

Application of High-Throughput Sequencing Technology in New Coronary Pneumonia

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Abstract: With the emergence of the epidemic at the beginning of the year and the continuous mutation of the virus, new disease characteristics have emerged, and many countries in the world have been forced to enter a state of tense public health defense. Under this circumstance, scientists from all over the world are united and united to fight the epidemic, and they are conducting research around the clock to find the best treatment for the sick. Molecular biology has played an important role in the prevention and control of this epidemic. The high-throughput sequencing technology contained in molecular biology has been continuously researched and developed and is becoming more and more perfect. It can be used in the determination and alignment of the nucleic acid sequence of the virus. Virus mutations play an important role in real-time detection. This article will first briefly introduce high-throughput sequencing technology, and then briefly analyze the specific application of high-throughput sequencing technology in new coronary pneumonia.

1. Introduction

The new type of coronavirus pneumonia is the first place where the new type of coronavirus pneumonia appeared in Wuhan, and it is also the place with the highest incidence. The early novel coronavirus in Wuhan was not well controlled, which caused a large number of people to be infected and spread. Wuhan has exported a large number of infected patients into other provinces and cities, leading to the gradual occurrence of new coronary pneumonia in other provinces and cities. But it has been strictly managed by the country. Soon after the outbreak, scientific researchers were able to control the development of the epidemic. The disease situation in Wuhan, Hubei Province, a major epidemic area, has gradually improved at a speed visible to the naked eye, and the number of new people added every day has been greatly reduced. The number of people cured is increasing. The main feature of the new type of coronary pneumonia is a new type of coronavirus infection. This type of coronavirus has not been seen before. The virus mainly causes inflammation of the lungs and produces patients with new coronary pneumonia, and the disease process is irreversible. In the early stage of the illness, the symptoms manifested include fever, cough, and difficulty breathing. Therefore, distinguishing the disease from influenza is also a necessary knowledge for people to cultivate before. Coughing often manifests as a dry cough, and it is generally difficult to breathe in about a week, threatening the life and health of the patient. Patients with more serious conditions will have symptoms such as septic shock and procoagulant

dysfunction. The new type of coronavirus pneumonia is caused by a new type of coronavirus infection. The treatment methods are mainly anti-viral, including anti-virus of Chinese medicine and anti-virus of western medicine. In addition, there is supportive treatment, including increasing immunity and correcting water and electrolyte balance. Disorders, isolation treatment, etc. If there is a bacterial infection, it needs to be treated with antibiotics. If you have difficulty breathing, you can choose to use a ventilator. If inflammation is not well controlled, it can be treated with a small amount of hormones. Although it is said that there is no specific medicine for the treatment of new coronavirus pneumonia, it is treatable and most of them heal well.

2. The Principle of Sequencing Technology in the Detection of New Coronavirus

High-throughput sequencing technology, also known as next-generation sequencing technology or deep sequencing. Compared with first-generation sequencing, second-generation sequencing is a revolutionary change. The definition of high-throughput is relative to first-generation sequencing, literally From the previous point of view, first-generation sequencing can only perform sequence detection and analysis on a sequence of one sample at a time, with a small amount of data, while high-throughput sequencing technology can generate dozens of hundreds of data at a time, with one-time sequencing. Compared with first-generation sequencing, the characteristics of multiple samples have increased throughput by at least tens of thousands of times, so it can be called high-throughput sequencing. The development of sequencing technology has also conformed to the progress of society and the changes of the times, and the remarkable feature of high-throughput sequencing technology is that it can conduct comprehensive and all-round observation and analysis of the genome of a certain species, which is based on the previous development conditions. Unimaginable. The specific application of this technology to the embodiment of the new coronavirus is capable of high-throughput sequencing of all nucleic acid molecules in the provided sample. After the sequencing is completed, all pathogenic microorganisms or their target sequences contained in the sample can be detected through bioinformatics analysis . Therefore, high-throughput sequencing technology relies on its high-throughput and high-accuracy characteristics to sequence and analyze all pathogenic microorganisms that may be infected. It plays an indispensable role in this new crown epidemic. Its sequencing results can detect new types of The gene sequence of all pathogenic microorganisms that may be infected, including the coronavirus.

3. The Method of Sequencing Technology in the Detection of New Coronavirus

Through high-throughput sequencing, whole-genome sequencing and other technologies, the entire genome sequence of the COVID-19 virus has been obtained. According to the sequence characteristics, it can be attributed to a beta coronavirus that has never appeared before, and high-throughput sequencing is used to find this The virus has about 88% homology with the virus in bats previously found in Zhoushan, Eastern China. The study found that the virus strain extracted from pangolins is 99% similar to the new coronavirus, which shows that pangolins are in It may be a latent host in this new coronavirus epidemic. Gene sequencing is the only way to dynamically track virus mutations, to show the route of virus transmission, and to use this technology to trace back to the source of infection. Compared with reverse transcription polymerase chain reaction, gene sequencing is more capable of real-time detection of virus mutations, and timely feedback information, and the feedback information is highly accurate and usable, which is more convenient for the next step of scientific research. Based on current research, the detection and research of high-throughput sequencing technology in the epidemic can be roughly classified into three methods: metagenomic sequencing, probe capture sequencing, and polymerase chain reaction

amplification technology. In terms of virus diagnosis, it is mainly sequencing diagnosis, using the technology provided by biological information to extract and identify the sequence information of the virus, and real-time monitoring and analysis of whether it has functional mutations. Sequencing technology has also made great achievements in vaccine development. Vaccine research needs to screen out truly immunogenic viral antigen nucleic acid sequences in advance, express viral proteins through nucleic acid sequences, and then identify specific regions of cell receptors, and induce host cells to develop an immune response. React, produce antibodies, in order to achieve the purpose of prevention.

