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Applications of Chemical Proteomics in New Drug Target Profiling

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Abstract

A critical need for novel drug targets has arisen as a result of the expanding demand for new treatment techniques in the medical and pharmaceutical domains. Contrarily, the targets of several medications that are currently commonly used in clinical practise have not been extensively documented. An integrated deconvolution of drug-target interactions is required for each drug since understanding a drug's interactions with biological components is essential for understanding the pharmacologic effects of that medication. An effective mass spectrometry (MS)-based affinity chromatography method for finding proteome-wide small molecule-protein interactions and linking these interactions to signalling and metabolic pathways is the developing discipline of chemical proteomics.

Keywords: Novel drug; Clinical practise; Chromatography; Metabolic pathways.

Introduction

The process of discovering new drugs is fundamentally complicated and has been around for thousands of years. However, the compounds' poor selectivity and unclear methods of action prevent their future use in clinical practise. It has been discovered that many medications operate on many targets, which inevitably leads to adverse effects and drug resistance throughout therapy [1]. The most infamous medication in history, thalidomide, was prescribed to treat morning sickness during pregnancy but it was later shown to cause severe birth abnormalities and congenital anomalies. In addition, the never-ending struggle against drug resistance in both antibiotics and cancer treatments best exemplifies the challenge of combining a variety of complex medications with the intended physiologic effects.

Pharmaceutical companies frequently utilise global proteomic techniques based on Mass Spectrometry (MS), which examine protein-protein interactions under various conditions, to find new therapeutic targets. A compound-centric approach, which focuses on characterising the characteristics of drug-target interactions, and activity-based protein profiling (ABPP), which concentrates on the enzymatic activity of specific proteins, have both been developed more recently as a complement to the more global approaches. An overview of innovative drug target profiling, large-scale chemical proteomics methodologies, and the aforementioned two strategies.

Conventional global proteome approaches, which quantitatively compare the levels of transcript and protein expression, have produced a wealth of insightful data, but these platforms are constrained in their ability to pinpoint changes in protein activity brought on by post-translational processes. Studies on cancer metabolism are further confounded by the possibility that enzymes carry out specific metabolic functions in tumour cells that may not be reflected in healthy physiology. These difficulties call for the development of innovative proteomic methods that will make it possible to accurately analyse the roles played by proteins in intricate biological systems like cancer cells [2].

The active site-directed covalent probe is the central component of the activity-based method. A reactive component that covalently binds to the target protein's active catalytic site, a linker region that can modulate reactivity and specificity, providing enough space for the reactive group to bind and preventing steric hindrance, and a tag for further identifying and purifying modified enzymes make up the general structure of these probes in their most basic form.

Compound-centric chemical proteomics (CCCP), in contrast to ABPP, focuses primarily on target identification. In this context, the identification of interacting components most frequently accomplished by affinity chromatography and sophisticated MS techniques is used to infer the mechanism of action of a bioactive chemical. The cellular targets for -lactones, anticancer drugs, and many natural compounds have all been effectively discovered using CCCP. This technique combines the long-established traditional drug affinity chromatography with statistics or bioinformatics for the subsequent identification of binding proteins [3]. Modern researchers combine high-resolution MS analysis with traditional drug affinity chromatography to provide more accurate and effective profiling. Therefore, this strategy is predicated in part on the enormous technical advancements in the MS sector, particularly in regards to the continuously growing sensitivity and throughput witnessed in recent years. Nano-electrospray ionisation (ESI) and quantification techniques have been developed over time [4]. Examples include stable isotope labelling, high-resolution, high-sensitive detection techniques like quadrupole time-of-flight or linear ion trap (LTQ), Fourier transform ion cyclotron resonance (FT-ICR), and LTQ/orbitrap mass spectrometers. However, the technologies must be usable by database management, statistical analysis, and systems designed specifically for laboratory information management.

The chemical proteomic method is well-suited for scientific study and has several advantages. By locating drug-target interactions, it offers a potent tool for profiling uncharacterized proteins. Additionally, this method may be used to examine the whole proteome or affirmative sub-proteomes and is not restricted to

panels of recombinant proteins. When tiny molecules interact with proteins in their unaltered, natural state, it is very helpful. Chemical proteomics can also be applied to any cell type, tissue, or species of interest, including bacteria and humans. Since tumour tissues are physiologically and clinically relevant sources, this approach makes it possible to explore important disease therapeutic processes in them. It may also be used to profile virulence in clinical samples [5].

Chemical methods can effectively identify particular types of proteins and serve as a useful tool for future protein separation from the proteome, even though global proteomic studies have long played a significant role in evaluating protein structure, function, and cellular connections. Chemical proteomics has been used to identify several compound targets, including those for kinase inhibitors and natural products.

Conclusion

Chemical proteomics is a crucial technique that aids in drug development and clinical trials. Particularly, chemical proteomics' discovery of kinase targets has been thoroughly studied in a variety of illnesses, from cancer to autoimmune disorders, emphasising the platform's potential therapeutic value. Chemical proteomics has recently been used to profile prospective new therapeutic targets for a more accurate knowledge of pharmacological side effects and treatment resistance under certain disease conditions, both *in vitro* and *in vivo*. To objectively evaluate how an unmodified medication interacts with its endogenous targets, conventional global proteome techniques are often used.There is no requirement for the reactive groups to covalently connect to proteins because the CCCP technique concentrates on detecting the interacting proteins. Therefore, the trifunctional probes utilised in CCCP give us the most precise and quick information about the biological targets since they can directly measure enzyme activity. On the other hand, ABPP is a renowned tool in drug development since, in contrast to CCCP, it can effectively describe the specific target classes.

References

1. Paulick MG, Bogyo M (2008) Application of activity-based probes to the study of enzymes involved in cancer progression. Curr Opin Genet Dev, 18(1):97-106.
2. Wilm M, Mann M (1996) Analytical properties of the nanoelectrospray ion source. Anal Chem, 68(1):1-8.
3. Ong SE, Mann M (2005) Mass spectrometry-based proteomics turns quantitative. Nat Chem Biol, 1(5):252-62.
4. Zhang J, Yang PL, Gray NS (2009) Targeting cancer with small molecule kinase inhibitors. Nat Rev Cancer, 9(1):28-39.
5. Johnson JD, Edman JC, Rutter WJ (1993) A receptor tyrosine kinase found in breast carcinoma cells has an extracellular discoidin I-like domain. Proc Natl Acad Sci USA, 90(12):5677-81.