major advances in medicine in the near future. Cancer, being a complex disease that affects a significant fraction of the population, is foreseen as a prime target for the new technologies, as tools for the high throughput analysis of genes and proteins might expedite the applications of basic research findings into daily clinical practice through translational research. In particular, proteomic technologies are expected to play a key role in the study and treatment of cancer, as they provide invaluable resources to define and characterize regulatory and functional networks, to investigate the precise molecular defect in diseased tissues and biological fluids, and for developing specific reagents to precisely pinpoint a particular disease or stage of a disease. For drug discovery, proteomics assist with powerful tools for identifying new clinically relevant drug targets, and provide functional insight for drug development.