

Research and Analysis on the Discovery of Effective Component of Traditional Chinese Medicine under the Guidance of Network Pharmacology

Xiaofan Li, Xiaoyu Wang, Bo Zhao, Wei Guo*
Ningxia Medical University, Yinchuan, 750000, China

Abstract: with the progress of medical pharmacology research and development, network pharmacology in China gradually occupies the frontier field of traditional Chinese medicine research, and also becomes one of the hotspots at present. Network pharmacology is put forward by foreign countries. China combines the principles of traditional Chinese medicine to analyze and expand. The study of network pathology is based on the analysis of high-throughput combinatorial data. It uses the way of computer virtual computing, on the basis of network database retrieval technology, to carry out the construction and analysis of biology and biological network and reveal the effectiveness and metabolism of traditional Chinese medicine. Network pharmacology has replaced a traditional model of drug treatment of a disease and established a new model with multiple targets and complex reticular relationships among multiple diseases.

Keywords: Network pharmacology; Traditional Chinese medicine; Effective component; Discovery and analysis

1. Introduction

In the past, the proportion of traditional Chinese medicine compound prescription is basically composed of more than two kinds of herbal medicines, so this kind of traditional Chinese medicine compound prescription has more complex chemical composition, and the pharmacological action has a variety of therapeutic approaches, and pharmacology has multi-targets and multi-levels. At present, there are often unclear substance research problems in the pharmacology of traditional Chinese medicine compound prescription, and the action mechanism of much pharmacology is not clear enough, so the basis of research and clinical application cannot be closely combined. The combination of holistic and systematic network pharmacology can make traditional Chinese medicine ingredients have more ideas, and network pharmacology can help traditional Chinese medicine compound prescription to explain the clear action mechanism of traditional Chinese medicine, so as to discover the active substances of traditional Chinese medicine and make medical workers better develop new drugs. At present, the research is still in its infancy, many aspects of data are not flexible and effective, and some databases have a more complex relationship, lack of relatively accurate biological models. This paper studies and analyzes the effective components of traditional Chinese medicine under the network pharmacology.

2. Application of Network Pharmacology in the Study of Traditional Chinese Medicine Components

Because the components of traditional Chinese medicine are various and have a variety of regulation ways, so there is a lot of information about the components of traditional Chinese medicine. The research idea of single target and single component of western medicine cannot be applied to the research field of traditional Chinese medicine, and it cannot better reflect the systematicness of traditional Chinese medicine and also cannot reflect the material basis of the efficacy of traditional Chinese medicine compound prescription better. Therefore it cannot play the law of the composition of traditional Chinese medicine. In the technology of network pharmacology, the research direction gradually changes to the overall research, turning into a more systematic regulation mode. After the integrated analysis of drugs and genes, their internal effects can be better analyzed, and the indirect interactions between drugs can be found by combining the interaction data between proteins. The research method of network pharmacology needs drug targets and uses the combination of multi-target interaction to play the role of synergism and reduction of toxicity. Network pharmacology needs to carry out problem research from

an interrelated point of view, which is consistent with the core idea of traditional Chinese medicine.

Combined with the complex network of drugs, we can analyze the action mechanism of drugs, change the traditional pharmacological research mechanism and turn to a comprehensive network. The use of network pharmacology, for the same disease at different stages of development, we can regulate combined with a variety of functional gene and protein. The chemical composition of the compound prescription of traditional Chinese medicine is relatively complex, and it has a multi-level pharmacological mechanism, which can be well integrated and compatible with network pharmacology. Network pharmacology can be analyzed as a whole to explain the compound action mechanism of traditional Chinese medicine. So it can better study the compound prescription of traditional Chinese medicine and expand the clinical indications for compound prescription of traditional Chinese medicine. The theories and methods of systems biology are developing rapidly, which can better support the research of biomedicine and promote the progress of Ming medicine. Systems biology can study the composition of biological systems, and the relationship between components can be established under a variety of environmental conditions. The mathematical model of computational biology can be used to describe the biological function to predict the phenotype. The study of systems biology should be based on high-throughput combinatorial data, combined with a large number of experimental data, in order to jointly support the physicochemical theoretical research and develop perfect computer technical support. Systems biology is a combination of multi-disciplines, combined with computational biology methods, it derives more branch subjects. Network pharmacology focuses on the analysis of the network integration of biological network and drug action, conducts specific analysis of the relationship in the network in order to carry out comprehensive network analysis. It conducts integrated analysis of the disease gene network and the action of drugs, explores the multi-target effects of drugs, and forms an interactive cross gene of drug diseases, so as to explore more complete network pharmacology and provide a mechanism for analyzing the action of drugs. Combined with the connection of nodes in the biological network, we can analyze the relationship between the networks and provide a more scientific description of the action mechanism of drugs.

