Received Date: 23 April 2020
Accepted Date: 02 May 2020
Published Date: 10 May 2020

Practique Clinique et Investigation

Misinterpretation and Misuse of Molecular Biology in the Traceability Issues of Novel Coronavirus

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ABSTRACT

Wuhan pneumonia has become a major and severe infectious disease threatening human health, and its viral source has become the focus of the world scientific community. The analysis of gene sequencing in molecular biology may be one of the key keys to solve this problem. However, due to the extreme complexity of its technology, it is often politicized and misinterpreted by nationalists. Through the typical examples that exist in this field, in this paper, it is believed that only by combining the epidemiological data, analyzing the evolutionary path of the virus, and conducting comprehensive analysis and research, can it be helpful to trace the origin of the unrecorded virus.

Keywords: *2019-nCoV /SARA-CoV -2; Source trace; Molecular biology; Gene sequencing; Misinterpretation; Buse*

INTRODUCTION

Since the outbreak of the new coronavirus pneumonia (COVID-19) in Wuhan, about the source of this new virus, how it spreads from the host in nature to people, and who is the "patient zero", has been the focus of attention from all walks of life.

There are still many mysteries about the origin of the new coronavirus and the initial development of the epidemic. Many observers and researchers are currently concerned about whether the virus leaked from the virus laboratory in Wuhan, China, where the epidemic originated. Initially, the Chinese media claimed that the outbreak occurred in the South China Seafood Wholesale Market in Wuhan. Later, researchers reported that the first batch of cases showed that the seafood market was not the source of the virus or the only source.

Due to the rising demand for legal accountability and economic compensation, related countries have shirked their responsibilities, making this issue seem confusing. This paper attempts to clarify the phenomenon that the achievements of molecular biology are misinterpreted and misused on the issue of traceability.

THE MISUSE OF MOLECULAR BIOLOGY IN THE TRACEABILITY PROBLEM

Since the outbreak of new coronavirus (COVID-19 or SARS-Cov-2) pneumonia in Wuhan, Hubei, China in December 2019, many people invariably focus on the P4 laboratory of Wuhan Institute of Virology, Chinese Academy of Sciences,

Citation: Jin-Zhong GONG, Misinterpretation and misuse of molecular biology in the traceability issues of novel coronavirus. Prac Clin Invest 3(2): 54-60.

especially Shi Zhengli's research team. In 2013, they discovered that cross-species infection could be achieved by altering the bat coronavirus spinous process S protein. Based on this, some people imagine that if a leak occurs during the experiment, it will most likely lead to a large-scale epidemic that sweeps the world.

Chinese officials have so far refused to conduct in-depth field investigations by international organizations; the military took over the P4 laboratory, Xi Jinping proposed to promote the publication of the Biosafety Law as soon as possible, all these seem to confirm the above inference.

Five hospitals affiliated to the seven Wuhan medical workers who died of early infection, a circle around the Chinese Academy of Sciences Wuhan Virus was formed, with a diameter of no more than 9 kilometers, and the shortest was only 2 miles. In the most densely infected areas of the epidemic-stricken areas, the earliest built "square cabin hospitals" once again formed another encirclement for the institute, with a diameter of 2-9 kilometers. This is evidence from the perspective of geographic information.

However, on February 27, it may be due to some pressure, Academician Zhong Nanshan, an expert in respiratory medicine, unexpectedly threw strange talk "The epidemic first appeared in China, and the source of the virus does not necessarily originate in China." This kind of high-level swing pot, stir muddy water, and confuse audio-visual, immediately stimulated a strong public opinion rebound.

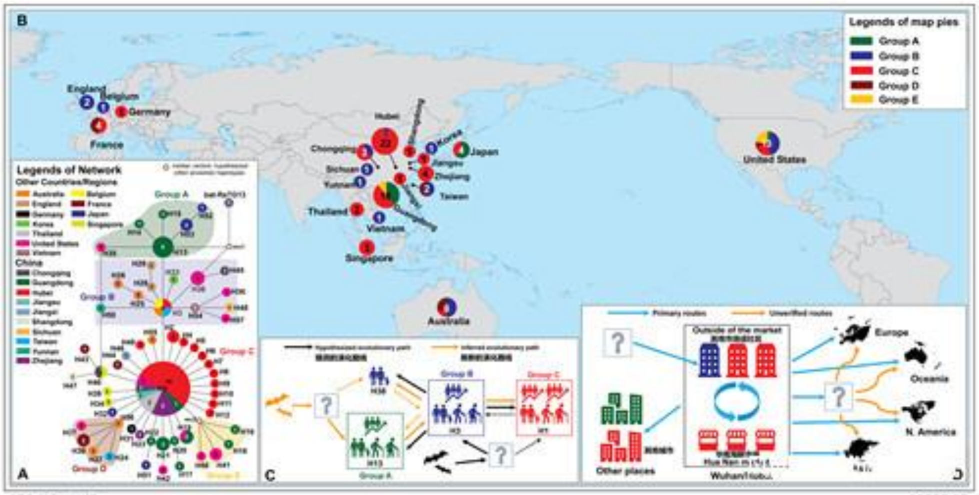

Figure 1: Evolution Relationship and Geographical Distribution Pattern of 58 Haplotypes of New Coronavirus (A, B) Possible evolutionary relationship between haplotypes (C), and the possible route of spread and spread of the new coronavirus (D) [1].

