The Application of Chemical Genomics and Chemical Proteomics in Cell Autophagy

Yinbing Zhang

Hubei University, Wuhan, 430062, China Email:1021946875@qq.com

Keywords: Chemical genomics; Chemical proteomics; Autophagy

Abstract: In recent years, he has conducted in-depth research on chemical genomics and chemical proteomics, cell autophagy, target identification, biosynthesis, and detection of early clinical drugs. Based on an overview of chemical genomics and chemical proteomics, combined with the recent clinical research results, this article clarifies the specific applications of chemical genomics and chemical proteomics in cell autophagy, providing significance reference for future clinical research.

Chemical genomics is simply defined as the reaction between the compound and the genome, which can play a significant role in the rapid identification and confirmation of clinical drug targets and in the design, synthesis and biological detection of compounds [1]. Chemical proteomics mainly refers to operating artificial control systems and conducting research on protein-related functional mechanisms. The goal of chemical genomics is to form interaction molecules between gene transcripts to achieve effective regulation of gene products. This article will review the application of chemical genomics and chemical proteomics in clinical autophagy in recent years.

1. Overview of Chemical Genomics and Chemical Proteomics

1.1 Chemical Genomics

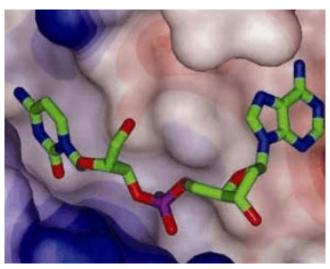


Figure 1. Schematic diagram of chemical genomics

Chemical genomics (Chemogenomics) is a new era of post-genome technology (see Figure 1), but also serves as a key pivotal bridge between the research of new drugs and the connection of the genome. It can complete the gene function analysis of small molecular compounds that are highly specific for determining the target protein, and discover new drug lead compounds as soon as possible [2]. Against the background of development in genomics, combinatorial omics, molecular biology, pharmacy and other fields, chemical genomics has been proposed to achieve multidisciplinary technical reorganization. It can use biologically active chemical small molecule ligands as a guide probe to further analyze Human genes, proteins, genes and other biological functions are explored in depth, and provide technical guidance for the development of new clinical

DOI: 10.38007/Proceedings.0001195 -891- ISBN: 978-1-80052-007-3

medicines, and to a large extent promote the development of China's pharmaceutical industry.

1.2 Chemical Proteomics

The fundamental goal of chemical proteomics is the development and application of biologically active targeted probes, which can study the functions of specific enzyme families existing in complex proteomes (see Figure 2) [3]. From a certain level, this type of chemical probe can bind the specificity of the target enzyme, which is convenient for further purification and identification. On the other hand, it can also covalently modify the target enzyme and its subfamily and look for differential functions and functions The enzyme [4]. With the subsequent development of chemical proteomics, the role of chemical probes has gradually appeared in the field of proteomics, and it has shown increasing targets for identification, verification, and new drug development.

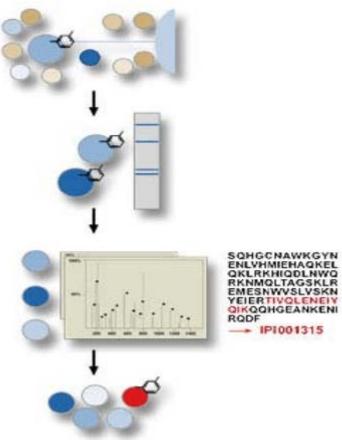


Figure 2. Schematic diagram of chemical proteomics

2. Applied research on chemical genomics and chemical proteomics

In the current research, chemical genomics and chemical proteomics technology can be used to design and successfully screen small molecules that mediate autophagy [5]. Liu Yuan et al. [6] studied the survival of rapamycin-sensitive yeast using HTS technology after the addition of small molecules, and found that it can successfully screen a total of 26 inhibitory mines from 16,350 small molecule compounds. Small molecule interactors of rapamycin, and 57 small molecules that enhance the effect of rapamycin. It was found that there were a total of 6 small-molecule interactors, which could successfully eliminate the presence of rapamycin and inhibit the proliferation of yeast. In the follow-up studies, there were also many researchers. In order to fully explain the clinical mechanism of SMIR, the whole genome mRNA profile was analyzed. It was found that after half an hour of SMIR and rapamycin treatment of yeast cells, a total of 492,588 gene expressions were up-regulated Down-regulated the situation and found that SMIR4 can effectively prevent intracellular physiological changes due to rapamycin.

Not only that, Gade TPF [7] and others also found that SMER10, 18, 28 and their analogs can all promote autophagy substrates such as the elimination of α -synuclein via mTOR-independent pathways or downstream regulators. In recent years, the clinic has been expected to become a drug that has a certain effect on Parkinson's disease. The results of this study indicate that chemical genomics and chemical proteomics have great therapeutic potential for discovering new cellular pathways and drug targets for autophagy-related diseases, and have entered the market trial regulatory phase. The mechanism of action of rapamycin is similar to that of everolimus and tamsulosin, and both have strong anticancer effects. Martin L Pall [8] and others have used cell screening technology to successfully screen autophagy small molecules such as perhexiline, niclosamide, and pharmacological molecular libraries that can activate the rich nutritional conditions of cancer cells. Such as small yards, such small molecules can hinder mTORCI, and will not affect the mTORC2 signaling pathway.