3. Advantages in the Field of Traditional Chinese Medicine under the Guidance of Network Pharmacology

Combined with the network pharmacology and the holistic view of traditional Chinese medicine, we use more dynamic analysis methods to realize the method of holistic view. Combined with network pharmacology and

systematic biomedical technology, database website technology of traditional Chinese medicine is used to diagnose traditional Chinese medicine diseases on the basis of computer software, then combined with traditional Chinese medicine formula treatment methods, network pharmacology analysis methods are used to analyze the components of traditional Chinese medicine compound prescription and find the effective mechanism of compound prescription to treat diseases, so as to better deal with the problems in the research of traditional Chinese medicine, and improve the technical level of traditional Chinese medicine research.

3.1. Select the active ingredients of traditional Chinese medicine compound prescription

As for the application of network pharmacology in pharmacokinetic aspect, the platform of data analysis can be used to screen out the effective components of traditional Chinese medicine compound prescription and explore the inherent target effect, so as to verify the characteristics of traditional Chinese medicine compound prescription in the treatment of diseases and analyze the principle of multi-components.

3.2. Analysis of the ways of compound preparation in the treatment of diseases

In the process of treating diseases with compound preparation, traditional Chinese medicine components should be combined to predict. We should clarify the pharmacological basis of drug action in the key target of diseases treatment. The action path of compound preparations in treating diseases is clearer. Network pharmacology can clarify many links. In view of the different processes of compound treatment of diseases, we should use multiple components and multi-targets to play a coordinated role, and use multi-ways to carry out the action mechanism.

3.3. Explore the mechanism of compound preparation in the treatment of diseases

Network pharmacology needs to check the prediction targets of diseases, and use computer software to identify the prediction targets of compound ingredients. The key targets of traditional Chinese medicine compound prescription in treating diseases are very important, and we should construct relevant network map, thus we can analyze the compound treatment of diseases more deeply and explore the potential mechanism of compound preparation.

3.4. Verify the rationality of the combination of prescriptions

The theoretical method of traditional Chinese medicine prescription compound has a profound influence, and the first principle of compound prescription is the mechanism of dispensing and usage of traditional Chinese medi-

cine. Combined with network pharmacology to verify the combination of prescriptions, we can clarify the importance of traditional Chinese medicine components and verify the rationality of traditional Chinese medicine compound prescription.

3.5. Explore the method of compound prescription

The advantage of traditional Chinese medicine is the multi-component compound method, and traditional Chinese medicine has the advantage of multi-target. The compatibility of various medicinal materials in the new prescription can be solved reasonably, so that the clinical application can be carried out smoothly and the obstacles in the development of traditional Chinese medicine can be solved. In the process of exploring theoretical support, it is necessary to explore the prescription methods of network pharmacology.

3.6. Relocate the compound preparation of traditional Chinese medicine

In the process of clinical treatment, we need the compound prescription of traditional Chinese medicine with a clearer structure, strictly approve the compound prescription of traditional Chinese medicine to enter the process of clinical use, and construct the disease scope of the development and research of traditional Chinese medicine and explore the role of new targets. Compared with the process of new drug development, the repositioning process of traditional Chinese medicine compound preparation is a process with a relatively short period, and the cost of repositioning is not high. Moreover, the repositioning success rate and safety of traditional Chinese medicine compound preparation are relatively high. At present, this technology has received more attention. At present, network pharmacology is based on the methods of systems biology and bioinformatics, and has the advantages of multi-targets and multi-approaches. It can better explore new targets for the treatment of diseases.