Yu Wenbin paper [1], it seems to provide a "solid scientific basis" for this argument.

This article states that, based on 120 mutation points, the 12 countries on four continents, Genomic data from 93 samples (as of February 12), and the researchers obtained 58 haplotypes. It is further divided into 5 families: 3 ancient super communicators H1, H3 and H13; 2 emerging super communicators H56 and mv2. "Old" haplotypes H13 and H38, via the intermediate vector mv1, associated with the new horseshoe bat virus RaTG13, with haplotypes H3, derived haplotypes H1 and H2, H8-H12, Became a new coronavirus in Wuhan South China Seafood Market（December 24, 2019 to January 5, 2020).

The Sina website public account A SIR accordingly concluded: The mainland China sample only has the offspring C, and the five groups three generations are present in the United States. In the electronic cigarette incident in June-October 2019, 200 patients died of pulmonary fibrosis, and they were New Coronary Pneumonia. Genetically inferred that the new coronavirus originated in the United States.

A Taiwanese TV station invited a video recorded by Taiwanese pharmacologist Dr. Pan Huaizong has received millions of hits on the mainland network.

In this regard, some people raised strong questions after carefully reading the original text.

(1) The basis for judging virus seniority in the family is not appropriate. First assume that bat coronavirus is the source, The fewer mutations there are, the closer to the ancestors. This ignores the variability of the new coronavirus.

(2)So-called ancestral viruses H13 and H38, both gene sequences can be traced back to Wuhan, China; H13 was carried by patients returning to Guangzhou from Wuhan, H38 was carried by a 35-year-old Chinese man returning from Wuhan to Washington State in the United States, in January 5.

(3)Wuhan patient sample sequence only H1, because these 20 samples were all patients with concentrated outbreak from December 24, 2019 to January 5, 2020.

(4) The US patients included all five groups of ABCDE sequences, which precisely indicates that the US was caused by imported cases.

(5) If the U.S. begins to spread the new coronavirus in September 2019, can their medical systems not be paralyzed?

In addition, if the virus is imported into China from a foreign country, why did it just erupt in Wuhan, Hubei, and then gradually spread, and not many places burst out at the same time?

MISREADING OF ACHIEVEMENTS IN MOLECULAR BIOLOGY

By mapping the genetic history of the new coronavirus from December 2019 to March 2020, Cambridge University Peter Forster et al. [2] discovered three different but closely related virus types A, B and C. Through 160 infection samples collected around the world, they discovered the trajectory of different types of new corona viruses spreading around the world.

Type A-the most primitive strain, most similar to the virus extracted from bats and pangolins. It was first discovered in China, and more often found in infected people in the United States and Australia. There are only a few cases of Type A in Wuhan, and it comes from Americans who have lived in Wuhan. The study found that two-thirds of American samples were infected with the virus A, and most of the infected patients were from the West Coast.

Type B is considered to be a variant of Type A in China, it is most common in East Asia. Of the 93 samples infected with type B, except for 19, all others are distributed in China or Asian countries.

Type C is considered to be derived from type B, which does not exist in the mainland China sample, but it is very common in Europe. Researchers think it may have spread through Singapore.

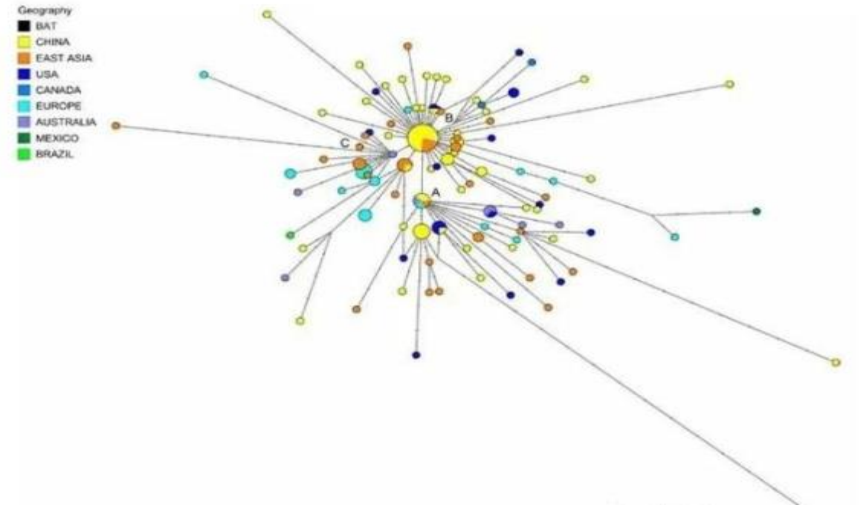

Figure 2: Regional distribution of three types of novel coronavirus
(Image Source: Phylogenetic network analysis of SARS-CoV-2 genomes).

The researchers believe that in order to accurately attack the immune system of different populations, the new coronavirus is constantly mutating.

