**Related works**

-Drs. Zhu, Zhang, W. Wang, Li, and Yang contributed equally to this article. And this work was supported by the grants from the National Key Research and Development Program of China and the National Major Project for the Control and the Prevention of Infectious Disease in China .

So in December 2019, a cluster of patients with pneumonia of unknown cause was linked to a seafood wholesale market in Wuhan, China. A previously unknown betacoronavirus was discovered through the use of unbiased sequencing in samples from patients with pneumonia. And human airway epithelial cells were used to isolate a novel coronavirus,That named 2019-nCoV, which formed a clade within the subgenus Orthocoronavirinae, sarbecovirus subfamily. Different from both MERS-CoV and SARS-CoV, 2019-nCoV is the 17th member of the family of coronaviruses that infect the humans. Enhanced surveillance and further investigation are ongoing. (Funded by the National Key Research and Development Program of China and the National Major Project for Control and Prevention of Infectious Disease in China.)

Coronaviruse causes respiratory, enteric, neurologic and hepatic diseases And we discovered that Coronaviruses are enveloped RNA viruses which are distributed among birds, And because of the frequent cross-species occasional and infections spillover events,The coronaviruses are likely to emerge in humans periodically.

In December 2019 and January 2020 we discovered Cov19 in china and this illness likely to have been caused by this COV was named “novel coronavirus-infected pneumonia”. We used Molecular techniques successfully to identify the infectious agents for many years.And we describe in this report the use of molecular techniques and unbiased DNA sequencing to discover the novel betacoronavirus that is likely to have been the cause of the severe pneumonia in the three patients in Wuhan, China. Although our study does not fulfill the Koch’s postulates,So our analyses provide the evidence implicating 2019-nCoV in the wuhan outbreak.

-Lu,R,Zhao,X,Li,J ..Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding.

We identify Coronavirus(Cov19) From the genomic surveillance of the clinical samples from the patients with the viral pneumonia in Wuhan, China.We discovered that the virus belongs to the subgenus Sarbecovirus from Our phylogenetic analysis of 2019-nCoV that sequenced from the nine patients' samples. The 2019-nCoV originated from one source in a very short period and was detected rapidly. However,as the virus transmits to more individuals we need a constant surveillance of mutations arising because the average evolutionary rate for the coronaviruses is roughly 10−4 nucleotide substitutions per site per year,1 in the typical RNA virus with the mutations arising during every replication cycle,So striking that the sequences of 2019-nCoV from different patients that described here were almost identical.As we discovered the genomic structure of the seventh human coronavirus that can cause a severe pneumonia for the human,

-A new coronavirus associated with human respiratory disease in Chinam, And these authors contributed equally: Fan Wu, Su Zhao, Bin Yu, Yan-Mei Chen, Wen Wang, Zhi-Gang Song. The patient studied was a 41-year-old man with no history of the hepatitis, diabetes or tuberculosis, And he was admitted to and hospitalized in the Central Hospital of Wuhan on 26 December 2019, 6 days after onset of disease. The patient was suffered from fever, chest tightness, unproductive cough, pain and weakness for 1 week , and these were normal to the physical examination of cardiovascular, abdominal and neurological characteristics. Also the patient suffered from mild hypoxaemia with oxygen levels and after a lot of rayes and examinations preliminary aetiological investigations excluded the presence of influenza virus, Chlamydia pneumoniae and Mycoplasma pneumoniae using commercial pathogen antigen-detection kits.

After investigating the possible aetiological agents associated with this disease we discovered a bat SARS-like coronavirus (CoV) which had previously been sampled in China.

-Rambaut,A,Holmes,EC,O'Toole,A .A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology.

the generation of tens of thousands of the virus genome sequences has resulted from the ongoing pandemic spread of the new human coronavirus, SARS-CoV-2, which is associated with severe pneumonia/disease(COV19).

yet there is currently no coherent nor accepted scheme for naming the expanding phylogenetic diversity of SARS-CoV-2. And we show a dynamic and rational virus nomenclature which uses a phylogenetic framework to identify those lineages that contribute to the active spread.

Also by focusing on the active virus lineages and those spreading to new locations, this nomenclature will assist in tracking and understanding the patterns and determinants of the global spread of SARS-CoV-2.