Chemical genomics and chemical proteomics are still of great value for related research on cell autophagy. Existing studies have found that ABO can significantly up-regulate the expression of annexin A7, and ANXA7 and the autophagosome marker LC3. In the cytoplasm, it can co-localize and successfully induce the accumulation of LC3-II. LC3-GFP screens the autophagy inhibitor MBCQ, and based on this molecule, the molecular synthesis of spautin-1 is further optimized. After research, it is concluded that the protein USP10, The molecular activity of 13 has a dependent effect. In addition, the existing literature also found that autophagy inhibitors can effectively delay the death of neurons caused by ESCRT-III. This finding also indicates that the accumulation of autophagosomes does not help neurons to survive better. ESCRT-III dysfunction is also prone to multiple neuropathic degenerative diseases [9].

3 Prospects of Chemical Genomics and Chemical Proteomics

High-throughput screening (HTS), as one of the emerging technologies that have been gradually developed in the last century to the present, has high sensitivity, specificity, and rapidity. Chemical genomics strategies can allow the use of a large number of different compounds to complete the processing of multiple genomic targets in parallel, effectively optimizing for drug development. By using HTS technology as one of the key technologies of chemical genomics technology platform, it is a technology developed based on target proteins, conforming to target genes, and bioactive small molecules, which greatly improve the speed of drug screening and provide new drugs, discover the way.

3.1 Combinatorial chemistry

Combinatorial chemistry technology can pass a reliable chemical reaction system to efficiently synthesize a large number of organic molecules, and according to the three-dimensional structure of a single receptor macromolecule, it can complete the design of differentiated lead compounds. Each type of lead compound can exist as a mother core. Then, the structure of the mother nucleus is modified and extended to different receptor positions of the mother nucleus, so that different compounds can be obtained. In this way, a series of molecular corresponding composite sample libraries are formed between the differentiated mother cores and structural fragments, which completes the establishment of the virtual composite sample library.

3.2 Bioinformatics

Under the background of the rapid development of information, science, and computer technology in recent years, bioinformatics has been produced. It can achieve the extraction, analysis, induction, and storage of biological and medical related information through the use of multiple technologies such as mathematics, informatics, and biology. And closely related to new drug targets, screening drugs and clinical trials. Genomics, proteomics, combination technology, and HTS technology all play a significant role in clinical research and development of new drugs, and accumulate a large amount of differentiated biological and chemical information.

3.3 Other new technologies

For the current research on chemical genomics, more and more new technologies are gradually proposed, such as capillary electrophoresis, differential scanning calorimetry, and atomic force microscope technology. Many new types of technology also provide strong support for the development of chemical genomics and chemical proteomics technology.

Conclusion:

In today's research on the application of chemical genomics and chemical proteomics in cellular autophagy, by deeply exploring the mechanism relationship between tumor diseases and cellular autophagy, it has been found that the application of chemical genomics technology can The shortcomings are effectively compensated. And related research on the discovery of autophagy chemical small molecules has advantages over other detection methods in terms of cell detection. Comparative studies of proteomes can also reveal that under differentiating conditions, the protein components are differentially expressed within the proteome. In the future, research in this field will be further developed to play a greater role in the treatment of clinical oncology diseases.

References:

- [1] Chen Suhong, Wang Hua. Application of ultra-high-throughput screening based on cell function in chemical genomics drug discovery [J]. Foreign Medical Sciences. Pharmaceutical Division, 2018, 29 (6): 42-45.
- [2] Ding Lina, Zhao Yang, Zhao Baoxiang, et al. Application of Chemical Genetics in Functional Genomics Research [J]. Chemistry of Life, 2017, 27 (1): 12-14.
- [3] Gautron J, Mann K, Righetti P G, et al. Application of functional genomics in identifying new egg proteins [J]. Chinese Poultry, 2018, 32 (7): 40-44.
- [4] Wu Xiaoge, Lu Xinyu. Application and development of mass spectrometry in proteomics [J]. Journal of Medical Postgraduates, 2017 (10): 74-76.
- [5] Wang Zejun, Luo Yao, Han Yuping, et al. Application of Nanoparticles in Cell Autophagy Regulation and Imaging Research [J]. SCIENCE CHINA: Chemistry, 2017 (06): 92-100.
- [6] Liu Yuan, Zhang Siping, Huang Xiaohui, et al. Construction of human Rab12 gene eukaryotic expression vector and its expression in HEK293 cells [J]. Genomics and Applied Biology, 2015, 34 (12).
- [7] Gade T P F, Tucker E, Nakazawa M S, et al. Ischemia-induced hepatocellular carcinoma quiescence and autophagy dependence [J]. Journal of International Medical Radiology, 2017 (04): 104.
- [8] Martin L Pall, Stephen Levine. Nrf2 is an important transcription factor that regulates cell protection mechanisms such as detoxification, anti-oxidation, and anti-inflammatory-its activity can be enhanced by health foods and other factors (English) [J]. Acta Physiologica Sinica, 2015 (1).
- [9] Ping Juan, Zhao Na, Wang Baoquan, et al. Study on the apoptosis-inducing effect of anti-sense oligonucleotides of bcr-abl gene of human chronic myelogenous leukemia on K562 cell line [J]. China Cancer Journal 2019, (03): 13-18.