The Type A virus did not spread in China, but it spread in large numbers in the United States. Some netizens in mainland China groundless speculation, and questioned whether the virus originated in the United States. This was further interpreted in China as the earliest virus did not come from China, but the United States. Some Chinese netizens said that the research report "finally proved China's sinlessness and returned a justice to China."

In this regard, the first author of the paper, Dr. Forster, stressed in an interview with the Global Times that this argument is a misinterpretation of the results of his team's research. Professor Lin Qingshun of the University of California, San Francisco (UCSF) School of Medicine pointed out in the media, The number of cases caused by the virus is not directly related to the source; In terms of quantitative ratio, the prevalence of the original virus strains in the United States is higher than in China, and no conclusion can be drawn on the origin of the virus. The largest ethnicity in the United States is now white, but would you say that the primitive ethnicity in the United States is not Indian? [3].

Peter Forster said in an interview with VOA, We can be sure that the new coronavirus was first spread in China, and the earliest epidemic location may be Guangdong. "What we are seeing is the" founder effect". Some people who travel to Canada and North America carry the A virus. It has not been discovered for a long time but it has spread and is infectious. Very strong. Then, suddenly, type A virus became the main type in the United States. The localization of type B virus in East Asia may also be caused by the "founder effect of genetic bottlenecks", which occurs when the virus establishes a new type from a small, isolated infected group. Another explanation is that the type B virus in Wuhan may be more immune and environmentally adaptable to a large part of the East Asian population [4].

The Scripps Research Institute molecular biologist Kristian Andersen analyzed the complete genes of 27 Wuhan pneumonia new corona viruses in China, It was found that the genomes of 24 samples from Wuhan, Thailand, Shenzhen and other places are very consistent, They "show very limited genetic variation, indicating that all of these virus strains have relatively new common ancestors." According to the molecular evolution clock, he calculated the time when the virus first began to spread widely from the crowd. The median value is December 2 and the earliest can be October 1 [5].

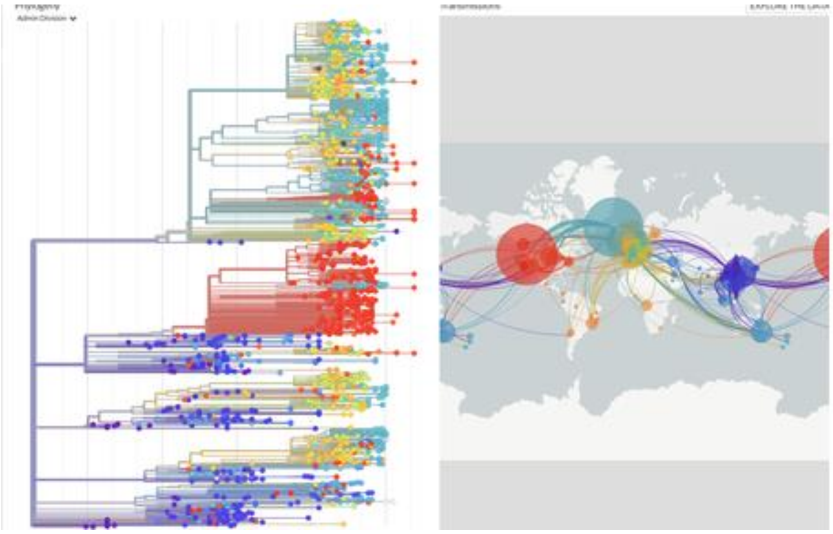

Figure 3: Statistics of new coronavirus on nextstrain.org website (Website screenshot, 2020-03-27)

The new coronavirus genome sequence spectrum-the new coronavirus gene evolution tree shows that all branches on the tree point to an ancestor-Wuhan, China.

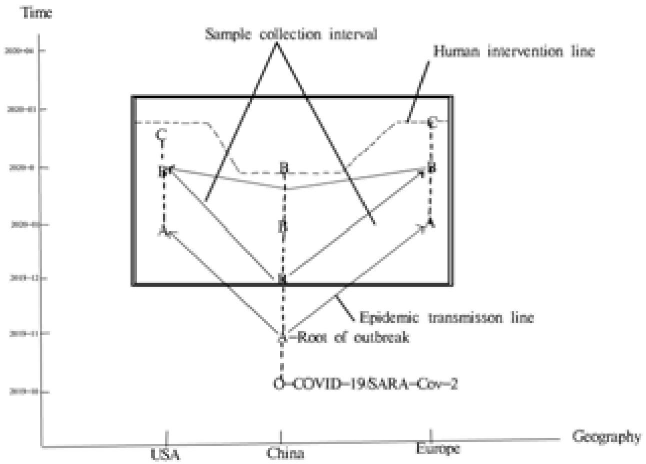

Figure 4: Interpretation model of new coronavirus type distribution around the world.

The author believes that to accurately understand the results of molecular biology research, we must also refer to epidemiological models.

In short, only by combining epidemiological data, analyzing the evolutionary path of the virus, and conducting comprehensive research to eliminate prejudice, we can help track down the source of unrecorded viruses.

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