4. The Significance of Sequencing Technology in the Detection of New Coronavirus

The advancement and perfection of sequencing technology can be said to be a revolutionary advancement in the field of biological research. This technology is helpful to reduce the manpower and material resources required for sequencing. In previous studies on human genome sequencing, the Human Genome Project conducted in 1990 successfully encoded the human genome, but the entire research process cost as much as 3 billion US dollars, and the research and development of second-generation sequencing technology has brought genome sequencing into the era of 10,000 yuan genomes. Such a low cost of single-base sequencing allows us to implement genome projects for more species to decrypt the genome genetic code of more biological species. At the same time, among the species that have completed the genome sequence determination, it has become possible to perform large-scale whole-genome resequencing of other species of this species. High-throughput sequencing technology can be regarded as a milestone in the development of sequencing technology, which can simultaneously sequence millions of DNA molecules. This makes it possible to perform detailed and comprehensive analysis of a species' transcriptome and genome. The birth of high-throughput sequencing technology can be said to be a landmark event in the field of genomics research. This technology allows the single-base cost of nucleic acid sequencing to drop sharply compared with the first-generation sequencing technology. Such a low single-base sequencing cost allows us to implement genome projects for more species to decrypt the genome genetic codes of more biological species. At the same time, among the species that have completed the genome sequence determination, it has become possible to perform large-scale whole-genome resequencing of other species of this species.

5. Advantages of High-Throughput Sequencing Technology

Compared with first-generation sequencing, high-throughput sequencing has the characteristics of high throughput and fast sequencing, but the accuracy of high-throughput sequencing is not high. The sequencing results often need to be further processed and corrected before they can be applied to the next research. With the continuous development of sequencing technology Development, one day in the future, will surely be able to solve the existing ones. The advantages of high-throughput sequencing technology are: First, it can be sequenced through a chip. The development of a chip is an advanced research in the field of scientific research. It is only the size of a fingernail but can store genetic information of millions of people. It can also read the sequencing results of multiple samples at the same time at one time, using the idea of parallel processing to the extreme, so it can also be called massively parallel sequencing, which is recognized by everyone. Second, high-throughput sequencing technology can quantitatively determine genes. Scientific researchers stipulate that the number of times a certain DNA in a sample is sequenced will reflect the content of this DNA in the sample. Third, save costs. According to incomplete statistics, the Human Genome Project carried out in the last century cost a total of 2.7 billion US dollars. Although it is lower than the estimated 3 billion US dollars before the start of the study, it is also a high-consumption study

and is still a A project that requires a lot of financial resources, and the current development of second-generation sequencing is only a small part of the first-generation sequencing, or even less than 1%.

6. Problems in the Development of High-Throughput Sequencing Technology

The rapid development of high-throughput sequencing technology and frequent use have brought great convenience to scientific research. At the same time, there are also some problems that still need to be solved. First, the accuracy of sequencing has been improved. Compared with the first-generation sequencing, the accuracy of the second-generation sequencing has been greatly improved. However, adhering to a rigorous and serious attitude towards scientific research, researchers are still working to improve the accuracy of sequencing, and the application of this technology is dominated by humans. A more serious attitude to solve the problems of human health. Second, the storage and analysis of sequencing data. As the virus continues to produce genetic mutations, a large amount of data will be generated, which has triggered scientific researchers to think about data storage and analysis. For the analysis of genetic information, although the analysis of the sequencing results has been completed, the accuracy is still Needs to be improved, the actual clinical application effect is still relatively small, and the current degree of data accumulation is far from enough compared with human data. Third, data security and information privacy. For data generated by individuals, if they cannot be protected, humans will lose trust in sequencing technology, which raises huge questions about how to store the generated data more safely and reliably.

7. Conclusion

With its high throughput and high accuracy, high-throughput sequencing has greatly helped scientific researchers in this epidemic, greatly speeding up the process of vaccine research and advent, and controlling the development of the epidemic, not only for us Provide virus sequence information, and greatly reduce the human and financial resources consumed in the research process. At present, there is still room for progress and development in high-throughput sequencing, which reflects many problems, such as whether the accuracy of sequencing can be improved, how can the results of sequencing be stored safely and reliably, and whether Let people trust and use continuous technology. These problems need to be solved. Only when we continue to enrich ourselves can we develop technology, bring progress to society, and become the talents that society needs.

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