3.7. Constructing the mechanism of traditional Chinese medicine

The timely property of traditional Chinese medicine is a key part of the current theoretical system of traditional Chinese medicine, and the pharmacological mechanism of traditional Chinese medicine can better guide clinical drug use. There are often many components of traditional Chinese medicine, and it has a multi-target action mechanism. There are many similarities between the research ideas of constructing the property mechanism of traditional Chinese medicine and the network pharmacology system, which can better contribute to the pharmacological theory research of traditional Chinese medicine.

4. Analysis of Network Pharmacology under the Active Components of Traditional Chinese Medicine

4.1. Zero code pure dry experiment

For the network pharmacology of traditional Chinese medicine, we should integrate prescriptions and traditional Chinese medicine to treat the corresponding diseases and explore the study of improving the molecular mechanism. The integrity of network pharmacology of traditional Chinese medicine is generally analyzed. First of all, we use the way of database, combined with methods of text mining and software prediction, to explore the effective target for traditional Chinese medicine. We use computer simulation technology, combined with perfect in vitro experiments, to verify the interaction sites between small molecules and target molecules of the drug. In addition, we screen the biological functions related to molecular pathways and target molecules by enrichment analysis, construct the pathway interaction network between drugs and active components, establish the interaction network system between active components and phenotypic diseases. The interaction network can also be target molecules. We should construct the interaction network centered on target molecules, combined with advanced analysis tools such as prediction websites plus the corresponding statistical values to predict each process.

4.2. Network pharmacology of traditional Chinese Medicine based on the dry-wet combination

The research method of dry-wet combination of network pharmacology pays more attention to the way of experimental research, taking network pharmacology as the screening target gene, combined with more biological functions and pathway prediction methods. This network pharmacology strategy is generally divided into three steps, each step of which needs to be verified by conventional molecular biology and integrated with cell biology technology.

4.3. Combined with network pharmacology and bioinformatics analysis

To integrate the methods of bioinformatics analysis with that of network pharmacology, first of all, we should use the way of database and text mining, combined with the means of software prediction to explore the effective targets in traditional Chinese medicine. The interaction sites between small molecules and target molecules in drugs can be verified by computer simulation technology and in vitro experiments. Then, we analyze the high-throughput sequencing of normal group and disease group to test the results of the chip, so as to screen out the differences of expressed genes. By obtaining the in-

tersection between the target molecules and the expressed genes, the drug-related target molecules will be successfully separated. Then, enrichment analysis is used to screen the biological functions of molecular pathways and target molecules.

Afterwards, we construct the interaction network between drugs and active components, and establish a complete target molecular interaction network system to predict the interaction network centered on target molecules, predict combined with website analysis tools and the corresponding statistical values, and analyze the related immune microenvironment and phenotypic analysis. Finally, for some clinical data, it is necessary to analyze the clinical correlation and predictive model.

5. Conclusions

To sum up, under the current development, a large number of combinatorial data have emerged in the effective components of traditional Chinese medicine, and the transfer, analysis and utilization of the data have shown an explosive growth. At present, after a period of summary and exploration of network pharmacology, more and more methods have emerged gradually, and there is a lack of more scientific evaluation methods. In this regard, in the process of practical application, we should make a correct choice to deal with these problems. In the process of carrying out the work, experts in many fields will be involved, and experts in various fields should be brought together, such as formic acid biologists and systems biologists, so that they can work closely together. The development of systems biology and network pharmacology can promote the treatment of various diseases, under-

stand the pathogenesis of a variety of complex diseases in an all-round way, so as to make more accurate diagnostic measures and provide more technical support for drug research and development.

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